



aaa gca cct gct atg ttc aat ata aga aat att gga aag acg ctc gtc	200
Lys Ala Pro Ala Met Phe Asn Ile Arg Asn Ile Gly Lys Thr Leu Val	
35 40 45	
acc agg acc caa gga acc aaa att gca tct gat ggt ctc aag ggt cgt	248
Thr Arg Thr Gln Gly Thr Lys Ile Ala Ser Asp Gly Leu Lys Gly Arg	
50 55 60 65	
gtg ttt gaa gtg agt ctt gct gat ttg cag aat gat gaa gtt gca ttt	296
Val Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Val Ala Phe	
70 75 80	
aga aaa ttc aag ctg att act gaa gat gtt cag ggt aaa aac tgc ctg	344
Arg Lys Phe Lys Leu Ile Thr Glu Asp Val Gln Gly Lys Asn Cys Leu	
85 90 95	
act aac ttc cat ggc atg gat ctt acc cgt gac aaa atg tgt tcc atg	392
Thr Asn Phe His Gly Met Asp Leu Thr Arg Asp Lys Met Cys Ser Met	
100 105 110	
gtc aaa aaa tgg cag aca atg att gaa gct cac gtt gat gtc aag act	440
Val Lys Lys Trp Gln Thr Met Ile Glu Ala His Val Asp Val Lys Thr	
115 120 125	
acc gat ggt tac ttg ctt cgt ctg ttc tgt gtt ggt ttt act aaa aaa	488
Thr Asp Gly Tyr Leu Leu Arg Leu Phe Cys Val Gly Phe Thr Lys Lys	
130 135 140 145	
cgc aac aat cag ata cgg aag acc tct tat gct cag cac caa cag gtc	536
Arg Asn Asn Gln Ile Arg Lys Thr Ser Tyr Ala Gln His Gln Gln Val	
150 155 160	
cgc caa atc cgg aag aag atg atg gaa atc atg acc cga gag gtg cag	584
Arg Gln Ile Arg Lys Lys Met Met Glu Ile Met Thr Arg Glu Val Gln	
165 170 175	
aca aat gac ttg aaa gaa gtg gtc aat aaa ttg att cca gac agc att	632
Thr Asn Asp Leu Lys Glu Val Val Asn Lys Leu Ile Pro Asp Ser Ile	
180 185 190	
gga aaa gac ata gaa aag gct tgc caa tct att tat cct ctc cat gat	680
Gly Lys Asp Ile Glu Lys Ala Cys Gln Ser Ile Tyr Pro Leu His Asp	
195 200 205	
gtc ttc gtt aga aaa gta aaa atg ctg aag aag ccc aag ttt gaa ttg	728
Val Phe Val Arg Lys Val Lys Met Leu Lys Lys Pro Lys Phe Glu Leu	
210 215 220 225	
gga aag ctc atg gag ctt cat ggt gaa ggc agt agt tct gga aaa gcc	776
Gly Lys Leu Met Glu Leu His Gly Glu Gly Ser Ser Ser Gly Lys Ala	
230 235 240	
act ggg gac gag aca ggt gct aaa gtt gaa cga gct gat gga tat gaa	824
Thr Gly Asp Glu Thr Gly Ala Lys Val Glu Arg Ala Asp Gly Tyr Glu	
245 250 255	
cca	827
Pro	

<210> 724  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> 54..305



<400> 724

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Met  
1  
gcg gtt ggc aag aac aag cgc ctt acg aaa ggc ggc aaa aag gga gcc 104  
Ala Val Gly Lys Asn Lys Arg Leu Thr Lys Gly Gly Lys Lys Gly Ala  
5 10 15  
aag aag aaa gtg gtt gat cca ttt tct aag aaa gat tgg tat gat gtg 152  
Lys Lys Lys Val Val Asp Pro Phe Ser Lys Lys Asp Trp Tyr Asp Val  
20 25 30  
aaa gca cct gct atg ttc aat ata aga aat att gga aag acg ctc gtc 200  
Lys Ala Pro Ala Met Phe Asn Ile Arg Asn Ile Gly Lys Thr Leu Val  
35 40 45  
acc agg acc caa gga acc aaa att gca tct gat ggt ctc aag ggt cgt 248  
Thr Arg Thr Gln Gly Thr Lys Ile Ala Ser Asp Gly Leu Lys Gly Arg  
50 55 60 65  
gtg ttt gag acc atc aga tgc aat ttc gct tca ctt ttc ctg gct gta 296  
Val Phe Glu Thr Ile Arg Cys Asn Phe Ala Ser Leu Phe Leu Ala Val  
70 75 80  
gag cgc ttt cc 307  
Glu Arg Phe

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<220>  
<221> CDS  
<222> 119..535

<400> 725

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ttggcaagaa caagcgcctt acgaaaggcg gcaaaaaggg agccaagaag aaagtaca 118  
atg rtt gaa gct cac gtt gat gtc aag act acc gat ggt tac ttg ctt 166  
Met Xaa Glu Ala His Val Asp Val Lys Thr Asp Gly Tyr Leu Leu  
1 5 10 15  
cgt ctg ttc tgt gtt ggt ttt act aaa aaa cgc aac aat cag ata cgg 214  
Arg Leu Phe Cys Val Gly Phe Thr Lys Lys Arg Asn Asn Gln Ile Arg  
20 25 30  
aag acc tct tat gct cag cac caa cag gtc cgc caa atc cgg aag aag 262  
Lys Thr Ser Tyr Ala Gln His Gln Gln Val Arg Gln Ile Arg Lys Lys  
35 40 45  
atg atg gaa atc atg acc cga gag gtg cag aca aat gac ttg aaa gaa 310  
Met Met Glu Ile Met Thr Arg Glu Val Gln Thr Asn Asp Leu Lys Glu  
50 55 60  
gtg gtc aat aaa ttg att cca gac agc att gga aaa gac ata gaa aag 358  
Val Val Asn Lys Leu Ile Pro Asp Ser Ile Gly Lys Asp Ile Glu Lys  
65 70 75 80  
gct tgc caa tct att tat cct ctc cat gat gtc ttc gtt aga aaa gta 406  
Ala Cys Gln Ser Ile Tyr Pro Leu His Asp Val Phe Val Arg Lys Val  
85 90 95



taggtatttg ctttctagtc tacataca atg aaa agg aaa aaa cgt cag ttc 232  
Met Lys Arg Lys Lys Arg Gln Phe  
1 5  
ctg aag ctc tct caa aac atc aac aga tgg aaa gac gtg ccn atg tcc 280  
Leu Lys Leu Ser Gln Asn Ile Asn Arg Trp Lys Asp Val Pro Met Ser  
10 15 20  
tcc cct ccc tcc act ctg ggg gct tgg aaa tgc tgc agc agg gag cag 328  
Ser Pro Pro Ser Thr Leu Gly Ala Trp Lys Cys Cys Ser Arg Glu Gln  
25 30 35 40  
gcc cca ggc tgg acc tgc cct gtc ctc acg acg agt gtg tgc naa gtg 376  
Ala Pro Gly Trp Thr Cys Pro Val Leu Thr Thr Ser Val Cys Xaa Val  
45 50 55  
aac aat aaa tca ttt caa aga 397  
Asn Asn Lys Ser Phe Gln Arg  
60

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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 203..484

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tcttgtttat cgagggtttt gggctggtgg tytcggcagc cagcttctgg tgactcagtc 120  
cgcagctata gttccagtaa gaactaaaaa acgtttcaca ytcctatatt atcaacctaa 180  
atttaaaaca gaaaaggagt tt atg caa cat gcc cgg aaa gca gga ttg gtt 232  
Met Gln His Ala Arg Lys Ala Gly Leu Val  
1 5 10  
att cct cca gaa aaa tcg gac cgt tcc ata cat ctg gcc tgt aca gct 280  
Ile Pro Pro Glu Lys Ser Asp Arg Ser Ile His Leu Ala Cys Thr Ala  
15 20 25  
ggc ata ttt gat gcc tat gtt cct cct gag ggt gat gca cgc ata tca 328  
Gly Ile Phe Asp Ala Tyr Val Pro Pro Glu Gly Asp Ala Arg Ile Ser  
30 35 40  
tct ctt tca aag gag gga ctg ata gag aga act gaa cga atg aag aag 376  
Ser Leu Ser Lys Glu Gly Leu Ile Glu Arg Thr Glu Arg Met Lys Lys  
45 50 55  
act atg gca tca caa gtg tca atc cgg agg ata aaa gac tat gat gcc 424  
Thr Met Ala Ser Gln Val Ser Ile Arg Arg Ile Lys Asp Tyr Asp Ala  
60 65 70  
aac ttt aaa ata aag gac ttc cct gaa aaa gct aag gat atc ttt att 472  
Asn Phe Lys Ile Lys Asp Phe Pro Glu Lys Ala Lys Asp Ile Phe Ile  
75 80 85 90  
gaa gct cac ctt t 485  
Glu Ala His Leu

<210> 729  
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<220>

<221> CDS

<222> 219..515

<400> 729

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ctctgcgacc ggcagccgcc aatgggaagg gagtgagtgc cacgaacagg ccaataagga      60
gggagcagtg cgggggtttaa atctgaggct aggcctggctc ttctcggcgt gctgcggcgg      120
aacggctgtt ggtttctgct ggktgtaggt ccttggtctgg tcgggcctcc ggtgttctgc      180
ttctccccgc tgagctgctg cctggtgaag aggaagcc atg gcg ctc cga gtc acc      236
                                Met Ala Leu Arg Val Thr
                                1           5
agg aac tcg aaa att aat gct gaa aat aag gcg aag atc aac atg gca      284
Arg Asn Ser Lys Ile Asn Ala Glu Asn Lys Ala Lys Ile Asn Met Ala
           10           15           20
ggc gca aag cgc gtt cct acg gcc cct gct gca acc tcc aag ccc gga      332
Gly Ala Lys Arg Val Pro Thr Ala Pro Ala Ala Thr Ser Lys Pro Gly
           25           30           35
ctg agg cca aga aca gct ctt ggg gac att ggt aac aaa gtc agt gaa      380
Leu Arg Pro Arg Thr Ala Leu Gly Asp Ile Gly Asn Lys Val Ser Glu
           40           45           50
caa ctg cag gcc aaa atg cct atg aag aag gaa gca aaa cct tca gct      428
Gln Leu Gln Ala Lys Met Pro Met Lys Lys Glu Ala Lys Pro Ser Ala
           55           60           65           70
act ggw aaa gtc att gat aaa aaa cta cca aaa cct ctt gaa aag gta      476
Thr Gly Lys Val Ile Asp Lys Lys Leu Pro Lys Pro Leu Glu Lys Val
           75           80           85
cct atg ctg gtg cca gtg cca gtg tct gag cca gtg cca g      516
Pro Met Leu Val Pro Val Pro Val Ser Glu Pro Val Pro
           90           95

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<210> 730

<211> 615

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 262..615

<400> 730

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atTTTTTTTT agcgcatgcg caagacatgc tagtctcttt tccggttagc gcggcgtgag      60
aagccatgag cagcaaagtc tctcgcgaca ccctgtacga ggcggtgcgg gaagtccctgc      120
acgggaacca gcgcaangcc gcaagttcct ggagacggtg gagttgcaga tcagcttgaa      180
gaactatgat cccagaagg acaagcgctt ctcgggcacc gtcagcactg tgacgaggct      240
aaggccgtgg atatccccca c atg gac atc gag gcg ctg aaa aaa ctc aac      291
                                Met Asp Ile Glu Ala Leu Lys Lys Leu Asn
                                1           5           10
aag aat ara aaa ctg gtc aag aag ctg gcc aag aag tat gat gcg ttt      339
Lys Asn Xaa Lys Leu Val Lys Lys Leu Ala Lys Lys Tyr Asp Ala Phe
           15           20           25

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ttg gcc tca gag tct ctg atc aag cag att cca cga atc ctc ggc cca	387
Leu Ala Ser Glu Ser Leu Ile Lys Gln Ile Pro Arg Ile Leu Gly Pro	
30 35 40	
ggt tta aat aag gca gga aag ttc cct tyc ctg ctc aca cac aac gaa	435
Gly Leu Asn Lys Ala Gly Lys Phe Pro Xaa Leu Leu Thr His Asn Glu	
45 50 55	
aac atg gtg gcc aaa gtg gat gag gtg aag tcc aca atc aag ttc caa	483
Asn Met Val Ala Lys Val Asp Glu Val Lys Ser Thr Ile Lys Phe Gln	
60 65 70	
atg aag aag gtg tta tgt ctg gct gta gct gtt ggt cac gtg aag atg	531
Met Lys Lys Val Leu Cys Leu Ala Val Ala Val Gly His Val Lys Met	
75 80 85 90	
aca gac gat gag ctt gtg tat aac att cac ctg gct gtc aac ttc ttg	579
Thr Asp Asp Glu Leu Val Tyr Asn Ile His Leu Ala Val Asn Phe Leu	
95 100 105	
gtg tca ttg ctc aag aaa aac tgg cag aat gtc cgg	615
Val Ser Leu Leu Lys Lys Asn Trp Gln Asn Val Arg	
110 115	

<210> 731  
 <211> 376  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 76..375

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ggascgggtg acagg atg gct ggg cac aga ttg gtg ttg gta tta gga gat	111
Met Ala Gly His Arg Leu Val Leu Val Leu Gly Asp	
1 5 10	
ctg cac atc cca cac cgg tgc aac agt ttg cca gct aaa ttc aaa aaa	159
Leu His Ile Pro His Arg Cys Asn Ser Leu Pro Ala Lys Phe Lys Lys	
15 20 25	
ctc ctg gtg cca gga aaa att cag cac att ctc tgc aca gga aac ctt	207
Leu Leu Val Pro Gly Lys Ile Gln His Ile Leu Cys Thr Gly Asn Leu	
30 35 40	
tgc acc aaa gag agt tat gac tat ctc aag act ctg gct ggt gat gtt	255
Cys Thr Lys Glu Ser Tyr Asp Tyr Leu Lys Thr Leu Ala Gly Asp Val	
45 50 55 60	
cat att gtg aga gga gac ttc gat gag aat ctg aat tat cca gaa cag	303
His Ile Val Arg Gly Asp Phe Asp Glu Asn Leu Asn Tyr Pro Glu Gln	
65 70 75	
aaa gtt gtg act gtt gga cag ttc aga ttc tca tgc aag gct cct tct	351
Lys Val Val Thr Val Gly Gln Phe Arg Phe Ser Ser Lys Ala Pro Ser	
80 85 90	
cac tcc cct ttc tca ggc cag gag g	376
His Ser Pro Phe Ser Gly Gln Glu	
95 100	

<210> 732

<211> 517  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 76..516

<400> 732  
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 ggascgggtg acagg atg ttg gtg ttg gta tta gga gat ctg cac atc cca 111  
 Met Leu Val Leu Val Leu Gly Asp Leu His Ile Pro  
 1 5 10  
 cac cgg tgc aac agt ttg cca gct aaa ttc aaa aaa ctc ctg gtg cca 159  
 His Arg Cys Asn Ser Leu Pro Ala Lys Phe Lys Lys Leu Leu Val Pro  
 15 20 25  
 gga aaa att cag cac att ctg tgc aca gga aac ctt tgc acc aaa gag 207  
 Gly Lys Ile Gln His Ile Leu Cys Thr Gly Asn Leu Cys Thr Lys Glu  
 30 35 40  
 agt tat gac tat ctg aag act ctg gct ggt gat gtt cat att gtg aga 255  
 Ser Tyr Asp Tyr Leu Lys Thr Leu Ala Gly Asp Val His Ile Val Arg  
 45 50 55 60  
 gga gac ttc gat gag aat ctg aat tat cca gaa cag aaa gtt gtg act 303  
 Gly Asp Phe Asp Glu Asn Leu Asn Tyr Pro Glu Gln Lys Val Val Thr  
 65 70 75  
 gtt gga cag ttc aaa att ggt ctg atc cat gga cat caa gtt att cca 351  
 Val Gly Gln Phe Lys Ile Gly Leu Ile His Gly His Gln Val Ile Pro  
 80 85 90  
 tgg gga gat atg gcc agc tta gcc ctg ttg cag agg caa ttt gat gtg 399  
 Trp Gly Asp Met Ala Ser Leu Ala Leu Leu Gln Arg Gln Phe Asp Val  
 95 100 105  
 gac att ctt atc tcg gga cac aca cac aaa ttt gaa gca ttt gag cat 447  
 Asp Ile Leu Ile Ser Gly His Thr His Lys Phe Glu Ala Phe Glu His  
 110 115 120  
 gaa aat aaa ttc tac att aat cca ggt tct gca ctg ggg cat ata atg 495  
 Glu Asn Lys Phe Tyr Ile Asn Pro Gly Ser Ala Leu Gly His Ile Met  
 125 130 135 140  
 ctt gga aac aaa cat tat tcc a 517  
 Leu Gly Asn Lys His Tyr Ser  
 145

<210> 733  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 76..408

<400> 733  
 tagtgggcgg gtcgccgagg agcctgagga agagggcggc gacggtggtg gtgactgagc 60

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ggascgggtg acagg atg gaa acc ttt gca cca aag aga gtt atg act atc      111
      Met Glu Thr Phe Ala Pro Lys Arg Val Met Thr Ile
            1             5             10
tma mga act ctg gct ggt gat gtt cat att gtg aga gga gac ttc gat      159
Xaa Arg Thr Leu Ala Gly Asp Val His Ile Val Arg Gly Asp Phe Asp
            15             20             25
gag aat ctg aat tat cca gaa cag aaa gtt gtg act gtt gga cag ttc      207
Glu Asn Leu Asn Tyr Pro Glu Gln Lys Val Val Thr Val Gly Gln Phe
            30             35             40
aaa att ggt ctg atc cat gga cat caa gtt att cca tgg gga gat atg      255
Lys Ile Gly Leu Ile His Gly His Gln Val Ile Pro Trp Gly Asp Met
            45             50             55             60
gcc agc tta gcc ctg ttg cag agg caa ttt gat gtg gac atn ctt atc      303
Ala Ser Leu Ala Leu Leu Gln Arg Gln Phe Asp Val Asp Xaa Leu Ile
            65             70             75
tcg gga cac aca crc aaa ttt gaa gca ttt gag cat gaa aat aaa ttc      351
Ser Gly His Thr Xaa Lys Phe Glu Ala Phe Glu His Glu Asn Lys Phe
            80             85             90
tac att aat cca ggt tct gca ctg ggg cat ata atg ctt gga aac aaa      399
Tyr Ile Asn Pro Gly Ser Ala Leu Gly His Ile Met Leu Gly Asn Lys
            95             100             105
cat tat tcc a
His Tyr Ser
            110

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<210> 734  
 <211> 277  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 69..275

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tctcttccct gaacgttttc ttctttccct ggacaggcag cctcctttgt gtgtattcag      60
aggcagtg atg act tgc tgt cca ggc agc tcc ctc ctg cac aca gaa tgc      110
      Met Thr Cys Cys Pro Gly Ser Ser Leu Leu His Thr Glu Cys
            1             5             10
tca ggg tca ctg aac cac tgc ttc tct ttt gaa agt aga gct agc tgc      158
Ser Gly Ser Leu Asn His Cys Phe Ser Phe Glu Ser Arg Ala Ser Cys
            15             20             25             30
cac ttt cac gtg gcc tcc gca gtg tct cca ccc acc cct gtg ctc ccc      206
His Phe His Val Ala Ser Ala Val Ser Pro Pro Thr Pro Val Leu Pro
            35             40             45
tgc cac kct gat ggc tca aga caa ggc tgg caa acc ctc cca kna aca      254
Cys His Xaa Asp Gly Ser Arg Gln Gly Trp Gln Thr Leu Pro Xaa Thr
            50             55             60
tct ctg gcc cag aaa gcc tct ct
Ser Leu Ala Gln Lys Ala Ser
            65

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<210> 735

<211> 401  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 70..399

<400> 735  
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 tggttgaag atg tgg cga gtg aaa aaa ctg agc ctc agc ctg tcg cct tcg 111  
 Met Trp Arg Val Lys Lys Leu Ser Leu Ser Leu Ser Pro Ser  
 1 5 10  
 ccc cag acg gga aaa cga tct atg aga act cct ctc cgt gaa ctt acc 159  
 Pro Gln Thr Gly Lys Arg Ser Met Arg Thr Pro Leu Arg Glu Leu Thr  
 15 20 25 30  
 ctg cag ccc ggt gcc ctc acc aac tct gga aaa aga tcc ccc gct tgc 207  
 Leu Gln Pro Gly Ala Leu Thr Asn Ser Gly Lys Arg Ser Pro Ala Cys  
 35 40 45  
 tcc tcg ctg acc cca tca ctg tgc aag ctg ggg ctg cag gaa ggc agc 255  
 Ser Ser Leu Thr Pro Ser Leu Cys Lys Leu Gly Leu Gln Glu Gly Ser  
 50 55 60  
 aac aac tca tct cca gtg gat ttt gta aat aac aag agg aca gac tta 303  
 Asn Asn Ser Ser Pro Val Asp Phe Val Asn Asn Lys Arg Thr Asp Leu  
 65 70 75  
 tct tca gaa cat ttc agt cat tcc tca aag tgg cta gaa act tgt cag 351  
 Ser Ser Glu His Phe Ser His Ser Ser Lys Trp Leu Glu Thr Cys Gln  
 80 85 90  
 cat gaa tca gat gag cag cct cta gat cca att ccc caa att agc tct 399  
 His Glu Ser Asp Glu Gln Pro Leu Asp Pro Ile Pro Gln Ile Ser Ser  
 95 100 105 110  
 ac 401

<210> 736  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 25..471

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 actagtggag tgagggggttaa caag atg gcg acc gag acg gtg gag ctc cat 51  
 Met Ala Thr Glu Thr Val Glu Leu His  
 1 5  
 aag cta aag ctt gcc gaa cta aag caa gaa tgt ctt gct cgt ggt ttg 99  
 Lys Leu Lys Leu Ala Glu Leu Lys Gln Glu Cys Leu Ala Arg Gly Leu  
 10 15 20 25  
 gag acc aag gga ata aag caa gat ctt atc cac aga ctc cag gca tat 147  
 Glu Thr Lys Gly Ile Lys Gln Asp Leu Ile His Arg Leu Gln Ala Tyr  
 30 35 40



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ctt gaa gaa cat gct gaa gag gag gca aat gaa gaa gat gta ctg gga      195
Leu Glu Glu His Ala Glu Glu Glu Ala Asn Glu Glu Asp Val Leu Gly
      45      50      55
gat gaa aca gag gaa gaa gaa aca aag ccc att gag ctc cct gtc aaa      243
Asp Glu Thr Glu Glu Glu Glu Thr Lys Pro Ile Glu Leu Pro Val Lys
      60      65      70
gag gaa gaa ccc cct gaa aaa act gtt gat gtg gca gca gag aag aaa      291
Glu Glu Glu Pro Pro Glu Lys Thr Val Asp Val Ala Ala Glu Lys Lys
      75      80      85
gtg gtg aaa att aca tct gaa ata cca cag act gag aga atg cag aag      339
Val Val Lys Ile Thr Ser Glu Ile Pro Gln Thr Glu Arg Met Gln Lys
      90      95      100      105
agg gct gaa cga tty aat gta cct gtg agc ttg gag agt aag aaa gct      387
Arg Ala Glu Arg Phe Asn Val Pro Val Ser Leu Glu Ser Lys Lys Ala
      110      115      120
gct cgg gca gct agg ttt ggg att tct tca gtt cca aca aaa ggt ctg      435
Ala Arg Ala Ala Arg Phe Gly Ile Ser Ser Val Pro Thr Lys Gly Leu
      125      130      135
tca tct gat aac aaa cct atg gtt aac ttg gat aag      471
Ser Ser Asp Asn Lys Pro Met Val Asn Leu Asp Lys
      140      145

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<210> 737  
 <211> 421  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 82..420

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gcggggcccta gcaaccagag cagtgcagct agcaaccgcc ggaatggcga aagcaacaac      60
aatcaaagaa gccttagcga g atg gga aga gaa aac tgg cca gag gca tct      111
      Met Gly Arg Glu Asn Trp Pro Glu Ala Ser
      1      5      10
gaa gcc aaa gag ata aaa ctt tat gcc cag att ccc cct ata gag aag      159
Glu Ala Lys Glu Ile Lys Leu Tyr Ala Gln Ile Pro Pro Ile Glu Lys
      15      20      25
atg gat gca tcc ttg tcc atg ctt gct aat tgc gag aag ctt tca ctg      207
Met Asp Ala Ser Leu Ser Met Leu Ala Asn Cys Glu Lys Leu Ser Leu
      30      35      40
tct aca aac tgc att gaa aaa att gcc aac ctg aat ggc tta aaa aac      255
Ser Thr Asn Cys Ile Glu Lys Ile Ala Asn Leu Asn Gly Leu Lys Asn
      45      50      55
ttg agg ata tta tct tta gga aga aac aac ata aag aac tta aat gga      303
Leu Arg Ile Leu Ser Leu Gly Arg Asn Asn Ile Lys Asn Leu Asn Gly
      60      65      70
ctg gag gca gta ggg gac aca tta gaa gaa ctg tgg atc tcc tac aat      351
Leu Glu Ala Val Gly Asp Thr Leu Glu Glu Leu Trp Ile Ser Tyr Asn
      75      80      85      90
ttt att gag aag ttg aaa ggg atc cac ata atg aag aaa ttg aag att      399
Phe Ile Glu Lys Leu Lys Gly Ile His Ile Met Lys Lys Leu Lys Ile

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<400> 739

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gtttttcagc tcgccattca cttegetgtg aag atg gcg tcg ggc agc ggg aca      54
                               Met Ala Ser Gly Ser Gly Thr
                               1           5
aaa aac ttg gac ttt cgc cga aag tgg gac aaa gat gaa tat gag aaa      102
Lys Asn Leu Asp Phe Arg Arg Lys Trp Asp Lys Asp Glu Tyr Glu Lys
          10           15           20
ctc gcc gag aag agg ctc acg gaa gag aga gaa aag aaa gat gga aaa      150
Leu Ala Glu Lys Arg Leu Thr Glu Glu Arg Glu Lys Lys Asp Gly Lys
          25           30           35
cca gtg cag cct gtc aag cga gag ctt tta cgg cat agg gac tac aag      198
Pro Val Gln Pro Val Lys Arg Glu Leu Leu Arg His Arg Asp Tyr Lys
          40           45           50           55
gtg gac ttg gaa tcc aag ctt ggg aag aca att gtc att acc aag aca      246
Val Asp Leu Glu Ser Lys Leu Gly Lys Thr Ile Val Ile Thr Lys Thr
          60           65           70
acc cct caa tct gag atg gga gga tat tac tgc aat gtc tgt ccc att      294
Thr Pro Gln Ser Glu Met Gly Gly Tyr Tyr Cys Asn Val Cys Pro Ile
          75           80           85
gtc tat ctg acc atc ttt ctc tta ctg tcc tct ttg tct agc tat ctg      342
Val Tyr Leu Thr Ile Phe Leu Leu Leu Ser Ser Leu Ser Ser Tyr Leu
          90           95           100
gcc tat ctg tcg atc cat ctt cgt gtc tgt ctt cag ccc cca cct gtt      390
Ala Tyr Leu Ser Ile His Leu Arg Val Cys Leu Gln Pro Pro Pro Val
          105           110           115
tgt cca tct gtc caa tta cct gtg act ctg tgc atc tt      428
Cys Pro Ser Val Gln Leu Pro Val Thr Leu Cys Ile
          120           125           130

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<210> 740

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 310..483

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cgaaagtggg acaaagatga atatgagarr ctgcccagaga agaggctcac ggaagagaga      180
gaaaagaaag atggaaaacc agtgcagcct gtcaagcgag agcttttacg gcatagggac      240
tacaaggtgg acttggaatc caagcttggg aagacaattg tcattaccaa gacaaccct      300
caatctgag atg gga gga tat tac tgc aat gtc tgt gac tgt gtg gtg aag      351
          Met Gly Gly Tyr Tyr Cys Asn Val Cys Asp Cys Val Val Lys
          1           5           10
gac tcc atc aac ttt ctg gat cac att aat gga arg aaa cat cag aga      399
Asp Ser Ile Asn Phe Leu Asp His Ile Asn Gly Xaa Lys His Gln Arg
          15           20           25           30
aac ctg ggc atg tct atg cgt gtg gaa cgt tcc acc ctg gat cag gtg      447
Asn Leu Gly Met Ser Met Arg Val Glu Arg Ser Thr Leu Asp Gln Val
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aag aaa cgt ttt gag gtc aac aag aag atg gaa 483  
 Lys Lys Arg Phe Glu Val Asn Lys Lys Lys Met Glu  
 50 55

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 acggaagtgt cccggggctg cattgtgcta cagctaga atg aag cac atc aac cta 176  
 Met Lys His Ile Asn Leu  
 1 5  
 tca ttt gca gcg tgt gga ttt ctg ggc att tac cac ttg ggg gca gca 224  
 Ser Phe Ala Ala Cys Gly Phe Leu Gly Ile Tyr His Leu Gly Ala Ala  
 10 15 20  
 tct gca ctt tgc aga cat ggc aaa aaa ctt gtg aag gat gtc aaa gcc 272  
 Ser Ala Leu Cys Arg His Gly Lys Lys Leu Val Lys Asp Val Lys Ala  
 25 30 35  
 ttc gct ggg gcg tct gcg gga tcg ttg gtt gct tct gtt ctg cta aca 320  
 Phe Ala Gly Ala Ser Ala Gly Ser Leu Val Ala Ser Val Leu Leu Thr  
 40 45 50  
 gca cca gaa aaa ata gag gaa tgt aac caa ttt acc tac aag ttt gcc 368  
 Ala Pro Glu Lys Ile Glu Glu Cys Asn Gln Phe Thr Tyr Lys Phe Ala  
 55 60 65 70  
 gaa gaa atc aga agg cag tct ttc ggg gca gta acg ccc ggt tat gac 416  
 Glu Glu Ile Arg Arg Gln Ser Phe Gly Ala Val Thr Pro Gly Tyr Asp  
 75 80 85  
 ttc atg gcc cga cta aga agt ggg atg gag tcg att ctt cct ccc agc 464  
 Phe Met Ala Arg Leu Arg Ser Gly Met Glu Ser Ile Leu Pro Pro Ser  
 90 95 100  
 gct cac gag ctg gcc cag aac cga ctg cac 494  
 Ala His Glu Leu Ala Gln Asn Arg Leu His  
 105 110

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004220"666E7550

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1					5					10							
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Gly	Leu	Arg	Ser	Arg	Leu	Gly	Gln	Pro	Leu	Thr	Gly	Arg	Arg	Ala	Gly		
15					20					25							
ttg	tgt	gaa	cag	gca	cgc	agc	tgc	aga	ttt	tat	tct	ggg	agt	gca	acc	148	
Leu	Cys	Glu	Gln	Ala	Arg	Ser	Cys	Arg	Phe	Tyr	Ser	Gly	Ser	Ala	Thr		
30					35					40							
ctc	tca	aag	gtt	gaa	gga	act	gat	gta	aca	ggg	att	gaa	gaa	gta	gta	196	
Leu	Ser	Lys	Val	Glu	Gly	Thr	Asp	Val	Thr	Gly	Ile	Glu	Glu	Val	Val		
45					50					55							
att	cca	aaa	aag	aaa	act	tgg	gat	aaa	gta	gcc	gtt	ctt	cag	gca	ctt	244	
Ile	Pro	Lys	Lys	Lys	Thr	Trp	Asp	Lys	Val	Ala	Val	Leu	Gln	Ala	Leu		
60					65					70							
gca	tcc	aca	gta	aac	agg	gat	acc	aca	gct	gtg	cct	tat	gtg	ttt	caa	292	
Ala	Ser	Thr	Val	Asn	Arg	Asp	Thr	Thr	Ala	Val	Pro	Tyr	Val	Phe	Gln		
75					80					85					90		
gat	gat	cct	tac	ctt	atg	cca	gca	tca	tct	ttg	gaa	tct	cgt	tca	ttt	340	
Asp	Asp	Pro	Tyr	Leu	Met	Pro	Ala	Ser	Ser	Leu	Glu	Ser	Arg	Ser	Phe		
95					100					105							
tta	ctg	gca	aag	aaa	tcc	ggg	gag	aat	gtg	gcc	aag	ttt	att	att	aat	388	
Leu	Leu	Ala	Lys	Lys	Ser	Gly	Glu	Asn	Val	Ala	Lys	Phe	Ile	Ile	Asn		
110					115					120							
tca	tac	ccc	aaa	tat	ttt	cag	aag	gac	ata	gct	gaa	cct	cat	ata	ccg	436	
Ser	Tyr	Pro	Lys	Tyr	Phe	Gln	Lys	Asp	Ile	Ala	Glu	Pro	His	Ile	Pro		
125					130					135							
tgt	tta	atg	cct	gag	tac	ttt	gaa	cct	cag	atc	aaa	gac	ata	agt		481	
Cys	Leu	Met	Pro	Glu	Tyr	Phe	Glu	Pro	Gln	Ile	Lys	Asp	Ile	Ser			
140					145					150							

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 <222> 72..254

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Met Ala Glu Phe Leu Asp Asp Gln Glu Thr Arg Leu Cys																											
1					5					10																	
gac	aac	tgc	aaa	aaa	gaa	att	cct	gtg	ttt	aac	ttt	acc	atc	cat	gag	158											
Asp	Asn	Cys	Lys	Lys	Glu	Ile	Pro	Val	Phe	Asn	Phe	Thr	Ile	His	Glu												
15					20					25																	
atc	cac	tgt	caa	agg	aac	att	ggg	atg	tgt	cct	acc	tgt	aag	gaa	cca	206											
Ile	His	Cys	Gln	Arg	Asn	Ile	Gly	Met	Cys	Pro	Thr	Cys	Lys	Glu	Pro												
30					35					40					45												
ttt	ccc	aaa	tct	gac	atg	gag	act	cac	atg	act	gca	gaa	cac	tgc	cag	g	255										
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 <222> 123..287

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 ag atg gac att ctg aaa tca gag atc ctt cgg aag cgg cag ctg gtg 167  
 Met Asp Ile Leu Lys Ser Glu Ile Leu Arg Lys Arg Gln Leu Val  
 1 5 10 15  
 gag gac agg aac ctg ctg gtg gaa aat aaa aaa tat ttc aag cgt agt 215  
 Glu Asp Arg Asn Leu Leu Val Glu Asn Lys Lys Tyr Phe Lys Arg Ser  
 20 25 30  
 gag ctc gcc aaa aaa gaa gag gaa gca tat ttt gaa aga tgt ggc tac 263  
 Glu Leu Ala Lys Lys Glu Glu Glu Ala Tyr Phe Glu Arg Cys Gly Tyr  
 35 40 45  
 aag ata cag cca aaa gag gag gac 287  
 Lys Ile Gln Pro Lys Glu Glu Asp  
 50 55

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 <222> 105..392

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 Met Pro Gly His  
 1  
 tta cag gaa ggc ttc ggc tgc gtg gtc acc aac cga ttc gac cag tta 164  
 Leu Gln Glu Gly Phe Gly Cys Val Val Thr Asn Arg Phe Asp Gln Leu  
 5 10 15 20  
 ttt gac gac gaa tcg gac ccc ttc gag gtg ctg aag gca gca gag aac 212  
 Phe Asp Asp Glu Ser Asp Pro Phe Glu Val Leu Lys Ala Ala Glu Asn  
 25 30 35  
 aag aaa aaa gaa gcc ggc ggc ggc ggc gtt ggc ggc cct ggc gcc aag 260  
 Lys Lys Lys Glu Ala Gly Gly Gly Gly Val Gly Gly Pro Gly Ala Lys  
 40 45 50  
 agc gca stc agg ccg cgg ccc aga cca act cca acg csg cag gca aac 308  
 Ser Ala Xaa Arg Pro Arg Pro Arg Pro Thr Pro Thr Xaa Gln Ala Asn  
 55 60 65

agc tgc gca agg agt ccc aga aag acc gca aga acc cgc tgc ccc cca	356
Ser Cys Ala Arg Ser Pro Arg Lys Thr Ala Arg Thr Arg Cys Pro Pro	
70 75 80	
gcg ttg gcg tgg ttg aca aga aag agg aga cgc agc c	393
Ala Leu Ala Trp Leu Thr Arg Lys Arg Arg Arg Ser	
85 90 95	

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gcggaagac tcatcggagc gtgtggattt gagccgccgc attttttaac cctagatctc	120
gaa atg cat cgt gat tcc tgt cca ttg gac tgt aag gtt tat gta ggc	168
Met His Arg Asp Ser Cys Pro Leu Asp Cys Lys Val Tyr Val Gly	
1 5 10 15	
aat ctt gga aac aat ggc aac aag acg gaa ttg gaa cgg gct ttt ggc	216
Asn Leu Gly Asn Asn Gly Asn Lys Thr Glu Leu Glu Arg Ala Phe Gly	
20 25 30	
tac tat gga cca ctc cga agt gtg tgg gtt gct aga aac cca ccc ggc	264
Tyr Tyr Gly Pro Leu Arg Ser Val Trp Val Ala Arg Asn Pro Pro Gly	
35 40 45	
ttt gct ttt gtt gaa ttt gaa gat ccc cga gat gca gct gat gca gtc	312
Phe Ala Phe Val Glu Phe Glu Asp Pro Arg Asp Ala Ala Asp Ala Val	
50 55 60	
cga gag cta gat gga aga aca cta tgt ggc tgc cgt gta aga gtg gaa	360
Arg Glu Leu Asp Gly Arg Thr Leu Cys Gly Cys Arg Val Arg Val Glu	
65 70 75	
ctg tcg aat ggt gaa aaa aga agt aga aat cgt ggc cca nct ccc tct	408
Leu Ser Asn Gly Glu Lys Arg Ser Arg Asn Arg Gly Pro Xaa Pro Ser	
80 85 90 95	
tgg ggt cgt cgc cct cga gat gat tat cgt agg agg agt cct cca mct	456
Trp Gly Arg Arg Pro Arg Asp Asp Tyr Arg Arg Arg Ser Pro Pro Xaa	
100 105 110	
cgt cgc aga tct cc	470
Arg Arg Arg Ser	
115	

<210> 747  
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 <212> DNA  
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<220>  
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004220"6667560

<400> 747

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actgggagac	tctgtgcctc	gctgaggaaa	aataactaaa	c atg ggc aaa gga gat		176
				Met Gly Lys Gly Asp		
				1	5	
cct aag aag ccg aga ggc aaa atg tca tca tat gca ttt ttt gtg caa						224
Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe Val Gln						
	10		15		20	
act tgt cgg gag gag cat aag aag aag cac cca gat gct tca gtc aac						272
Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn						
	25		30		35	
ttc tca gag ttt tct aag aag tgc tca gag agg tgg aag acc atg tct						320
Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser						
	40		45		50	
gct aaa gag aaa gga aaa ttt gaa gat atg gca aaa gcg gac aag gcc						368
Ala Lys Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala						
	55		60		65	
cgt tat gaa aga gaa atg aaa acc tat atc cct ccc aaa ggg gag aca						416
Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr						
	70		75		80	
aaa aag aag ttc aag grt ccc aat gca ccc aag agg cct cct tgc gcc						464
Lys Lys Lys Phe Lys Xaa Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala						
	90		95		100	
ttc ttc ctc ttc tgc tct gag tat cgc c						492
Phe Phe Leu Phe Cys Ser Glu Tyr Arg						
	105		110			

<210> 748

<211> 713

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 383..712

<400> 748

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cggcgggggt	gccatggacc	ctctccgcg	gcgcggcctt	cacagctggg	ccgcgcccgg	180
catccgtagt	ccgctctccc	aaagcctcgg	tggagctgaa	gctgccacag	agtgcattgt	240
cacaaagggt	catcacacac	ggagctgccc	ctccctgtct	ccctagagcc	catcttcgas	300
gccaggggct	tttctaccas	gattctgggg	tgktctctct	cctttctctcc	ctcccagatc	360
ktctcacgaa	aaataactaa	ac atg ggc aaa gga gat	cct aag aag ccg aga			412
		Met Gly Lys Gly Asp	Pro Lys Lys Pro Arg			
		1	5		10	
ggs raa atg tca tca tat gsr ttt ttt gtg caa act tgt cgg gag gag						460
Gly Xaa Met Ser Ser Tyr Xaa Phe Phe Val Gln Thr Cys Arg Glu Glu						
	15		20		25	
cat aag arg aag cac cca gat gct tca gtc aac ttc tca gag ttt tct						508
His Lys Xaa Lys His Pro Asp Ala Ser Val Asn Phe Ser Glu Phe Ser						



	30		35		40	
aag aag tgc tca gag agg tgg aag acc atg tct gct aaa gag aaa gga						556
Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Gly						
	45		50		55	
aaa ttt gaa gat atg gca aaa gcg gac aag gcc cgt tat gaa aga gaa						604
Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu						
	60		65		70	
atg aaa acc tat atc cct ccc aaa ggg gag aca aaa aag aag ttc aag						652
Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys						
	75		80		85	
grt ccc aat gca ccc aag agg cct cct tcg gcy ttc ttc ctc ttc tgc						700
Xaa Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys						
	95		100		105	
tct gag tat cgc c						713
Ser Glu Tyr Arg						
	110					

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ccattgcagt acattgagct ccatagagac agcgccgggg caagtgagag cgggacgggc	120
actgggcgac tctgtgcctc gctgaggacc atg tct gct aaa gag aaa gga aaa	174
Met Ser Ala Lys Glu Lys Gly Lys	
	1 5
ttt gaa gat atg gca aaa gcg gac aag gcc cgt tat gaa aga gaa atg	222
Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met	
	10 15 20
aaa acc tat atc cct ccc aaa ggg gag aca aaa aag aag ttc aag ggt	270
Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Gly	
	25 30 35 40
ccc aat gca ccc aag agg cct cct tcg gcc ttc ttc ctc ttc tgc tct	318
Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser	
	45 50 55
gag tat cgc c	328
Glu Tyr Arg	

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&lt;400&gt; 750

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tcactgctcc caaaa atg gcg gac gca ttc gga gat gag ctg ttc agc gtg   111
          Met Ala Asp Ala Phe Gly Asp Glu Leu Phe Ser Val
                1             5             10
ttc gag ggc gac tcg acc act gcg gcg gga acc aaa aaa gac aag gaa   159
Phe Glu Gly Asp Ser Thr Thr Ala Ala Gly Thr Lys Lys Asp Lys Glu
          15             20             25
aag gac aag ggg aaa tgg aag ggg cct cca ggg tct gca gac aag gca   207
Lys Asp Lys Gly Lys Trp Lys Gly Pro Pro Gly Ser Ala Asp Lys Ala
          30             35             40
ggg aaa cgt ttt gat ggt aaa tta caa tca gaa tca act aat aat gga   255
Gly Lys Arg Phe Asp Gly Lys Leu Gln Ser Glu Ser Thr Asn Asn Gly
          45             50             55             60
aaa aat aag aga g
Lys Asn Lys Arg   268

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&lt;210&gt; 751

&lt;211&gt; 739

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 343..738

&lt;400&gt; 751

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caccagagtc ggcgtaacta tcgcctgaca gggatatctga agtaaaaggg gcatttaaata   180
caaacgggat tgagatggat tgggttankr aaacataatg gtccaaatga cgctagtgat   240
gggacagtac gacttcgtgg actaccattt ggttcagca aagaggaaak rgttcagttc   300
tttcaagggg tggaatcgt gccaaatggg ataacattga cg atg gac tac cag   354
          Met Asp Tyr Gln
                1
ggg aga agc aca ggg gag gcc ttc gtg cag ttt gct tca aag gag ata   402
Gly Arg Ser Thr Gly Glu Ala Phe Val Gln Phe Ala Ser Lys Glu Ile
          5             10             15             20
gca gaa aat gct ctg ggg aaa cac aag gaa aga ata ggg cac agg tat   450
Ala Glu Asn Ala Leu Gly Lys His Lys Glu Arg Ile Gly His Arg Tyr
          25             30             35
att gag atc ttc aga agt agc agg agt gaa atc aaa gga ttt tat gat   498
Ile Glu Ile Phe Arg Ser Ser Arg Ser Glu Ile Lys Gly Phe Tyr Asp
          40             45             50
cca cca aga aga ttg ctg gga cag cga ccg gga cca tat gat aga cca   546
Pro Pro Arg Arg Leu Leu Gly Gln Arg Pro Gly Pro Tyr Asp Arg Pro
          55             60             65
ata gga gga aga ggg ggt tat tat gga gct ggg cgt gga agt atg tat   594
Ile Gly Gly Arg Gly Gly Tyr Tyr Gly Ala Gly Arg Gly Ser Met Tyr
          70             75             80
gac aga atg cga cga gga ggt gat gga tat gat ggt ggt tat gga ggt   642
Asp Arg Met Arg Arg Gly Gly Asp Gly Tyr Asp Gly Gly Tyr Gly Gly

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85		90		95		100	
ttt gat gac tat ggt ggc tat aat aat tac ggc tat ggg aat gat ggc							690
Phe Asp Asp Tyr Gly Gly Tyr Asn Asn Tyr Gly Tyr Gly Asn Asp Gly							
	105		110		115		
ttt gat gaa aga aag aag aca agg aaa agg agg agg agg aag agg aga a							739
Phe Asp Glu Arg Lys Lys Thr Arg Lys Arg Arg Arg Arg Lys Arg Arg							
	120		125		130		

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 <222> 429..599

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caccagagtc ggcgtaacta tcgcctgaca gggatatctga agtaaaaggg gcattttaat	180
caaacgggat tgagatggat tgggttatga aacataatgg tccaaatgac gctagtgatg	240
ggacagtacg acttcgtgga ctaccatttg gttgcagcaa agaggaaata gttcagttct	300
ttcaagggtat attgaratct tcagaagtag caggagtga atcaaaggat tttatgatcc	360
accaagaaga ttgctgggac agcgaccggg accatatgat agaccaatag gaggaagagg	420
gggttatt atg gag ctg ggc gtg gaa gta tgt atg aca gaa tgc gac gag	470
Met Glu Leu Gly Val Glu Val Cys Met Thr Glu Cys Asp Glu	
1 5 10	
gag gtg atg gat atg atg gtg gtt atg gag gtt ttg atg act atg gtg	518
Glu Val Met Asp Met Met Val Val Met Glu Val Leu Met Thr Met Val	
15 20 25 30	
gct ata ata att acg gct atg gga atg atg gct ttg atg aaa gaa aga	566
Ala Ile Ile Ile Thr Ala Met Gly Met Met Ala Leu Met Lys Glu Arg	
35 40 45	
aga caa gga aaa gga gga gga gga aga gga gaa	599
Arg Gln Gly Lys Gly Gly Gly Gly Arg Gly Glu	
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<210> 753  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 172..342

<400> 753	
cactaataca tttatgctga aacctgtacc ttaaaacatt tttaaatagg tatattgaga	60
tcttcagaag tagcaggagt gaaatcaaag gattttatga tccaccaaga agattgctgg	120
gacagcgacc gggaccatat gatagaccaa taggaggaag aggggggttat t atg gag	177
	Met Glu

ctg ggc gtg gaa gta tgt atg aca gaa tgc gac gag gag gtg atg gat	1	225
Leu Gly Val Glu Val Cys Met Thr Glu Cys Asp Glu Glu Val Met Asp		
5 10 15		
atg atg gtg gtt atg gag gtt ttg atg act atg gtg gct ata ata att	273	
Met Met Val Val Met Glu Val Leu Met Thr Met Val Ala Ile Ile Ile		
20 25 30		
acg gct atg gga atg atg gct ttg atg aaa gaa aga aga caa gga aaa	321	
Thr Ala Met Gly Met Met Ala Leu Met Lys Glu Arg Arg Gln Gly Lys		
35 40 45 50		
gga gga gga gga aga gga gaa	342	
Gly Gly Gly Gly Arg Gly Glu		
55		

<210> 754  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 325..720

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ttgtggcgag cgctacacga ggcaaacgac ttctcccttc tttgaactgg accccgcgag	120
caccagaagt cggcgtaact atcgccctgac aggcatttaa atcaaacggg attgagatgg	180
attgggttat gaaacataat ggtccaaatg acgctagtga tgggacagta cgacttcgtg	240
gactaccatt tggttgcagc aaagaggaaa tagttcagtt ctttcaaggg ttggaaatcg	300
tgccaaaatg ggataacatt gacg atg gac tac cag ggg aga agc aca ggg	351
Met Asp Tyr Gln Gly Arg Ser Thr Gly	
1 5	
gag gcc ttc gtg cag ttt gct tca aag gag ata gca gaa aat gct ctg	399
Glu Ala Phe Val Gln Phe Ala Ser Lys Glu Ile Ala Glu Asn Ala Leu	
10 15 20 25	
ggg aaa cac aag gaa aga ata ggg cac agg tat att gag atc ttc aga	447
Gly Lys His Lys Glu Arg Ile Gly His Arg Tyr Ile Glu Ile Phe Arg	
30 35 40	
agt agc agg agt gaa atc aaa gga ttt tat gat cca cca aga aga ttg	495
Ser Ser Arg Ser Glu Ile Lys Gly Phe Tyr Asp Pro Pro Arg Arg Leu	
45 50 55	
ctg gga cag cga ccg gga cca tat gat aga cca ata gga gga aga ggg	543
Leu Gly Gln Arg Pro Gly Pro Tyr Asp Arg Pro Ile Gly Gly Arg Gly	
60 65 70	
ggg tat tat gga gct ggg cgt gga agt atg tat gac aga atg cga cga	591
Gly Tyr Tyr Gly Ala Gly Arg Gly Ser Met Tyr Asp Arg Met Arg Arg	
75 80 85	
gga ggt gat gga tat gat ggt ggt tat gga ggt ttt gat gac tat ggt	639
Gly Gly Asp Gly Tyr Asp Gly Gly Tyr Gly Gly Phe Asp Asp Tyr Gly	
90 95 100 105	
ggc tat aat aat tac ggc tat ggg aat gat ggc ttt gat gaa aga aag	687
Gly Tyr Asn Asn Tyr Gly Tyr Gly Asn Asp Gly Phe Asp Glu Arg Lys	
110 115 120	

aag aca agg aaa agg agg agg agg aag agg aga a  
 Lys Thr Arg Lys Arg Arg Arg Arg Lys Arg Arg  
 125 130

721

<210> 755  
 <211> 1036  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 112..1035

<400> 755

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 cttgcagttc agcgaccacg tttgtttcga cgccggaccg cgtaagagac g atg atg 117  
 Met Met  
 1  
 ttg ggc acg gaa ggt gga gag gga ttc gtg gtg aag gtc cgg ggc ttg 165  
 Leu Gly Thr Glu Gly Gly Glu Gly Phe Val Val Lys Val Arg Gly Leu  
 5 10 15  
 ccc tgg tct tgc tcg gcc gat gaa gtg cag agg ttt ttt tct gac tgc 213  
 Pro Trp Ser Cys Ser Ala Asp Glu Val Gln Arg Phe Phe Ser Asp Cys  
 20 25 30  
 aaa att caa aat ggg gct caa ggt att cgt ttc atc tac acc aga gaa 261  
 Lys Ile Gln Asn Gly Ala Gln Gly Ile Arg Phe Ile Tyr Thr Arg Glu  
 35 40 45 50  
 ggc aga cca agt ggc gag gct ttt gtt gaa ctt gaa tca gaa gat gaa 309  
 Gly Arg Pro Ser Gly Glu Ala Phe Val Glu Leu Glu Ser Glu Asp Glu  
 55 60 65  
 gtc aaa ttg gcc ctg aaa aaa gac aga gaa act atg gga cac aga tat 357  
 Val Lys Leu Ala Leu Lys Lys Asp Arg Glu Thr Met Gly His Arg Tyr  
 70 75 80  
 gtt gaa gta ttc aag tca aac aac gtt gaa atg gat tgg gtg ttg aag 405  
 Val Glu Val Phe Lys Ser Asn Asn Val Glu Met Asp Trp Val Leu Lys  
 85 90 95  
 cat act ggt cca aat agt cct gac acg gcc aat gat ggc ttt gta cgg 453  
 His Thr Gly Pro Asn Ser Pro Asp Thr Ala Asn Asp Gly Phe Val Arg  
 100 105 110  
 ctt aga gga ctt ccc ttt gga tgt agc aag gaa gaa att gtt cag ttc 501  
 Leu Arg Gly Leu Pro Phe Gly Cys Ser Lys Glu Glu Ile Val Gln Phe  
 115 120 125 130  
 ttc tca ggg ttg gaa atc gtg cca aat ggg ata aca ttg ccg gtg gac 549  
 Phe Ser Gly Leu Glu Ile Val Pro Asn Gly Ile Thr Leu Pro Val Asp  
 135 140 145  
 ttc cag ggg agg agt acg ggg gag gcc ttc gtg cag ttt gct tca cag 597  
 Phe Gln Gly Arg Ser Thr Gly Glu Ala Phe Val Gln Phe Ala Ser Gln  
 150 155 160  
 gaa ata gct gaa aag gct cta aag aaa cac aag gaa aga ata ggg cac 645  
 Glu Ile Ala Glu Lys Ala Leu Lys Lys His Lys Glu Arg Ile Gly His  
 165 170 175  
 agg tat att gar atc tty aag agy agy mga gct gaa gtt mga acy cay 693  
 Arg Tyr Ile Glu Ile Phe Lys Ser Ser Arg Ala Glu Val Arg Thr His

004220 6562560

180	185	190	
tat gat ccm ccw cga aag cty atg gcy atg cag cgg cca ggt ccy tat			741
Tyr Asp Pro Pro Arg Lys Leu Met Ala Met Gln Arg Pro Gly Pro Tyr			
195	200	205	210
gat agg ccg ggg gct ggc aga ggg tat aat agc att ggc aga gga gct			789
Asp Arg Pro Gly Ala Gly Arg Gly Tyr Asn Ser Ile Gly Arg Gly Ala			
215	220	225	
ggg ttt gaa agg atg agg cgt ggt gcc tat ggt gga ggg tat gga ggc			837
Gly Phe Glu Arg Met Arg Arg Gly Ala Tyr Gly Gly Gly Tyr Gly Gly			
230	235	240	
tat gat gac tat ggt ggc tat aat gat gga tat ggc ttt ggg tct gat			885
Tyr Asp Asp Tyr Gly Gly Tyr Asn Asp Gly Tyr Gly Phe Gly Ser Asp			
245	250	255	
aga ttt gga aga gac ctc aat tac tgt ttt tca gga atg tct gat cat			933
Arg Phe Gly Arg Asp Leu Asn Tyr Cys Phe Ser Gly Met Ser Asp His			
260	265	270	
aga tac gga gat ggt ggg tcc agt ttc cag agc acc aca ggg cac tgt			981
Arg Tyr Gly Asp Gly Gly Ser Ser Phe Gln Ser Thr Thr Gly His Cys			
275	280	285	290
gta cac atg agg ggg tta cct tac aga gcc act gag aat gat att tat			1029
Val His Met Arg Gly Leu Pro Tyr Arg Ala Thr Glu Asn Asp Ile Tyr			
295	300	305	
rat ttc t			1036
Xaa Phe			

<210> 756  
 <211> 721  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 494..721

<400> 756

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gaggggaagaa	ggaggaaaat	taccgcgtac	accaaattg	cattgagcca	aacttgccac	120
caagagccca	acaatcacca	tgatgstgag	cacggaaggc	aggaggggt	tcgtggtgaa	180
ggtcaggggc	ctaccctggt	cctgctcagc	cgatgaagt	atgcgcttct	tctctgattg	240
caagatccaa	aatggcacat	caggtattcg	tttcatctac	accagagaag	gcagaccaag	300
tggtgaagca	tttggtgaac	ttgaatctga	agaggamgtg	aaattsgctt	acgtgagcag	360
aagtagttct	ggtcgctcgt	taccgtctcg	ctatagccgt	ttgagggaag	aaggaggaaa	420
attaccgggt	atcgtttagag	ctacacaaa	attgcattga	gccaaacttg	ccaccaagag	480
cccaacaatc	acc atg atg ctg agc acg gaa ggc agg gag ggg ttc gtg					529
	Met Met Leu Ser Thr Glu Gly Arg Glu Gly Phe Val					
	1	5	10			
gtg aag gtc agg ggc cta ccc tgg tcc tgc tca gcc gat gaa gtg atg						577
Val Lys Val Arg Gly Leu Pro Trp Ser Cys Ser Ala Asp Glu Val Met						
15	20	25				
cgc ttc ttc tct gat tgc aag atc caa aat ggc aca tca ggt att cgt						625
Arg Phe Phe Ser Asp Cys Lys Ile Gln Asn Gly Thr Ser Gly Ile Arg						
30	35	40				
ttc atc tac acc aga gaa ggc aga cca agt ggt gaa gca ttt gtt gaa						673

Phe	Ile	Tyr	Thr	Arg	Glu	Gly	Arg	Pro	Ser	Gly	Glu	Ala	Phe	Val	Glu	
45					50				55						60	
ctt	gaa	tct	gaa	gag	gaa	gtg	aaa	ttg	gct	ttg	aag	aag	gac	aga	gaa	721
Leu	Glu	Ser	Glu	Glu	Glu	Val	Lys	Leu	Ala	Leu	Lys	Lys	Asp	Arg	Glu	
			65					70						75		

<210> 757  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 78..359

<400> 757																
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atcgagcaa	gaagtct	atg	tgc	ccc	agg	atc	ctg	gat	tac	ctg	agg	aag				110
		Met	Cys	Pro	Arg	Ile	Leu	Asp	Tyr	Leu	Arg	Lys				
		1				5						10				
aag	agr	rtc	arg	gaa	raa	aaa	ccc	acc	agt	caa	gga	aag	tca	agt	agc	158
Lys	Arg	Xaa	Xaa	Glu	Xaa	Lys	Pro	Thr	Ser	Gln	Gly	Lys	Ser	Ser	Ser	
			15					20					25			
aag	aag	gaa	atg	tct	aaa	aga	gat	ggc	aag	gag	aaa	aaa	gac	aga	gga	206
Lys	Lys	Glu	Met	Ser	Lys	Arg	Asp	Gly	Lys	Glu	Lys	Lys	Asp	Arg	Gly	
		30					35					40				
gtg	acg	agg	ttt	cag	gaa	aat	gcc	agt	gaa	ggg	aag	gcc	cct	gca	gaa	254
Val	Thr	Arg	Phe	Gln	Glu	Asn	Ala	Ser	Glu	Gly	Lys	Ala	Pro	Ala	Glu	
	45				50					55						
gac	gtc	ttt	aag	aag	ccc	ctg	cct	cct	act	gtg	aag	aag	gaa	gag	agt	302
Asp	Val	Phe	Lys	Lys	Pro	Leu	Pro	Pro	Thr	Val	Lys	Lys	Glu	Glu	Ser	
	60				65				70					75		
ncc	cct	cca	cct	aaa	gtg	gta	aac	cca	ctg	atc	ggc	ntc	ttg	ggg	gaa	350
Xaa	Pro	Pro	Pro	Lys	Val	Val	Asn	Pro	Leu	Ile	Gly	Xaa	Leu	Gly	Glu	
			80					85					90			
tat	gga	gga	g													360
Tyr	Gly	Gly														

<210> 758  
 <211> 459  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 103..459

<400> 758																
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ctctgcgtgg	gggctgctc	cccggctccc	ggtgcagaca	cc	atg	tac	gga	ttt								114
					Met	Tyr	Gly	Phe								
					1											

gtg aat cac gcc ctg gag ttg ctg gtg atc cgc aat tac ggc ccc gar	162
Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn Tyr Gly Pro Glu	
5 10 15 20	
gtg tgg gaa gac atc aaa aaa gag gca cag tta gat gaa gaa gga cag	210
Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp Glu Glu Gly Gln	
25 30 35	
ttt ctt gtc aga ata ata tat gat gac tcc aaa act tat gat ttg gtt	258
Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr Tyr Asp Leu Val	
40 45 50	
gct gct gca agc aaa gtc ctc aat ctc aat gct gga gaa atc ctc caa	306
Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly Glu Ile Leu Gln	
55 60 65	
atg ttt ggg aag atg ttt ttc gtc ttt tgc caa gaa tct ggt tat gat	354
Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu Ser Gly Tyr Asp	
70 75 80	
aca atc ttg cgt gtc ctg ggc tct aat gtc aga gaa ttt cta cag aac	402
Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu Phe Leu Gln Asn	
85 90 95 100	
ctt gat gct ctg cac gac cac ctt gct acc atc tas yca gga atg cgt	450
Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Xaa Xaa Gly Met Arg	
105 110 115	
gca cct tcc	459
Ala Pro Ser	
<210> 759	
<211> 709	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 55..708	
<400> 759	
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Met	
1	
gtg ttc agg cgc ttc gtg gag gtt ggc cgg gtg gcc tat gtc tcc ttt	105
Val Phe Arg Arg Phe Val Glu Val Gly Arg Val Ala Tyr Val Ser Phe	
5 10 15	
gga cct cat gcc gga aaa ttg gtc gcg att gta gat gtt att gat cag	153
Gly Pro His Ala Gly Lys Leu Val Ala Ile Val Asp Val Ile Asp Gln	
20 25 30	
aac agg gct ttg gtc gat gga cct tgc act caa gtg agg aga cag gcc	201
Asn Arg Ala Leu Val Asp Gly Pro Cys Thr Gln Val Arg Arg Gln Ala	
35 40 45	
atg cct ttc aag tgc atg cag ctc act gat ttc atc ctc aag ttt ccg	249
Met Pro Phe Lys Cys Met Gln Leu Thr Asp Phe Ile Leu Lys Phe Pro	
50 55 60 65	
cac agt gcc cac cag aag tat gtc cga caa gcc tgg cag aag gca gac	297
His Ser Ala His Gln Lys Tyr Val Arg Gln Ala Trp Gln Lys Ala Asp	
70 75 80	
atc aat aca aaa tgg gca gcc aca cga tgg gcc aag aag att gaa gcc	345



Ile Asn Thr Lys Trp Ala Ala Thr Arg Trp Ala Lys Lys Ile Glu Ala	
85 90 95	
aga gaa agg aaa gcc aag atg aca gat ttt gat cgt ttt aaa gtt atg	393
Arg Glu Arg Lys Ala Lys Met Thr Asp Phe Asp Arg Phe Lys Val Met	
100 105 110	
aag gca aag aaa atg agg aac aga ata atc aag aat gaa gtt aag aag	441
Lys Ala Lys Lys Met Arg Asn Arg Ile Ile Lys Asn Glu Val Lys Lys	
115 120 125	
ctt caa aag gca gct ctc ctg aaa gct tct ccc aaa aaa gca cct ggt	489
Leu Gln Lys Ala Ala Leu Leu Lys Ala Ser Pro Lys Lys Ala Pro Gly	
130 135 140 145	
act aag ggt act gct gct gct gct gct gct gct gct gct gct gct gct	537
Thr Lys Gly Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala	
150 155 160	
gct gct gct aaa gtt cca gca aaa aag atc acc gcc gcg agt aaa aag	585
Ala Ala Ala Lys Val Pro Ala Lys Lys Ile Thr Ala Ala Ser Lys Lys	
165 170 175	
gct cca gcc cag aar gtt cct gcc cag aaa gcc aca ggc cag aaa gca	633
Ala Pro Ala Gln Lys Val Pro Ala Gln Lys Ala Thr Gly Gln Lys Ala	
180 185 190	
gcg cct gct cna aaa gct cag aag ggt caa aaa gct cca gcc cag aaa	681
Ala Pro Ala Xaa Lys Ala Gln Lys Gly Gln Lys Ala Pro Ala Gln Lys	
195 200 205	
gca cct gct cca aag gca tct ggc aam g	709
Ala Pro Ala Pro Lys Ala Ser Gly Xaa	
210 215	
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<221> CDS	
<222> 55..360	
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Met	
1	
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Val Phe Arg Arg Phe Val Glu Val Gly Arg Val Ala Tyr Val Ser Phe	
5 10 15	
gga cct cat gcc gga aaa ttg gtc gcg att gta gat gtt att gat cag	153
Gly Pro His Ala Gly Lys Leu Val Ala Ile Val Asp Val Ile Asp Gln	
20 25 30	
aac agg gct ttg gtc gat gga cct tgc act caa gtg agg aga cag gcc	201
Asn Arg Ala Leu Val Asp Gly Pro Cys Thr Gln Val Arg Arg Gln Ala	
35 40 45	
atg cct ttc aag tgc atg cag ctc act gat ttc atc ctc aag ttt ccg	249
Met Pro Phe Lys Cys Met Gln Leu Thr Asp Phe Ile Leu Lys Phe Pro	
50 55 60 65	
cac agt gcc cac cag aag tat gtc cga caa gcc tgg cag aag gca gac	297

His Ser Ala His Gln Lys Tyr Val Arg Gln Ala Trp Gln Lys Ala Asp  
 70 75 80  
 atc aat aca aaa tgg gca rcc aca cgm tgg gca ctt ctc cat ttc cta 345  
 Ile Asn Thr Lys Trp Ala Xaa Thr Arg Trp Ala Leu Leu His Phe Leu  
 85 90 95  
 ctg gag gat tta ttt  
 Leu Glu Asp Leu Phe 360  
 100

<210> 761  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 55..480

<400> 761  
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 Met  
 1  
 gtg ttc agg cgc ttc gtg gag gtt ggc cgg gtg gcc tat gtc tcc ttt 105  
 Val Phe Arg Arg Phe Val Glu Val Gly Arg Val Ala Tyr Val Ser Phe  
 5 10 15  
 gga cct cat gcc gga aaa ttg gtc gcg att gta gat gtt att gat cag 153  
 Gly Pro His Ala Gly Lys Leu Val Ala Ile Val Asp Val Ile Asp Gln  
 20 25 30  
 aac agg gct ttg gtc gat gga cct tgc act caa gtg agg aga cag gcc 201  
 Asn Arg Ala Leu Val Asp Gly Pro Cys Thr Gln Val Arg Arg Gln Ala  
 35 40 45  
 atg cct ttc aag tgc atg cag ctc act gat ttc atc ctc aag ttt ccg 249  
 Met Pro Phe Lys Cys Met Gln Leu Thr Asp Phe Ile Leu Lys Phe Pro  
 50 55 60 65  
 cac agt gcc cac cag aag tat gtc cga caa gcc tgg cag aag gca gac 297  
 His Ser Ala His Gln Lys Tyr Val Arg Gln Ala Trp Gln Lys Ala Asp  
 70 75 80  
 atc aat aca aaa tgg gca gcc aca cga tgg gcc aag aag att gaa gcc 345  
 Ile Asn Thr Lys Trp Ala Ala Thr Arg Trp Ala Lys Lys Ile Glu Ala  
 85 90 95  
 aga gaa agg aaa gcc aag atg aca gat ttt gat cgt ttt aaa gtt atg 393  
 Arg Glu Arg Lys Ala Lys Met Thr Asp Phe Asp Arg Phe Lys Val Met  
 100 105 110  
 aag gca aag aaa atg agg aac aga ata atc aag aat gaa gtt aag aag 441  
 Lys Ala Lys Lys Met Arg Asn Arg Ile Ile Lys Asn Glu Val Lys Lys  
 115 120 125  
 ctt caa aag gca gct ctg gaa ata aga tta ttc ctt ttt 480  
 Leu Gln Lys Ala Ala Leu Glu Ile Arg Leu Phe Leu Phe  
 130 135 140

<210> 762  
 <211> 730  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 55..729

<400> 762

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Met  
1  
gtg ttc agg cgc ttc gtg gag gtt ggc cgg gtg gcc tat gtc tcc ttt 105  
Val Phe Arg Arg Phe Val Glu Val Gly Arg Val Ala Tyr Val Ser Phe  
5 10 15  
gga cct cat gcc gga aaa ttg gtc gcg att gta gat gtt att gat cag 153  
Gly Pro His Ala Gly Lys Leu Val Ala Ile Val Asp Val Ile Asp Gln  
20 25 30  
aac agg gct ttg gtc gat gga cct tgc act caa gtg agg aga cag gcc 201  
Asn Arg Ala Leu Val Asp Gly Pro Cys Thr Gln Val Arg Arg Gln Ala  
35 40 45  
atg cct ttc aag tgc atg cag ctc act gat ttc atc ctc aag ttt ccg 249  
Met Pro Phe Lys Cys Met Gln Leu Thr Asp Phe Ile Leu Lys Phe Pro  
50 55 60 65  
cac agt gcc cac cag aag tat gtc cga caa gcc tgg cag aag gca gac 297  
His Ser Ala His Gln Lys Tyr Val Arg Gln Ala Trp Gln Lys Ala Asp  
70 75 80  
atc aat aca aaa tgg gca gcc aca cga tgg gcc aag aag att gaa gcc 345  
Ile Asn Thr Lys Trp Ala Ala Thr Arg Trp Ala Lys Lys Ile Glu Ala  
85 90 95  
aga gaa agg aaa gcc aag atg aca gat ttt gat cgt ttt aaa gtt atg 393  
Arg Glu Arg Lys Ala Lys Met Thr Asp Phe Asp Arg Phe Lys Val Met  
100 105 110  
aag gca aag aaa atg agg aac aga ata atc aag aat gaa gtt aag aag 441  
Lys Ala Lys Lys Met Arg Asn Arg Ile Ile Lys Asn Glu Val Lys Lys  
115 120 125  
ctt caa aag gca gct ctc ctg aaa gct tct ccc aaa aaa gca cct ggt 489  
Leu Gln Lys Ala Ala Leu Lys Ala Ser Pro Lys Lys Ala Pro Gly  
130 135 140 145  
act aag ggt act gct gct gct gct gct gct gct gct gct gct gct gct 537  
Thr Lys Gly Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala  
150 155 160  
gct gct gct gct gct gct gct gct gct gct aaa gtt cca gca aaa aag 585  
Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Val Pro Ala Lys Lys  
165 170 175  
atc acc gcc gcg agt aaa aag gct cca gcc cag aar gtt cct gcc cag 633  
Ile Thr Ala Ala Ser Lys Lys Ala Pro Ala Gln Lys Val Pro Ala Gln  
180 185 190  
aaa gcc aca ggc cag aaa gca gcg cct gct cna aaa gct cag aag ggt 681  
Lys Ala Thr Gly Gln Lys Ala Ala Pro Ala Xaa Lys Ala Gln Lys Gly  
195 200 205  
caa aaa gct cca gcc cag aaa gca cct gct cca aag gca tct ggc aam g 730  
Gln Lys Ala Pro Ala Gln Lys Ala Pro Ala Pro Lys Ala Ser Gly Xaa  
210 215 220 225

004220 " 666T550

<210> 763  
 <211> 820  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 166..819

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 ggaagctgag gcgccgaacg gctcccagag ggtcccggga agcgc atg gtg ttc agg 177  
 Met Val Phe Arg  
 1  
 cgc ttc gtg gag gtt ggc cgg gtg gcc tat gtc tcc ttt gga cct cat 225  
 Arg Phe Val Glu Val Gly Arg Val Ala Tyr Val Ser Phe Gly Pro His  
 5 10 15 20  
 gcc gga aaa ttg gtc gcg att gta gat gtt att gat cag aac agg gct 273  
 Ala Gly Lys Leu Val Ala Ile Val Asp Val Ile Asp Gln Asn Arg Ala  
 25 30 35  
 ttg gtc gat gga cct tgc act caa gtg agg aga cag gcc atg cct ttc 321  
 Leu Val Asp Gly Pro Cys Thr Gln Val Arg Arg Gln Ala Met Pro Phe  
 40 45 50  
 aag tgc atg cag ctg act gat ttc atc ctg aag ttt ccg cac agt gcc 369  
 Lys Cys Met Gln Leu Thr Asp Phe Ile Leu Lys Phe Pro His Ser Ala  
 55 60 65  
 cas cag aag tat gtc cga caa gcc tgg cag aag gca gac atc aat aca 417  
 Xaa Gln Lys Tyr Val Arg Gln Ala Trp Gln Lys Ala Asp Ile Asn Thr  
 70 75 80  
 aaa tgg gca gcc aca cga tgg gcc aag aag att gaa gcc aga gaa agg 465  
 Lys Trp Ala Ala Thr Arg Trp Ala Lys Lys Ile Glu Ala Arg Glu Arg  
 85 90 95 100  
 aaa gcc aag atg mnk gat ttt gat cgt ttt aaa gtt atg aag gca aag 513  
 Lys Ala Lys Met Xaa Asp Phe Asp Arg Phe Lys Val Met Lys Ala Lys  
 105 110 115  
 aaa atg agg aac aga ata atc aag aat gaa gtt aag aag ctt caa aag 561  
 Lys Met Arg Asn Arg Ile Ile Lys Asn Glu Val Lys Lys Leu Gln Lys  
 120 125 130  
 gca gct ctg ctg aaa gct tct ccc aaa aaa gca cct ggt act aag ggt 609  
 Ala Ala Leu Leu Lys Ala Ser Pro Lys Lys Ala Pro Gly Thr Lys Gly  
 135 140 145  
 act gct gct gct gct gct gct gct gct gct gct gct gct gct gct 657  
 Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala  
 150 155 160  
 aaa gtt cca gca aaa aag atc acc gcc gcg agt aaa aag gct cca gcc 705  
 Lys Val Pro Ala Lys Lys Ile Thr Ala Ala Ser Lys Lys Ala Pro Ala  
 165 170 175 180  
 cag aar gtt cct gcc cag aaa gcc aca ggc cag aaa gca gcg cct gct 753  
 Gln Lys Val Pro Ala Gln Lys Ala Thr Gly Gln Lys Ala Ala Pro Ala  
 185 190 195  
 cna aaa gct cag aag ggt caa aaa gct cca gcc cag aaa gca cct gct 801  
 Xaa Lys Ala Gln Lys Gly Gln Lys Ala Pro Ala Gln Lys Ala Pro Ala

004220-024400

200 205 210 820  
 cca aag gca tct ggc aam g  
 Pro Lys Ala Ser Gly Xaa  
 215

<210> 764  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 129..449

<400> 764  
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 tcttccttcg ctaacgcctc ccggtctctg tcagcctccc gccggccgtc tccttaacac 120  
 cgaacacc atg cct tca att aag ttg cag agt tct gat gga gag ata ttt 170  
 Met Pro Ser Ile Lys Leu Gln Ser Ser Asp Gly Glu Ile Phe  
 1 5 10  
 gaa gtt gat gtg gaa att gcc aaa caa tct gtg act att aag acc atg 218  
 Glu Val Asp Val Glu Ile Ala Lys Gln Ser Val Thr Ile Lys Thr Met  
 15 20 25 30  
 ttg gaa gat ttg gga atg gat gat gaa gga gat gat gac cca gtt cct 266  
 Leu Glu Asp Leu Gly Met Asp Asp Glu Gly Asp Asp Asp Pro Val Pro  
 35 40 45  
 cta cca aat gtg aat gca gca ata tta aaa aag gtc att cag tgg tgc 314  
 Leu Pro Asn Val Asn Ala Ala Ile Leu Lys Lys Val Ile Gln Trp Cys  
 50 55 60  
 acc cac cac aag gat gac cct cct cct cct gaa gat gat gag aac aaa 362  
 Thr His His Lys Asp Asp Pro Pro Pro Glu Asp Asp Glu Asn Lys  
 65 70 75  
 gaa aag cga aca gat gat atc cct gtt tgg gac caa gaa ttc ctg aaa 410  
 Glu Lys Arg Thr Asp Asp Ile Pro Val Trp Asp Gln Glu Phe Leu Lys  
 80 85 90  
 gtt gac caa gga cac ttt ttg aac tca ttc tgg ctg caa a 450  
 Val Asp Gln Gly His Phe Leu Asn Ser Phe Trp Leu Gln  
 95 100 105

<210> 765  
 <211> 518  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 198..518

<400> 765  
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 ccgacgcaga aaggagctgg ggaggaaaaa gctgctgcct tttgcgctgg agattcgtgg 120  
 gcaaggcttc tcattttccc aggctgcttc cctcccggg tgaggagcgt cctgagacta 180

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aggaaaagagc ctggaaa atg gag cag acc tgg acg aga gat tat ttt gca      230
                Met Glu Gln Thr Trp Thr Arg Asp Tyr Phe Ala
                1          5          10
gag gat gat ggg gag atg gta ccc aga acg agt cac aca gca gct ttt      278
Glu Asp Asp Gly Glu Met Val Pro Arg Thr Ser His Thr Ala Ala Phe
                15          20          25
ctt agt gac act aaa gat cga ggc cct cca gtg cag tca cag atc tgg      326
Leu Ser Asp Thr Lys Asp Arg Gly Pro Pro Val Gln Ser Gln Ile Trp
                30          35          40
aga agt ggt gaa aag gtc ccg ttt gtg cag aca tat tcc ttg aga gca      374
Arg Ser Gly Glu Lys Val Pro Phe Val Gln Thr Tyr Ser Leu Arg Ala
                45          50          55
ttt gag aaa ccc cct cag gta cag acc cag gct ctt cga gac ttt gag      422
Phe Glu Lys Pro Pro Gln Val Gln Thr Gln Ala Leu Arg Asp Phe Glu
                60          65          70          75
aag cac ctc aat gac ctg aag aag gag aac ttc agc ctc aag ctg cgc      470
Lys His Leu Asn Asp Leu Lys Lys Glu Asn Phe Ser Leu Lys Leu Arg
                80          85          90
atc tac ttc ctg gag gag cgc atg caa cag aag tat gag gcc agc cgg      518
Ile Tyr Phe Leu Glu Glu Arg Met Gln Gln Lys Tyr Glu Ala Ser Arg
                95          100          105

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<210> 766  
 <211> 470  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 166..468

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<400> 766
gggtcacgct aacgccgcgg tttcctccgc tcgattgggt ctactgtggg tctggactga      60
tctccatgtc ctgttggtgg gcttttacag cctttggatt gtgaaaactg ctgagagaga      120
cttgcaatcm agtymcataa gtataataaa gaaatattgg tcctc atg gaa gaa gag      177
                Met Glu Glu Glu
                1
caa gat tta cca gag caa cca gtg aaa aaa gcc aag atg cag gaa tca      225
Gln Asp Leu Pro Glu Gln Pro Val Lys Lys Ala Lys Met Gln Glu Ser
                5          10          15          20
gga gag caa act ata agt caa gta agc aat cca gat gtc agt gat cag      273
Gly Glu Gln Thr Ile Ser Gln Val Ser Asn Pro Asp Val Ser Asp Gln
                25          30          35
aag cct gaa aca tca agc ctt gct tca aac ctt ccc atg tca gag gaa      321
Lys Pro Glu Thr Ser Ser Leu Ala Ser Asn Leu Pro Met Ser Glu Glu
                40          45          50
att atg aca tgc acc gat tac atc cct cgc tca tcc aat gat tat acc      369
Ile Met Thr Cys Thr Asp Tyr Ile Pro Arg Ser Ser Asn Asp Tyr Thr
                55          60          65
tca caa atg tat tct gca aaa cct tat gca cat att ctc tca gtt cct      417
Ser Gln Met Tyr Ser Ala Lys Pro Tyr Ala His Ile Leu Ser Val Pro
                70          75          80
gtt tcg gaa act gct tac cct gga cag act caa tac cag aca cta cag      465

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Val Ser Glu Thr Ala Tyr Pro Gly Gln Thr Gln Tyr Gln Thr Leu Gln  
 85 90 95 100  
 cag ac 470  
 Gln

<210> 767  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 83..379

<400> 767  
 asaggagcag gaactggaac cctggccgag tccgaaaaaa gccagatctg gaaggtggct 60  
 gcggaacggg tttaagcgga ag atg gag gag ccg gag gaa ccg gcg gac agt 112  
 Met Glu Glu Pro Glu Glu Pro Ala Asp Ser  
 1 5 10  
 ggg cag tcg ctg gtc ccg gtt tat atc tat agt ccc gag tat gtc agt 160  
 Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser  
 15 20 25  
 atg tgt gac tcc ctg gcc aag atc ccc aaa ccg gcc agt atg gtg cat 208  
 Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met Val His  
 30 35 40  
 tct ttg att gaa gca tat gca ctg cat aag car atg agg ata gtt aag 256  
 Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile Val Lys  
 45 50 55  
 cct aaa gtg gcc tcc atg gag gag atg gcc acc ttc cac act gat gct 304  
 Pro Lys Val Ala Ser Met Glu Glu Met Ala Thr Phe His Thr Asp Ala  
 60 65 70  
 tat ctg cag cat ctc cag aag gtc agc caa gag ggc gat gat gat cat 352  
 Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp Asp His  
 75 80 85 90  
 ccg gac tcc ata gaa tat ggg cta ggt ta 381  
 Pro Asp Ser Ile Glu Tyr Gly Leu Gly  
 95

<210> 768  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 262..453

<400> 768  
 gatggctgca taccwgaag ggacagcagc tgggcagtc gagtgggctt gggtaaatac 60  
 aagtattggt gcacttaggg tgcggtattc cgtgtgtgca cgtctggtgg gggctttata 120  
 aagtgttttc gaggtgagct gctggggaaa agggaaacgg gagccctgca aatggagcga 180  
 cggggaggaa gagcgagggt ccagagccaa acccgtcact gacccccag cccaggcgcc 240

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cagccactcc ccaccgctac c atg gcc gaa gac gca gac atg cgc aat gag      291
                        Met Ala Glu Asp Ala Asp Met Arg Asn Glu
                        1                    5                    10
ctg gag gag atg cag cga agg gct gac cag ttg gct gat gag tcg ctg      339
Leu Glu Glu Met Gln Arg Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu
                        15                    20                    25
gaa agc acc cgt cgt atg ctg caa ctg gtt gaa gag agt aaa gat gct      387
Glu Ser Thr Arg Arg Met Leu Gln Leu Val Glu Glu Ser Lys Asp Ala
                        30                    35                    40
ggt atc agg act ttg gtt atg ttg gat gaa caa gga gaa caa ctg gaa      435
Gly Ile Arg Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Glu
                        45                    50                    55
cgc att gag gaa ggg atg g
Arg Ile Glu Glu Gly Met
                        60

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<210> 769  
 <211> 249  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 29..247

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<400> 769
actttttttt tccaagcggc tgccgaag atg gcg gag gtg cag gtc ctg gtg      52
                        Met Ala Glu Val Gln Val Leu Val
                        1                    5
ctt gat ggt cga ggc cat ctc ctg ggc cgc ctg gcg gcc atc gtg gct      100
Leu Asp Gly Arg Gly His Leu Leu Gly Arg Leu Ala Ala Ile Val Ala
                        10                    15                    20
aaa cag gta ctg ctg ggc cgg aag gtg gtg gtc gta cgc tgt gaa ggc      148
Lys Gln Val Leu Leu Gly Arg Lys Val Val Val Arg Cys Glu Gly
                        25                    30                    35                    40
atc atc ctc cgc aag cgg atg aac acc aac cct tcc cga ggc ccc tac      196
Ile Ile Leu Arg Lys Arg Met Asn Thr Asn Pro Ser Arg Gly Pro Tyr
                        45                    50                    55
cac ttc cgg gcc ccc agc cgc atc ttc tgg cgg acc gtg cga ggt atg      244
His Phe Arg Ala Pro Ser Arg Ile Phe Trp Arg Thr Val Arg Gly Met
                        60                    65                    70
ctg cc
Leu

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<210> 770  
 <211> 406  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 20..406



&lt;400&gt; 770

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agcgggtgggc tgagctaaa atg gct gag gag aga gtc gcg acg wga act caa      52
                        Met Ala Glu Glu Arg Val Ala Thr Xaa Thr Gln
                        1           5           10
ttt cct gta tct act gag tct caa aaa ccc cgg cag aaa aaa gct cca      100
Phe Pro Val Ser Thr Glu Ser Gln Lys Pro Arg Gln Lys Lys Ala Pro
                        15           20           25
gag ttt cct att ttg gag aag cag aac tgg ttg rtt cat ctt cat tat      148
Glu Phe Pro Ile Leu Glu Lys Gln Asn Trp Leu Xaa His Leu His Tyr
                        30           35           40
atc cgg aaa gat tat gaa gcc tgc aag gct gtt atc aaa gaa cag ctt      196
Ile Arg Lys Asp Tyr Glu Ala Cys Lys Ala Val Ile Lys Glu Gln Leu
                        45           50           55
caa gag act cag gga ttg tgt gaa tat gct atc tat gtc caa gca ttg      244
Gln Glu Thr Gln Gly Leu Cys Glu Tyr Ala Ile Tyr Val Gln Ala Leu
60                        65                        70                        75
ata ttt cgc cta gaa gga aat atc caa gaa tcc cta gaa ctc ttc cag      292
Ile Phe Arg Leu Glu Gly Asn Ile Gln Glu Ser Leu Glu Leu Phe Gln
                        80                        85                        90
aca tgt gca gtt ctt agt cct cag agt gct gat aac ctc aag cag gtg      340
Thr Cys Ala Val Leu Ser Pro Gln Ser Ala Asp Asn Leu Lys Gln Val
                        95           100           105
gcc aga tct tta ttt ctt ttg gga aaa cat aaa gct gcc att gaa gta      388
Ala Arg Ser Leu Phe Leu Leu Gly Lys His Lys Ala Ala Ile Glu Val
                        110           115           120
tat aat gaa gca gct aaa
Tyr Asn Glu Ala Ala Lys
                        125

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&lt;210&gt; 771

&lt;211&gt; 276

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 86..274

&lt;400&gt; 771

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atTTTTTTTTtg ccgcaagtta ttggcaagtt cccctgcagt tgTTTTgggct gtccctgtgg      60
ctggttcttg ggtgtgcggc cagcc atg gag cgc tct ggg ccc agc gaa gtg      112
                        Met Glu Arg Ser Gly Pro Ser Glu Val
                        1           5
aca ggc tca gac gcg tcg gga ccg gac ccg cag ctt gcg gtc acc atg      160
Thr Gly Ser Asp Ala Ser Gly Pro Asp Pro Gln Leu Ala Val Thr Met
10                        15                        20                        25
ggc ttc acg ggg ttc ggt aaa aaa gct cgc aca ttt gac ttg gaa gca      208
Gly Phe Thr Gly Phe Gly Lys Lys Ala Arg Thr Phe Asp Leu Glu Ala
                        30           35           40
atg ttt gaa caa act cga agg aca gct gtg gaa aga agt cgc aaa aca      256
Met Phe Glu Gln Thr Arg Arg Thr Ala Val Glu Arg Ser Arg Lys Thr
                        45                        50                        55

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ctg gaa gca aga gaa aaa ga  
 Leu Glu Ala Arg Glu Lys  
 60

276

<210> 772  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 242..463

<400> 772  
 agggccctct ttgtggctgc agttggcaag atggcgccgg tgggggtggc agaagaagct 60  
 gctgctaggt cccaacgggc ccgcggtggc ggccgcccgc gacctgacca gtgaggagga 120  
 ggaaggccag agcctatggt cctccattct gagcgaagtg tccaccgcgc ccaggtccaa 180  
 gctgccgtcc ggcaagaaca tcctggtctt cggatgaagat ggttctggtg aaacaaccct 240  
 c atg act aaa cta caa gga gct gag cat ggc aaa aaa gga aga ggc cta 289  
 Met Thr Lys Leu Gln Gly Ala Glu His Gly Lys Lys Gly Arg Gly Leu  
 1 5 10 15  
 gaa tat ctc tac ctc agt gtc cat gat gag gac cga gat gat cac acg 337  
 Glu Tyr Leu Tyr Leu Ser Val His Asp Glu Asp Arg Asp Asp His Thr  
 20 25 30  
 cgc tgc aac gtg tgg att ctg gat gga gac ttg tac cac aaa ggc ctg 385  
 Arg Cys Asn Val Trp Ile Leu Asp Gly Asp Leu Tyr His Lys Gly Leu  
 35 40 45  
 ctg aaa ttt gca gtt tct gct gaa tcc ttg cca gag acc ctc gtc att 433  
 Leu Lys Phe Ala Val Ser Ala Glu Ser Leu Pro Glu Thr Leu Val Ile  
 50 55 60  
 ttt gtt gca gac atg tct aga cct tgg act 463  
 Phe Val Ala Asp Met Ser Arg Pro Trp Thr  
 65 70

<210> 773  
 <211> 295  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 98..295

<400> 773  
 agccacaaac ggatgtgagg tgaggcagga gcggcgacct ttgaaggaaa aaaggaagtg 60  
 tttggacgac agcgagcggg agaagcgggg tcaagaa atg gaa gat aaa gtg act 115  
 Met Glu Asp Lys Val Thr  
 1 5  
 agt cca gag aaa gca gaa gaa gca aaa tta aaa gca aga tat cct cat 163  
 Ser Pro Glu Lys Ala Glu Glu Ala Lys Leu Lys Ala Arg Tyr Pro His  
 10 15 20  
 ctg gga caa aag cct gga ggt tca gat ttc tta agg aaa cgg ttg cag 211

Leu	Gly	Gln	Lys	Pro	Gly	Gly	Ser	Asp	Phe	Leu	Arg	Lys	Arg	Leu	Gln	
		25					30					35				
aaa	ggg	caa	aaa	tat	ttt	gat	tct	ggg	gat	tac	aac	atg	gct	aaa	gca	259
Lys	Gly	Gln	Lys	Tyr	Phe	Asp	Ser	Gly	Asp	Tyr	Asn	Met	Ala	Lys	Ala	
		40					45				50					
aaa	atg	aag	aac	aag	caa	ctt	cct	act	gca	gct	ccg					295
Lys	Met	Lys	Asn	Lys	Gln	Leu	Pro	Thr	Ala	Ala	Pro					
55					60					65						

<210> 774  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 105..350

<400> 774																
agccacaaac	ggatgtgagg	tgaggcagga	gcggcgacct	ttgaaggaaa	aaaggaagtg		60									
tttggacgac	agcgagcggg	agaagcgggg	tcaaagggag	cact	atg	tct	gcg	gaa		116						
								Met	Ser	Ala	Glu					
gtc	ccc	gag	gca	gcc	tcc	gcg	gag	gag	cag	aag	gaa	atg	gaa	gat	aaa	164
Val	Pro	Glu	Ala	Ala	Ser	Ala	Glu	Glu	Gln	Lys	Glu	Met	Glu	Asp	Lys	
5					10					15					20	
gtg	act	agt	cca	gag	aaa	gca	gaa	gaa	gca	aaa	tta	aaa	gca	aga	tat	212
Val	Thr	Ser	Pro	Glu	Lys	Ala	Glu	Glu	Ala	Lys	Leu	Lys	Ala	Arg	Tyr	
					25					30					35	
cct	cat	ctg	gga	caa	aag	cct	gga	ggt	tca	gat	ttc	tta	agg	aaa	cgg	260
Pro	His	Leu	Gly	Gln	Lys	Pro	Gly	Gly	Ser	Asp	Phe	Leu	Arg	Lys	Arg	
			40					45					50			
ttg	cag	aaa	ggg	caa	aaa	tat	ttt	gat	tct	ggg	gat	tac	aac	atg	gct	308
Leu	Gln	Lys	Gly	Gln	Lys	Tyr	Phe	Asp	Ser	Gly	Asp	Tyr	Asn	Met	Ala	
		55				60					65					
aaa	gca	aaa	atg	aag	aac	aag	caa	ctt	cct	act	gca	gct	ccg			350
Lys	Ala	Lys	Met	Lys	Asn	Lys	Gln	Leu	Pro	Thr	Ala	Ala	Pro			
	70					75					80					

<210> 775  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 105..407

<400> 775															
agccacaaac	ggatgtgagg	tgaggcagga	gcggcgacct	ttgaaggaaa	aaaggaagtg		60								
tttggacgac	agcgagcggg	agaagcgggg	tcaaagggag	cact	atg	tct	gcg	gaa		116					
								Met	Ser	Ala	Glu				

```

                                1
gtc ccc gag gca gcc tcc gcg gag gag cag aag agt gaa cac aac atg      164
Val Pro Glu Ala Ala Ser Ala Glu Glu Gln Lys Ser Glu His Asn Met
5                                10                                15                                20
ctc cct tgg tct ctg caa cca tcg att cct aac agc cta gag gaa atg      212
Leu Pro Trp Ser Leu Gln Pro Ser Ile Pro Asn Ser Leu Glu Glu Met
25                                30                                35
gaa gat aaa gtg act agt cca gag aaa gca gaa gaa gca aaa tta aaa      260
Glu Asp Lys Val Thr Ser Pro Glu Lys Ala Glu Glu Ala Lys Leu Lys
40                                45                                50
gca aga tat cct cat ctg gga caa aag cct gga ggt tca gat ttc tta      308
Ala Arg Tyr Pro His Leu Gly Gln Lys Pro Gly Gly Ser Asp Phe Leu
55                                60                                65
agg aaa cgg ttg cag aaa ggg caa aaa tat ttt gat tct ggg gat tac      356
Arg Lys Arg Leu Gln Lys Gly Gln Lys Tyr Phe Asp Ser Gly Asp Tyr
70                                75                                80
aac atg gct aaa gca aaa atg aag aac aag caa ctt cct act gca gct      404
Asn Met Ala Lys Ala Lys Met Lys Asn Lys Gln Leu Pro Thr Ala Ala
85                                90                                95                                100
ccg
Pro
407

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<210> 776  
 <211> 341  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 96..341

<400> 776

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gggccckkkgg agagctggga cgggcggcgg cggggtggcc tcggccaccc kctaattgca      60
tcttttcccg gcgtctcgtc tgcagaggga gcact atg tct gcg gaa gtc ccc      113
                                Met Ser Ala Glu Val Pro
                                1                                5

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gag gca gcc tcc gcg gag gag cag aag gaa atg gaa gat aaa gtg act      161
Glu Ala Ala Ser Ala Glu Glu Gln Lys Glu Met Glu Asp Lys Val Thr
10                                15                                20
agt cca gag aaa gca gaa gaa gca aaa tta aaa gca aga tat cct cat      209
Ser Pro Glu Lys Ala Glu Glu Ala Lys Leu Lys Ala Arg Tyr Pro His
25                                30                                35
ctg gga caa aag cct gga ggt tca gat ttc tta agg aaa cgg ttg cag      257
Leu Gly Gln Lys Pro Gly Gly Ser Asp Phe Leu Arg Lys Arg Leu Gln
40                                45                                50
aaa ggg caa aaa tat ttt gat tct ggg gat tac aac atg gct aaa gca      305
Lys Gly Gln Lys Tyr Phe Asp Ser Gly Asp Tyr Asn Met Ala Lys Ala
55                                60                                65                                70
aaa atg aag aac aag caa ctt cct act gca gct ccg
Lys Met Lys Asn Lys Gln Leu Pro Thr Ala Ala Pro
75                                80

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<210> 777

<211> 520  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 365..520

<400> 777  
 aaccagactg cgagcggaga agcggagttt gcagcctcgg aattggctag agcgccagag 60  
 ccgagtcagc cataaagcta cgcgctaggc tcttgccctt gacgtgagga gcgcagagat 120  
 ggcknannng aatagttttc aacgtctatt tcattccctg cttcagagga cctctttaat 180  
 ctttgatttt ggtccctggt tctaagaaaa gcaactgaaa aggtcgtaat accgccctg 240  
 agaaaaaagg agcagcgcta aataatcgag aaaatgcctc ctcttgaaac ggatatagag 300  
 atggaaacaa gatataagaa ggattgagaa tcatataata caggagctta aacacctatg 360  
 cgcg atg ata aag agg gta cta tta gag cgc ttg gaa aat acc agg aag 409  
 Met Ile Lys Arg Val Leu Leu Glu Arg Leu Glu Asn Thr Arg Lys  
 1 5 10 15  
 ttg aga gag tta aca gaa ggg cgc acg ctg gat tgg cca caa aat cga 457  
 Leu Arg Glu Leu Thr Glu Gly Arg Thr Leu Asp Trp Pro Gln Asn Arg  
 20 25 30  
 att act gaa gta agt gca aaa cga caa att gtc aca gaa tac aga gaa 505  
 Ile Thr Glu Val Ser Ala Lys Arg Gln Ile Val Thr Glu Tyr Arg Glu  
 35 40 45  
 aag ggg aaa aga aat 520  
 Lys Gly Lys Arg Asn  
 50

<210> 778  
 <211> 549  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 256..549

<400> 778  
 agccgccctt ccccccagct agtgagtgcg cgaacgagaa aggaggaggg cgctccagga 60  
 gacagcactg cagacgccat tctctctgtt ttctctgctg caccgacctc gacgtcttgc 120  
 ctgtgtccca cttgttcgcg gcctataggc tactgcagca ctgggggtgtc agttgttggt 180  
 ccgaccagaa acgcttcagt tctgctctgc aaggatatat aataactgat tgggtgtgcc 240  
 gtttaataaaa agaat atg gaa act gaa cag cca gaa gaa acc ttc cct aac 291  
 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn  
 1 5 10  
 act gaa acc aat ggt gaa ttt ggt aaa cgc cct gca gaa gat atg gaa 339  
 Thr Glu Thr Asn Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu  
 15 20 25  
 gag gaa caa gca ttt aaa aga tct aga aac act gat gag atg gtt gaa 387  
 Glu Glu Gln Ala Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu  
 30 35 40  
 tta cgc att ctg ctt cag agc aag aat gct ggg gca gtg att gga aaa 435

Leu Arg Ile Leu Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys  
 45 50 55 60  
 gga ggc aag aat att aag gct ctc cgt aca gac tac aat gcc agt gtt 483  
 Gly Gly Lys Asn Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val  
 65 70 75  
 tca gtc cca gac agc agt ggc ccc gag cgc ata ttg agt atc agt gct 531  
 Ser Val Pro Asp Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala  
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 Asp Ile Glu Thr Ile Gly 549  
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 ttctgctctg caaggatata taataactga ttggtgtgcc cgtttaataa aagaat atg 179  
 Met  
 1  
 gaa act gaa cag cca gaa gaa acc ttc cct aac act gaa acc aat ggt 227  
 Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn Gly  
 5 10 15  
 gaa ttt ggt aaa cgc cct gca gaa gat atg gaa gag gaa caa gca ttt 275  
 Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala Phe  
 20 25 30  
 aaa aga tct aga aac act gat gag atg gtt gaa tta cgc att ctg ctt 323  
 Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu Leu  
 35 40 45  
 cag agc aag aat gct ggg gca gtg att gga aaa gga ggc aag aat att 371  
 Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn Ile  
 50 55 60 65  
 aag gct ctc cgt aca gac tac aat gcc agt gtt tca gtc cag aca gca 419  
 Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Gln Thr Ala  
 70 75 80  
 gtg gcc ccg aag cgc ata ttg agt atc agt gct gat att gaa aca att 467  
 Val Ala Pro Lys Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr Ile  
 85 90 95  
 gga gaa att ctg aag aa  
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<210> 780  
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**SECRET**

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Gly Ser Gly Cys Glu Glu Lys Arg His Glu Gly Ser Ser Ser Glu Ser					
10                                15                                20                                25					
gtg cca ccc ggc act acc att tcg agg gtg aag ctc ctc gac acc atg	147				
Val Pro Pro Gly Thr Thr Ile Ser Arg Val Lys Leu Leu Asp Thr Met					
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gtg gac act ttt ctt cag aag ctg gtc gcc gcc ggc agc tac cag aga	195				
Val Asp Thr Phe Leu Gln Lys Leu Val Ala Ala Gly Ser Tyr Gln Arg					
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ttc act gac tgc tat aag tgc ttc tac cag ttg cag cct gcg atg aca	243				
Phe Thr Asp Cys Tyr Lys Cys Phe Tyr Gln Leu Gln Pro Ala Met Thr					
				60                                65                                70	
cag caa atc tat gac aag ttt ata gct cag ttg cag aca tct atc cgg	291				
Gln Gln Ile Tyr Asp Lys Phe Ile Ala Gln Leu Gln Thr Ser Ile Arg					
				75                                80                                85	
gag gaa atc tct gac atc aaa gag gag ggg aac cta gaa gct gtc ttg	339				
Glu Glu Ile Ser Asp Ile Lys Glu Glu Gly Asn Leu Glu Ala Val Leu					
				90                                95                                100                                105	
aat gcc ttg gat aaa att gtg gaa gaa ggc aaa gtc cgc aaa gag cca	387				
Asn Ala Leu Asp Lys Ile Val Glu Glu Gly Lys Val Arg Lys Glu Pro					
				110                                115                                120	
gcc tgg cgc ccc agc ggg atc cca gag aag gat ctg cac agt gtt atg	435				
Ala Trp Arg Pro Ser Gly Ile Pro Glu Lys Asp Leu His Ser Val Met					
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aaaccggaaa	aaaggccagg	aacctgaata	cgacctaata	gctgtttccg	agggggcaac	180
ttccacggag	arccttctgc	cctggtaacg	gccaaagagg	aggagatggc	gccagtcagg	240
gagcgcccg	ggcccagaca	gtgaggaagc	gcgaaggcgg	agcaaccgag	gaatcctccg	300

gagaagaatc agagccgtcg ctaccgccac taccgccacc acc atg gaa gga gca 355  
 Met Glu Gly Ala  
 1  
 aag ccg aca ttg cag ctc gtg tac cag gca gtg cag gcg ctt tac cac 403  
 Lys Pro Thr Leu Gln Leu Val Tyr Gln Ala Val Gln Ala Leu Tyr His  
 5 10 15 20  
 gac cca gat ccc agc gga aag gag cgc gcc tct ttt tgg ctt ggg gag 451  
 Asp Pro Asp Pro Ser Gly Lys Glu Arg Ala Ser Phe Trp Leu Gly Glu  
 25 30 35  
 ctg cag cgt tcg gtt cat gca tgg gag atc tca gac cag ttg tta cag 499  
 Leu Gln Arg Ser Val His Ala Trp Glu Ile Ser Asp Gln Leu Leu Gln  
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 Met Pro Ser Glu Thr Leu Trp Glu Ile Ala  
 1 5 10  
 aaa gct gaa gtg gaa aaa agg gga att aat gga agt gaa ggt gat gga 160  
 Lys Ala Glu Val Glu Lys Arg Gly Ile Asn Gly Ser Glu Gly Asp Gly  
 15 20 25  
 gct gaa att gca gaa aaa ttt gtt ttc ttc att ggc agt aaa aat ggg 208  
 Ala Glu Ile Ala Glu Lys Phe Val Phe Phe Ile Gly Ser Lys Asn Gly  
 30 35 40  
 gga aag act act att att cta agg tgt ctt gac aga gat gaa cca cca 256  
 Gly Lys Thr Thr Ile Ile Leu Arg Cys Leu Asp Arg Asp Glu Pro Pro  
 45 50 55  
 aaa cca acc tta gct ttg gaa tat aca tat gga aga aga gca aaa ggg 304  
 Lys Pro Thr Leu Ala Leu Glu Tyr Thr Tyr Gly Arg Arg Ala Lys Gly  
 60 65 70  
 cac aac aca cca aaa gat atc gct ca 330  
 His Asn Thr Pro Lys Asp Ile Ala  
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<210> 783  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS



<222> 89..412

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gcacactgtc ctttgccac cggacatc atg cct ccc aag aag gat gtt ccc	112
Met Pro Pro Lys Lys Asp Val Pro	
1 5	
gtg aag aaa cca gca ggg ccc tcc atc tcc aaa cct gct gct aag cca	160
Val Lys Lys Pro Ala Gly Pro Ser Ile Ser Lys Pro Ala Ala Lys Pro	
10 15 20	
gca gca gca ggg gct cct cca gcc aag acc aaa gct gag cca gct gtc	208
Ala Ala Ala Gly Ala Pro Pro Ala Lys Thr Lys Ala Glu Pro Ala Val	
25 30 35 40	
ccc cag gcc cct cag aaa acc cag gag cct cca gtc gat ctc tcc aaa	256
Pro Gln Ala Pro Gln Lys Thr Gln Glu Pro Pro Val Asp Leu Ser Lys	
45 50 55	
gtg gtg atc gag ttt aac aag gac cag ctg gag gag ctg aag tcg cgg	304
Val Val Ile Glu Phe Asn Lys Asp Gln Leu Glu Glu Leu Lys Ser Arg	
60 65 70	
cgt gtg gac ttt gag act ttc ctg ccc atg ctc cag gca gtg gcc aag	352
Arg Val Asp Phe Glu Thr Phe Leu Pro Met Leu Gln Ala Val Ala Lys	
75 80 85	
aac cga ggc caa ggc aca tat gag gac tac ttg gar ggg ttt cgt gtg	400
Asn Arg Gly Gln Gly Thr Tyr Glu Asp Tyr Leu Glu Gly Phe Arg Val	
90 95 100	
ttt gac aag gaa g	413
Phe Asp Lys Glu	
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<210> 784

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<221> CDS

<222> 30..227

<400> 784

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1 5	
ttt ggt gag cgg cct cca cct aaa cga ctt act agg gaa gct atg cga	101
Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr Arg Glu Ala Met Arg	
10 15 20	
aat tat tta aaa gag cga ggg gat caa aca gta ctt att ctt cat gca	149
Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val Leu Ile Leu His Ala	
25 30 35 40	
aaa gtt gca cag aag tca tat gga aat gaa aaa agg ttt ttt tgc cca	197
Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys Arg Phe Phe Cys Pro	
45 50 55	
cct cct tgt gta tat ctt atg ggc agc gca tg	229

Pro Pro Cys Val Tyr Leu Met Gly Ser Ala  
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tcctccgact caagatattt gtcaaattt ttcagaag atg gct gat cct tgg cag 116  
Met Ala Asp Pro Trp Gln  
1 5  
gaa tgc atg gat tat gca gta act cta gca aga caa gct gga gag gta 164  
Glu Cys Met Asp Tyr Ala Val Thr Leu Ala Arg Gln Ala Gly Glu Val  
10 15 20  
gtt tgt gaa gct ata aaa aat gaa atg aat gtt atg ctg aaa agt tct 212  
Val Cys Glu Ala Ile Lys Asn Glu Met Asn Val Met Leu Lys Ser Ser  
25 30 35  
cca gtt gat ttg gta act gct acg gac caa aaa gtt gaa aaa atg ctt 260  
Pro Val Asp Leu Val Thr Ala Thr Asp Gln Lys Val Glu Lys Met Leu  
40 45 50  
atc tct tcc ata aag gaa aag tat cca tct cac agt ttc att ggt gaa 308  
Ile Ser Ser Ile Lys Glu Lys Tyr Pro Ser His Ser Phe Ile Gly Glu  
55 60 65 70  
gaa tct gtg gca gct ggg gaa aaa agt atc tta acc gac aac ccc aca 356  
Glu Ser Val Ala Ala Gly Glu Lys Ser Ile Leu Thr Asp Asn Pro Thr  
75 80 85  
tkn atc att gac cct att gat gga aca act aac ttt gta cat aga ttt 404  
Xaa Ile Ile Asp Pro Ile Asp Gly Thr Thr Asn Phe Val His Arg Phe  
90 95 100  
cct ttt gta gct gtt tca att ggc ttt gct gta aat aaa aag ata gaa 452  
Pro Phe Val Ala Val Ser Ile Gly Phe Ala Val Asn Lys Lys Ile Glu  
105 110 115  
ttt gga gtt gtg tac agt tgt 473  
Phe Gly Val Val Tyr Ser Cys  
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<210> 786  
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<212> DNA  
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<220>  
<221> CDS  
<222> 91..315

<400> 786

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 gccctgctt tccctagttc cagttccaag atg ggg aaa tcc ttc gcc aac ttc 114  
 Met Gly Lys Ser Phe Ala Asn Phe  
 1 5  
 atg tgc aag aaa gac ttt cat cct gcc tcc aaa tcc aat atc aaa aaa 162  
 Met Cys Lys Lys Asp Phe His Pro Ala Ser Lys Ser Asn Ile Lys Lys  
 10 15 20  
 gta tgg atg gca gaa cag aaa ata tca tat gat aag aag aaa caa gaa 210  
 Val Trp Met Ala Glu Gln Lys Ile Ser Tyr Asp Lys Lys Lys Gln Glu  
 25 30 35 40  
 gaa ttg atg cag caa tat ctt aaa gaa caa gaa tca tat gat aat aga 258  
 Glu Leu Met Gln Gln Tyr Leu Lys Glu Gln Glu Ser Tyr Asp Asn Arg  
 45 50 55  
 ttg ctt atg gga gat gaa cgt gta aag aat ggc ctt aat ttc atg tat 306  
 Leu Leu Met Gly Asp Glu Arg Val Lys Asn Gly Leu Asn Phe Met Tyr  
 60 65 70  
 gaa gcc ccc 315  
 Glu Ala Pro  
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<210> 787  
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 <212> DNA  
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 Met  
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 Leu Arg Ser Arg Ser Xaa Xaa Ser Leu Gln Lys Gln Pro Pro Cys Gln  
 5 10 15  
 tct cta agt gcc caa aaa agt cgg agt ccc tgt gga agg ggt ggg acc 153  
 Ser Leu Ser Ala Gln Lys Ser Arg Ser Pro Cys Gly Arg Gly Gly Thr  
 20 25 30  
 gga agg ccc aga gga acg gcc tgc gga gca ggt ata cgc tgt gaa tgg 201  
 Gly Arg Pro Arg Gly Thr Ala Cys Gly Ala Gly Ile Arg Cys Glu Trp  
 35 40 45  
 cga cta cta tgt ggg cga gtg gaa gga caa cgt gaa aca cgg g 244  
 Arg Leu Leu Cys Gly Arg Val Glu Gly Gln Arg Glu Thr Arg  
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<210> 788  
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<222> 96..392

<400> 788

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ttctcggaac ccgaggagaa gcggcgctccg gggct atg gct gtg act ctg gac 113  
Met Ala Val Thr Leu Asp  
1 5  
aaa gac gct tat tat cgg cga gtg aag aga ctg tac agc aat tgg cgg 161  
Lys Asp Ala Tyr Tyr Arg Arg Val Lys Arg Leu Tyr Ser Asn Trp Arg  
10 15 20  
aaa gga gaa gat gag tat gcc aac gtt gat gcc att gtt gta tca gtg 209  
Lys Gly Glu Asp Glu Tyr Ala Asn Val Asp Ala Ile Val Val Ser Val  
25 30 35  
ggg gtt gat gaa gaa att gtt tat gcc aaa tca act gcc tta cag aca 257  
Gly Val Asp Glu Glu Ile Val Tyr Ala Lys Ser Thr Ala Leu Gln Thr  
40 45 50  
tgg ctc ttt ggt tat gaa cta act gat act atc atg gtc ttt tgt gat 305  
Trp Leu Phe Gly Tyr Glu Leu Thr Asp Thr Ile Met Val Phe Cys Asp  
55 60 65 70  
gac aaa atc atc ttt atg gcc agc aag aaa aaa gtg gag ttc ttg aaa 353  
Asp Lys Ile Ile Phe Met Ala Ser Lys Lys Lys Val Glu Phe Leu Lys  
75 80 85  
cag att gcc aac act aag ggc aat gag aat gct aat gga 392  
Gln Ile Ala Asn Thr Lys Gly Asn Glu Asn Ala Asn Gly  
90 95

<210> 789

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 165..506

<400> 789

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aatttgaacc ttttgagct gtgtgctaaa tcttcagtgg gaca atg ggt tca gac 176  
Met Gly Ser Asp  
1  
aaa aga gtg agt aga aca gag cgt agt gga aga tac ggt tcc atc ata 224  
Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile Ile  
5 10 15 20  
gac agg gat gac cgt gat gag cgt gaa tcc cga agc agg cgg agg gac 272  
Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser Arg Arg Arg Asp  
25 30 35  
tca gat tac aaa aga tct agt gat gat cgg agg ggt gat aga tat gat 320  
Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr Asp  
40 45 50  
gac tac cga gac tat gac agt cca gag aga gag cgt gaa aga agg aac 368  
Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg Asn

55	60	65	
agt gac cga tcc gaa gat ggc tac cat tca gat ggt gac tat ggt gag			416
Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly Glu			
70	75	80	
cac gac tat agg cat gac atc agt gac gag agg gmg aca aga cca tca			464
His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Xaa Thr Arg Pro Ser			
85	90	95	100
tgc tgc gcg gcc ttc cca tca mca tca cag aga gcg ata ttc ga			508
Cys Cys Ala Ala Phe Pro Ser Xaa Ser Gln Arg Ala Ile Phe			
105	110		

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	Met Phe Pro Arg Val
	1 5
tcg acg ttc cta cct ctt cgc ccc ctt tcc cgc cac cct ttg tcc tct	104
Ser Thr Phe Leu Pro Leu Arg Pro Leu Ser Arg His Pro Leu Ser Ser	
	10 15 20
gga agc ccg gag aca tca gcg gct gcg att atg cta ctc act gtt cgg	152
Gly Ser Pro Glu Thr Ser Ala Ala Ala Ile Met Leu Leu Thr Val Arg	
	25 30 35
cac gga aca gtc agg tac cgc agt tca gcg ctg ttg gcc cgg aca aaa	200
His Gly Thr Val Arg Tyr Arg Ser Ser Ala Leu Leu Ala Arg Thr Lys	
	40 45 50
aat aac atc caa aga tat ttt ggc act aac agt gtg atc tgt agc aag	248
Asn Asn Ile Gln Arg Tyr Phe Gly Thr Asn Ser Val Ile Cys Ser Lys	
	55 60 65
aaa gat aag cag tct gtt cga act gag gag act tcc aag gag act tca	296
Lys Asp Lys Gln Ser Val Arg Thr Glu Glu Thr Ser Lys Glu Thr Ser	
	70 75 80 85
gag agc caa gac agt gaa aag gaa aat acg aaa aaa gac ttg tta ggc	344
Glu Ser Gln Asp Ser Glu Lys Glu Asn Thr Lys Lys Asp Leu Leu Gly	
	90 95 100
att att aag ggc atg aaa gtt gaa tta agc aca gta aat gta cga aca	392
Ile Ile Lys Gly Met Lys Val Glu Leu Ser Thr Val Asn Val Arg Thr	
	105 110 115
aca aag ccc ccc aaa aga aga cc	415
Thr Lys Pro Pro Lys Arg Arg	
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<220>  
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 ggaagcccgg agacatcagc ggctgcaatt atg cta ctc act gtt cgg cac gga 174  
 Met Leu Leu Thr Val Arg His Gly  
 1 5  
 aca gtc agg tac cgc agt tca gcg ctg ttg gcc cgg aca aaa aat aac 222  
 Thr Val Arg Tyr Arg Ser Ser Ala Leu Leu Ala Arg Thr Lys Asn Asn  
 10 15 20  
 atc caa aga tat ttt ggc act aac agt gtg atc tgt agc aag aaa gat 270  
 Ile Gln Arg Tyr Phe Gly Thr Asn Ser Val Ile Cys Ser Lys Lys Asp  
 25 30 35 40  
 aag cag tct gtt cga act gag gag act tcc aag gag act tca gag agc 318  
 Lys Gln Ser Val Arg Thr Glu Glu Thr Ser Lys Glu Thr Ser Glu Ser  
 45 50 55  
 caa gac agt gaa aag gaa aat acg aaa aaa gac ttg tta ggc att att 366  
 Gln Asp Ser Glu Lys Glu Asn Thr Lys Lys Asp Leu Leu Gly Ile Ile  
 60 65 70  
 aag ggc atg aaa gtt gaa tta agc aca gta aat gta cga aca aca aag 414  
 Lys Gly Met Lys Val Glu Leu Ser Thr Val Asn Val Arg Thr Thr Lys  
 75 80 85  
 ccc ccc aaa aga aga cc 431  
 Pro Pro Lys Arg Arg  
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<220>  
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 Met Thr Val Leu Tyr  
 1 5  
 aag tca aaa aat aca tgc ctg cct cgt agt gaa gtt gta gcn ctc cgt 164  
 Lys Ser Lys Asn Thr Cys Leu Pro Arg Ser Glu Val Val Ala Leu Arg  
 10 15 20  
 aat atg tat att tta ctc agt ttt caa cat ttt gtg aat gtt gac tac 212  
 Asn Met Tyr Ile Leu Leu Ser Phe Gln His Phe Val Asn Val Asp Tyr  
 25 30 35  
 ctg aag ttc ctt ttt aga tgw gct att aac att ctg ttg gat tca gag g 261  
 Leu Lys Phe Leu Phe Arg Xaa Ala Ile Asn Ile Leu Leu Asp Ser Glu

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45

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<220>  
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 <222> 3..212

<400> 793  
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 Met Glu Lys Phe Asn Leu Asp Leu Ser Thr Val Thr Gln Ala Phe  
 1 5 10 15  
 cta aaa aat agt ggt gag ctg gag gct act tcc gcc ttc tta gcg tct 95  
 Leu Lys Asn Ser Gly Glu Leu Glu Ala Thr Ser Ala Phe Leu Ala Ser  
 20 25 30  
 ggt cag aga gct gat gga tat ccc att tgg tcc cga caa gat gac ata 143  
 Gly Gln Arg Ala Asp Gly Tyr Pro Ile Trp Ser Arg Gln Asp Asp Ile  
 35 40 45  
 gat ttg caa aaa gat gat gar gat acc aga gag gca ttg gtc aaa aaa 191  
 Asp Leu Gln Lys Asp Asp Glu Asp Thr Arg Glu Ala Leu Val Lys Lys  
 50 55 60  
 ttt ggt gct cag aat gta gct cg 214  
 Phe Gly Ala Gln Asn Val Ala  
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<210> 794  
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 <212> DNA  
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<220>  
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 gggacgcgca cgccagagga gacgaaagga acccggggtcg gaccagatcg gaaccactga 180  
 ccattgccc atg gcg gcc cta ggc cct agc agc cag aat gtc act gaa tac 231  
 Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr  
 1 5 10  
 gtc gtt cga gtt cct aag aat aca acc aaa aaa tat aac atc atg gct 279  
 Val Val Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala  
 15 20 25 30  
 ttt aat gca gcc gac aaa gtc aac ttt gct acg tgg aat cag gct cgg 327  
 Phe Asn Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg  
 35 40 45  
 ctg gag cgg gac ttg agc aac aag ann kct acc aag agg agg aga tgc 375  
 Leu Glu Arg Asp Leu Ser Asn Lys Xaa Xaa Thr Lys Arg Arg Arg Cys

50	55	60	
ccg aat cgg gcg cgg gca gtg agt tca acc gca agc ttc ggg agg agg			423
Pro Asn Arg Ala Arg Ala Val Ser Ser Thr Ala Ser Phe Gly Arg Arg			
65	70	75	
ctc gga gga aga agt acg gca tcg t			448
Leu Gly Gly Arg Ser Thr Ala Ser			
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Val Leu Phe Thr Ala Gly Glu Arg Trp Arg Cys Phe Leu Thr Pro Ser	
5 10 15 20	
agg tca tcc ctg tac tgg gcc tta cat aat ttc tgc tgt cgg aaa aaa	150
Arg Ser Ser Leu Tyr Trp Ala Leu His Asn Phe Cys Cys Arg Lys Lys	
25 30 35	
tcc act aca cct aag aaa att act ccc aat gtt act ttt tgt gat gaa	198
Ser Thr Thr Pro Lys Lys Ile Thr Pro Asn Val Thr Phe Cys Asp Glu	
40 45 50	
aat gca aag gag ccc gaa aat gca ctt gac aag ctc ttc tct tca gaa	246
Asn Ala Lys Glu Pro Glu Asn Ala Leu Asp Lys Leu Phe Ser Ser Glu	
55 60 65	
cag cag gct tcc atc ttg cat gtg ttg aat aca gca tct act aaa gaa	294
Gln Gln Ala Ser Ile Leu His Val Leu Asn Thr Ala Ser Thr Lys Glu	
70 75 80	
ctt gaa gct ttc cga ttg ctt cgt gga aga ag	326
Leu Glu Ala Phe Arg Leu Leu Arg Gly Arg	
85 90	

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<220>  
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agccagattt cacctctgca aat atg aga gat tct gca gaa ggt cct aaa gaa      173
                        Met Arg Asp Ser Ala Glu Gly Pro Lys Glu
                        1           5           10
gac gaa gag aag cct tca gcc tca gca ctt gag cag ccg gcc acc ctc      221
Asp Glu Glu Lys Pro Ser Ala Ser Ala Leu Glu Gln Pro Ala Thr Leu
                        15           20           25
cag gag gtg gcc agt cag gag gtg cct cca gaa cta gca acc cct gcc      269
Gln Glu Val Ala Ser Gln Glu Val Pro Pro Glu Leu Ala Thr Pro Ala
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Pro Ala Trp Glu Pro Gln Pro Glu Pro Asp
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                        Met Lys Cys Val Phe Val
                        1           5
acc gta ggg acc acc agc ttt gac gac ctc att gcg tgt gtg tcg gcg      164
Thr Val Gly Thr Thr Ser Phe Asp Asp Leu Ile Ala Cys Val Ser Ala
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ccc gac agt ctg caa aaa atc gag agc ctt ggt tac aac cga ctt atc      212
Pro Asp Ser Leu Gln Lys Ile Glu Ser Leu Gly Tyr Asn Arg Leu Ile
                        25           30           35
ctg caa att ggt aga gga acg gtg gta cct gaa ccc ttc agt act gag      260
Leu Gln Ile Gly Arg Gly Thr Val Val Pro Glu Pro Phe Ser Thr Glu
                        40           45           50
tcg ttt act ctg gat gtt tac agg tac aag gat tcc ttg aaa gaa gac      308
Ser Phe Thr Leu Asp Val Tyr Arg Tyr Lys Asp Ser Leu Lys Glu Asp
55           60           65           70
att cag aaa gca gat ctt gtt att agt cac gca ggt gca gga agc tgt      356
Ile Gln Lys Ala Asp Leu Val Ile Ser His Ala Gly Ala Gly Ser Cys
                        75           80           85
ttg gag act ctg gaa aaa gga aag cca ctc gta gtg gtt ata aac gaa      404
Leu Glu Thr Leu Glu Lys Gly Lys Pro Leu Val Val Val Ile Asn Glu
                        90           95           100
aag ttg atg aac aat cat cag ctg gaa ctg gca aag cag cta cac aaa      452
Lys Leu Met Asn Asn His Gln Leu Glu Leu Ala Lys Gln Leu His Lys
                        105           110           115
gag ggt cat ctc ttc tat tgt acc tgc agc acg ctt cct ggg ctg tta      500
Glu Gly His Leu Phe Tyr Cys Thr Cys Ser Thr Leu Pro Gly Leu Leu
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cag
Gln
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135

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Lys Lys Gly Gly Glu Lys Lys Lys Gly Arg Ser Ala Ile Asn Glu Val  
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nta acc cga gaa tac acc atc aac att cac aag cgc atc cat gga gtg 151  
Xaa Thr Arg Glu Tyr Thr Ile Asn Ile His Lys Arg Ile His Gly Val  
25 30 35  
ggc ttc aag aag cgt gca cct cgg gca ctc aaa gag att cgg aaa ttt 199  
Gly Phe Lys Lys Arg Ala Pro Arg Ala Leu Lys Glu Ile Arg Lys Phe  
40 45 50  
gcc atg aag gag atg gga act cca gat gtg cgc att gac acc agg ctc 247  
Ala Met Lys Glu Met Gly Thr Pro Asp Val Arg Ile Asp Thr Arg Leu  
55 60 65  
aac aaa gct gtc tgg gcc aaa gga ata agg tgc waa agt tat ctg tat 295  
Asn Lys Ala Val Trp Ala Lys Gly Ile Arg Cys Xaa Ser Tyr Leu Tyr  
70 75 80  
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Ser Xaa Val Asn Phe Cys Xaa Asp Thr  
85 90

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Lys Lys Gly Gly Glu Lys Lys Lys Gly Arg Ser Ala Ile Asn Glu Val  
5 10 15 20  
gta acc cga gaa tac acc atc aac att cac aag cgc atc cat gga gtg 151  
Val Thr Arg Glu Tyr Thr Ile Asn Ile His Lys Arg Ile His Gly Val

	25		30		35	
ggc ttc aag aag cgt gca cct cgg gca ctc aaa gag att cgg aaa ttt						199
Gly Phe Lys Lys Arg Ala Pro Arg Ala Leu Lys Glu Ile Arg Lys Phe						
	40		45		50	
gcc atg aag gag atg gga act cca gat gtg cgc att gac acc agg ctc						247
Ala Met Lys Glu Met Gly Thr Pro Asp Val Arg Ile Asp Thr Arg Leu						
	55		60		65	
aac aaa gct gtc tgg gcc aaa gga ata agg aat gtg cca tac cga atc						295
Asn Lys Ala Val Trp Ala Lys Gly Ile Arg Asn Val Pro Tyr Arg Ile						
	70		75		80	
cgt gtg cgg ctg tcc aga aaa cgt aat gag gat gaa gat tca cca aat						343
Arg Val Arg Leu Ser Arg Lys Arg Asn Glu Asp Glu Asp Ser Pro Asn						
	85		90		95	100
aag cta tat act ttg ktt acc tat acw gtc aat gtg g						380
Lys Leu Tyr Thr Leu Xaa Thr Tyr Thr Val Asn Val						
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ggc att gtt tca att att aaa agt gtg ggg gca gtg ggc gga aca aac	95
Gly Ile Val Ser Ile Ile Lys Ser Val Gly Ala Val Gly Gly Thr Asn	
	20 25 30
gcg ccg act aca gag gct gga cgt aag ctt agc ggt ggc gcg cgt gcg	143
Ala Pro Thr Thr Glu Ala Gly Arg Lys Leu Ser Gly Gly Ala Arg Ala	
	35 40 45
cag cgc cgg ccc gag ttg cca aaa caa agg gga ttt ggt gat gga ggc	191
Gln Arg Arg Pro Glu Leu Pro Lys Gln Arg Gly Phe Gly Asp Gly Gly	
	50 55 60
ttt gtt aga agg aat aca aaa tcg agg gca tgg tgg ggg att ttt gac	239
Phe Val Arg Arg Asn Thr Lys Ser Arg Ala Trp Trp Gly Ile Phe Asp	
	65 70 75
atc ttg cga asa gaa cta cag gag ctc atg aaa cag att gac ata atg	287
Ile Leu Arg Xaa Glu Leu Gln Glu Leu Met Lys Gln Ile Asp Ile Met	
	80 85 90 95
gtg gct cat aaa aaa tct gaa tgg gaa gga cgg tac aca	326
Val Ala His Lys Lys Ser Glu Trp Glu Gly Arg Tyr Thr	
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<220>  
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 <222> 194..496

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 tggaggccag ttctggagct attgcagcct cggttgcccg gccggggacc cgagccgaaa 180  
 agttatcgtc aga atg tcg ggc aaa gac cga att gaa atc ttt ccc tcg 229  
 Met Ser Gly Lys Asp Arg Ile Glu Ile Phe Pro Ser  
 1 5 10  
 cga atg gca cag acc atc atg aag gct cgt tta aag gga gca cag aca 277  
 Arg Met Ala Gln Thr Ile Met Lys Ala Arg Leu Lys Gly Ala Gln Thr  
 15 20 25  
 ggt cga aac ctg ctg aag aaa aaa tct gat gcc tta act ctt cga ttt 325  
 Gly Arg Asn Leu Leu Lys Lys Lys Ser Asp Ala Leu Thr Leu Arg Phe  
 30 35 40  
 cga cag atc cta aag aag ata ata gag act aaa atg ttg atg ggc gaa 373  
 Arg Gln Ile Leu Lys Lys Ile Ile Glu Thr Lys Met Leu Met Gly Glu  
 45 50 55 60  
 gtg atg aga gaa gct gcc ttt tca cta gct gaa gcc aag ttc aca gca 421  
 Val Met Arg Glu Ala Ala Phe Ser Leu Ala Glu Ala Lys Phe Thr Ala  
 65 70 75  
 ggt gac ttc agc act aca gtt atc caa aat gtc aat aaa gcg caa gtg 469  
 Gly Asp Phe Ser Thr Thr Val Ile Gln Asn Val Asn Lys Ala Gln Val  
 80 85 90  
 aag att cga gcg aag aaa gat aat gta g 497  
 Lys Ile Arg Ala Lys Lys Asp Asn Val  
 95 100

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 Met Val Leu Trp  
 1  
 aaa gtt gtg ttc aac cga gac aaa caa gga gag tat cgg ttc agc acc 165  
 Lys Val Val Phe Asn Arg Asp Lys Gln Gly Glu Tyr Arg Phe Ser Thr  
 5 10 15 20  
 aca cag cca ccg cag gag tca gtg gat cgg tgg gga aaa tgc tgc tta 213  
 Thr Gln Pro Pro Gln Glu Ser Val Asp Arg Trp Gly Lys Cys Cys Leu  
 25 30 35  
 ccc tgg gcc ctg ggc tgt aga aag aag aca cca aag gca aag tac atg 261

Pro Trp Ala Leu Gly Cys Arg Lys Lys Thr Pro Lys Ala Lys Tyr Met  
 40 45 50

tat ctg gcg cag gag ctc ttg gtt gat cca gaa tgg cc 299

Tyr Leu Ala Gln Glu Leu Leu Val Asp Pro Glu Trp  
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<210> 803

<211> 488

<212> DNA

<213> Homo sapiens

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<222> 214..486

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 ggtagtgggc cacaagcccc cagtccaga ggcgtgattt tctggcatcc ttaaactctg 180  
 tgtcaaggat tggttataat ataaccagaa acc atg acg gcg gct gag aac gta 234

Met Thr Ala Ala Glu Asn Val

1 5  
 tgc tac acg tta att aac gtg cca atg gat tca gaa cca cca tct gaa 282  
 Cys Tyr Thr Leu Ile Asn Val Pro Met Asp Ser Glu Pro Pro Ser Glu

10 15 20  
 att agc tta aaa aat gat cta gaa aaa gga gat gta aag tca aag act 330  
 Ile Ser Leu Lys Asn Asp Leu Glu Lys Gly Asp Val Lys Ser Lys Thr  
 25 30 35

gaa gct ttg aag aaa gta atc att atg att ctg aat ggt gaa aaa ctt 378  
 Glu Ala Leu Lys Lys Val Ile Ile Met Ile Leu Asn Gly Glu Lys Leu  
 40 45 50 55

cct gga ctt ctg atg acc atc att cgt ttt gtg cta cct ctt cag gat 426  
 Pro Gly Leu Leu Met Thr Ile Ile Arg Phe Val Leu Pro Leu Gln Asp  
 60 65 70

cac act atc aag aaa tta ctt ctn gka ttt tgg gaa att gtt cct aaa 474  
 His Thr Ile Lys Lys Leu Leu Leu Xaa Phe Trp Glu Ile Val Pro Lys  
 75 80 85

aca act cca gat gg 488  
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<211> 453

<212> DNA

<213> Homo sapiens

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<222> 179..451

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gattttctgg catccttaaa tcttgtgtca aggattggtt ataataaac cagaaacc 178  
atg acg gcg gct gag aac gta tgc tac acg tta att aac gtg cca atg 226  
Met Thr Ala Ala Glu Asn Val Cys Tyr Thr Leu Ile Asn Val Pro Met  
1 5 10 15  
gat tca gaa cca cca tct gaa att agc tta aaa aat gat cta gaa aaa 274  
Asp Ser Glu Pro Pro Ser Glu Ile Ser Leu Lys Asn Asp Leu Glu Lys  
20 25 30  
gga gat gta aag tca aag act gaa gct ttg aag aaa gta atc att atg 322  
Gly Asp Val Lys Ser Lys Thr Glu Ala Leu Lys Lys Val Ile Ile Met  
35 40 45  
att ctg aat ggt gaa aaa ctt cct gga ctt ctg atg acc atc att cgt 370  
Ile Leu Asn Gly Glu Lys Leu Pro Gly Leu Leu Met Thr Ile Ile Arg  
50 55 60  
ttt gtg cta cct ctt cag gat cac act atc aag aaa tta ctt ctn gka 418  
Phe Val Leu Pro Leu Gln Asp His Thr Ile Lys Lys Leu Leu Leu Xaa  
65 70 75 80  
ttt tgg gaa att gtt cct aaa aca act cca gat gg 453  
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<212> DNA  
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<222> 70..444

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atctgtgaa atg cag tta aca cat cag ctg gac cta ttt ccc gaa tgc agg 111  
Met Gln Leu Thr His Gln Leu Asp Leu Phe Pro Glu Cys Arg  
1 5 10  
gta acc ctt ctg tta ttt aaa gat gta aaa aat gcg gga gac ttg aga 159  
Val Thr Leu Leu Leu Phe Lys Asp Val Lys Asn Ala Gly Asp Leu Arg  
15 20 25 30  
aga aag gcc atg gaa ggc acc atc gat gga tca ctg ata aat cct aca 207  
Arg Lys Ala Met Glu Gly Thr Ile Asp Gly Ser Leu Ile Asn Pro Thr  
35 40 45  
gtg att gtt gat cca ttt cag ata ctt gtg gca gca aac aaa gca gtt 255  
Val Ile Val Asp Pro Phe Gln Ile Leu Val Ala Ala Asn Lys Ala Val  
50 55 60  
cac ctc tac aaa ctg gga aaa atg aag aca aga act cta tct act gaa 303  
His Leu Tyr Lys Leu Gly Lys Met Lys Thr Arg Thr Leu Ser Thr Glu  
65 70 75  
att att ttc aac ctt tcc cca aat aac aat att tca gag gct ttg aaa 351  
Ile Ile Phe Asn Leu Ser Pro Asn Asn Asn Ile Ser Glu Ala Leu Lys  
80 85 90  
aaa ttt ggt atc tca gca aat gac act tca att cta att gtt tac att 399  
Lys Phe Gly Ile Ser Ala Asn Asp Thr Ser Ile Leu Ile Val Tyr Ile  
95 100 105 110

gaa gag gga gaa aaa caa ata aat caa gaa tac cta ata tct caa g 445  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 76..414

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 Met Glu Thr Ala Pro Lys Pro Gly Lys Asp Val Pro  
 1 5 10  
 ccc aag aaa gac aaa ctt cag acc aag aga aag aaa ccg ccg cga tac 159  
 Pro Lys Lys Asp Lys Leu Gln Thr Lys Arg Lys Lys Pro Arg Arg Tyr  
 15 20 25  
 tgg gag gaa gag acc gtt ccg acc aca gcc gga gcc tct cca ggg cct 207  
 Trp Glu Glu Glu Thr Val Pro Thr Thr Ala Gly Ala Ser Pro Gly Pro  
 30 35 40  
 cct cgt aac aag aag aat ccg gag ctc cgt cct cag aga cca aaa aat 255  
 Pro Arg Asn Lys Lys Asn Arg Glu Leu Arg Pro Gln Arg Pro Lys Asn  
 45 50 55 60  
 gct tac atc tta aag aag tct ccg atc tct aag aag cct cag gtc ccg 303  
 Ala Tyr Ile Leu Lys Lys Ser Arg Ile Ser Lys Lys Pro Gln Val Pro  
 65 70 75  
 aag aaa ccc cga gaa tgg aag aac ccg gag tcc cag cgc ggc ttg tcc 351  
 Lys Lys Pro Arg Glu Trp Lys Asn Pro Glu Ser Gln Arg Gly Leu Ser  
 80 85 90  
 ggg gcc caa gat cca ttc cca ggc ccc rcc ccc gtc cct gtg gaa gtg 399  
 Gly Ala Gln Asp Pro Phe Pro Gly Pro Xaa Pro Val Pro Val Glu Val  
 95 100 105  
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 Val Gln Lys Phe Cys  
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<210> 807  
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 <212> DNA  
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<220>  
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Glu	Arg	Leu	Tyr	Gln	Xaa	Lys	Asp	Gly	Ser	Gln	Arg	Gly	Gly	Ile	Phe	
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agc	cag	ttt	gca	aat	cag	aat	ctg	agc	aag	aaa	atc	cct	gga	gtg	aaa	465
Ser	Gln	Phe	Ala	Asn	Gln	Asn	Leu	Ser	Lys	Lys	Ile	Pro	Gly	Val	Lys	
85				90					95					100		
ctc	tgt	gaa	agc	att	gta	tat	gga	gaa	gtc							495
Leu	Cys	Glu	Ser	Ile	Val	Tyr	Gly	Glu	Val							
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 <212> DNA  
 <213> Homo sapiens

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accctgacta	cgggagttgg	gaggaccg	gacaccgcac	agccrggaa	atg gac tcr		178								
					Met Asp Ser										
					1										
gtg gcm	ttt gag	gat gtr	gmt gtg	aac ttc	acc cak	gag gag	tgg gct								
Val Ala	Phe Glu	Asp Val	Xaa Val	Asn Phe	Thr Xaa	Glu Glu	Trp Ala								
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Leu Leu	Xaa Pro	Ser Gln	Lys Asn	Leu Tyr	Arg Asp	Val Met	Trp Glu								
20		25		30		35									
acc atg	agg aat	ctg gcc	tct ata	ggg aaa	aaa tgg	aag gac	cag aac								
Thr Met	Arg Asn	Leu Ala	Ser Ile	Gly Lys	Lys Trp	Lys Asp	Gln Asn								
		40		45		50									
att aaa	gat cac	tac aaa	cac cga	ggg aga	aat cta	aga agt	cat atg								
Ile Lys	Asp His	Tyr Lys	His Arg	Gly Arg	Asn Leu	Arg Ser	His Met								
	55		60		65										
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Leu Glu	Arg Leu	Tyr Gln	Xaa Lys	Asp Gly	Ser Gln	Arg Gly	Gly Ile								
70			75		80										
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Phe Ser	Gln Phe	Ala Asn	Gln Asn	Leu Ser	Lys Lys	Ile Pro	Gly Val								
85		90		95											
aaa ctc	tgt gaa	agc att	gta tat	gga gaa	gtc										
Lys Leu	Cys Glu	Ser Ile	Val Tyr	Gly Glu	Val		499								
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gctccagccc caggaaggac ccaggacacc cggaagccgg aa atg gac tca gtg 174  
Met Asp Ser Val

gcc ttt gag gat gtg gct gtg aac ttc acc cag gag gag tgg gct ttg 222  
Ala Phe Glu Asp Val Ala Val Asn Phe Thr Gln Glu Glu Trp Ala Leu  
5 10 15 20

ctg agt cct tcc cag aag aat ctc tac aga gat gtg acg ctg gaa acc 270  
Leu Ser Pro Ser Gln Lys Asn Leu Tyr Arg Asp Val Thr Leu Glu Thr  
25 30 35

ttc agg aac ctg gcc tcg gtc gga atc caa tgg aaa gac cag gac att 318  
Phe Arg Asn Leu Ala Ser Val Gly Ile Gln Trp Lys Asp Gln Asp Ile  
40 45 50

gag aat ctg tac caa aac ctg ggg att aag cta aga agt ctg gtg gag 366  
Glu Asn Leu Tyr Gln Asn Leu Gly Ile Lys Leu Arg Ser Leu Val Glu  
55 60 65

aga c  
Arg 370

<210> 811

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 162..431

<400> 811

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ttgacgcgtc aggttgctgt acccctgcat cggatgcgct gtaccctgcg ctggctccgt 120  
gaaccttagg gacaacaccg ggacaccgc gaggccgaa a atg gac tca gtg gct 176  
Met Asp Ser Val Ala

ttt gag gat gtg tct gtg agc ttc agc cag gag gag tgg gct ctg ctg 224  
Phe Glu Asp Val Ser Val Ser Phe Ser Gln Glu Glu Trp Ala Leu Leu  
10 15 20

gct cct tcw yag aag aaa ctc tac aga gat gtg atg cag gaa aca ttc 272  
Ala Pro Ser Xaa Lys Lys Leu Tyr Arg Asp Val Met Gln Glu Thr Phe  
25 30 35

aag aac ctg gca tct ata ggg gaa aaa tgg gaa gac ccg aat gtt gaa 320  
Lys Asn Leu Ala Ser Ile Gly Glu Lys Trp Glu Asp Pro Asn Val Glu  
40 45 50

gat caa cac aaa aac caa gga cga aat cta aga agc cat acg gga gag 368  
Asp Gln His Lys Asn Gln Gly Arg Asn Leu Arg Ser His Thr Gly Glu  
55 60 65

aga ctc tgt gaa ggt aaa gaa ggt agt caa tgt gca gaa aac ttc agt 416  
Arg Leu Cys Glu Gly Lys Glu Gly Ser Gln Cys Ala Glu Asn Phe Ser

70                      75                      80                      85                      431  
ccc aat ctc agt gtg  
Pro Asn Leu Ser Val  
90

<210> 812  
<211> 338  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 107..337

<400> 812  
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gacctgggttc ctctgcccag gcttctgtca ctctgtcacc tacgct atg ccc tgc 115  
Met Pro Cys  
1  
tgt agt cac agg agg tgt aga gag gmc ccc ggg aca tct gaa agc cag 163  
Cys Ser His Arg Arg Cys Arg Glu Xaa Pro Gly Thr Ser Glu Ser Gln  
5 10 15  
gaa atg gac cca gtg gcc ttt gat gat gtt gct gtg aac ttc acc cag 211  
Glu Met Asp Pro Val Ala Phe Asp Asp Val Ala Val Asn Phe Thr Gln  
20 25 30 35  
gag gag tgg gct ttg ctg gat att tcc cag agg aaa ctc tac aag gaa 259  
Glu Glu Trp Ala Leu Leu Asp Ile Ser Gln Arg Lys Leu Tyr Lys Glu  
40 45 50  
gtg atg ctg gaa act ttc agg aac ctg acc tct gta gga aaa agt tgg 307  
Val Met Leu Glu Thr Phe Arg Asn Leu Thr Ser Val Gly Lys Ser Trp  
55 60 65  
aaa gac cag aac att gaa tat gag tac caa a 338  
Lys Asp Gln Asn Ile Glu Tyr Glu Tyr Gln  
70 75

<210> 813  
<211> 411  
<212> DNA  
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<220>  
<221> CDS  
<222> 84..410

<400> 813  
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tctgttacct aaagcaataa aaa atg gcc aga gga tca gtg tcc gat gag gaa 113  
Met Ala Arg Gly Ser Val Ser Asp Glu Glu  
1 5 10  
atg atg gag ctc aga gaa gct ttt gcc aaa gtt gat act gat ggc aat 161  
Met Met Glu Leu Arg Glu Ala Phe Ala Lys Val Asp Thr Asp Gly Asn  
15 20 25

004220"666ET560

gga tac atc agc ttc aat gag ttg aat gac ttg ttc aag gct gct tgc	209
Gly Tyr Ile Ser Phe Asn Glu Leu Asn Asp Leu Phe Lys Ala Ala Cys	
30 35 40	
ttg cct ttg cct ggg tat aga gta cga gan att aca gaa aac ctg atg	257
Leu Pro Leu Pro Gly Tyr Arg Val Arg Xaa Ile Thr Glu Asn Leu Met	
45 50 55	
gct aca ggt gat ctg gac caa gat gga agg atc agc ttt gat gag ttt	305
Ala Thr Gly Asp Leu Asp Gln Asp Gly Arg Ile Ser Phe Asp Glu Phe	
60 65 70	
atc rag att ttc cat ggc cta aaa agc aca gat gtt gcc aag acc ttt	353
Ile Xaa Ile Phe His Gly Leu Lys Ser Thr Asp Val Ala Lys Thr Phe	
75 80 85 90	
aga raa gcr atc aat aag aag gaw ggg att tgt gca atc ggt ggt act	401
Arg Xaa Ala Ile Asn Lys Lys Xaa Gly Ile Cys Ala Ile Gly Gly Thr	
95 100 105	
tca gag cag t	
Ser Glu Gln	411

<210> 814  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 121..453

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cccgcgaccc ggagcagctc ggaggcgggtg aataatagct cttcaagtct gcaataaaaa	120
atg gcc tcc aac aaa act aca ttg caa aaa atg gga aaa aaa cag aat	168
Met Ala Ser Asn Lys Thr Thr Leu Gln Lys Met Gly Lys Lys Gln Asn	
1 5 10 15	
gga aag agt aaa aaa gtt gaa gag gca gag cct gaa gaa ttt gtc gtg	216
Gly Lys Ser Lys Lys Val Glu Glu Ala Glu Pro Glu Glu Phe Val Val	
20 25 30	
gaa aaa gta cta gat cga cgt gta gtg aat ggg aaa gtg gaa tat ttc	264
Glu Lys Val Leu Asp Arg Arg Val Val Asn Gly Lys Val Glu Tyr Phe	
35 40 45	
ctg aag tgg aag gga ttt aca gat gct gac aat act tgg gaa cct gaa	312
Leu Lys Trp Lys Gly Phe Thr Asp Ala Asp Asn Thr Trp Glu Pro Glu	
50 55 60	
gaa aat tta gat tgt cca gaa ttg att gaa gcg ttt ctt aac tct cag	360
Glu Asn Leu Asp Cys Pro Glu Leu Ile Glu Ala Phe Leu Asn Ser Gln	
65 70 75 80	
aaa gct ggc aaa gaa aaa gat ggt aca aaa aga aaa tct tta tct gac	408
Lys Ala Gly Lys Glu Lys Asp Gly Thr Lys Arg Lys Ser Leu Ser Asp	
85 90 95	
agt gaa tct gat gac agc aaa tca aag aag aaa aga gat gct gct g	454
Ser Glu Ser Asp Asp Ser Lys Ser Lys Lys Arg Asp Ala Ala	
100 105 110	

<210> 815

<211> 719  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 347..718

<400> 815  
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 tgaaggaggc tgggataact agcttgaaag aaattcagtc tagttataga catctttggc 120  
 attaactctga tgtttactag tgatatctca tgctaggcag ttatgctttg cttctagggg 180  
 cttctctttt taaaacaaaa gaaagctctt ttcgttttct gtgtgctgca tgctccagtg 240  
 tgtgtgttta caccatcggg tcttctccct ctagagatta gcataactcc ctttgctgtt 300  
 ggattgttat tttgagcaat atgttttgga aagggttggtt ttcatac atg agt gca 355  
 Met Ser Ala

1  
 cgc aaa tca tca gat gca tct gct tgc tcc tct tca gaa ata tct gtg 403  
 Arg Lys Ser Ser Asp Ala Ser Ala Cys Ser Ser Ser Glu Ile Ser Val  
 5 10 15  
 aaa gag ttt cta gcc aaa gcc aaa gaa gac ttt ttg aaa aaa tgg gag 451  
 Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu  
 20 25 30 35  
 aat cca act cag aat aat gcc gga ctt gaa gat ttt gaa agg aaa aaa 499  
 Asn Pro Thr Gln Asn Asn Ala Gly Leu Glu Asp Phe Glu Arg Lys Lys  
 40 45 50  
 acc ctt gga aca ggt tca ttt gga aga gtc atg ttg gta aaa cac aaa 547  
 Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys  
 55 60 65  
 gcc act gan ngg tat tat gcc atg aag atc tta gat aag cag aag gtt 595  
 Ala Thr Xaa Xaa Tyr Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val  
 70 75 80  
 gtt aaa ctg aag caa ata gag cat act ttg aat gag aaa aga ata tta 643  
 Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu  
 85 90 95  
 cag gca gtg aat ttt cct ttc ctt gtt cga ctg gag tat gct ttt aag 691  
 Gln Ala Val Asn Phe Pro Phe Leu Val Arg Leu Glu Tyr Ala Phe Lys  
 100 105 110 115  
 gat aat tct aat twa tac atg gtt atg g 719  
 Asp Asn Ser Asn Xaa Tyr Met Val Met  
 120

<210> 816  
 <211> 312  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 109..312

<400> 816

acacagcatt ttaatatcag tgaggtccac agctagcagt aagagctggt gtaattgaaa 60  
gacgttttagg tgcaatcatt ctgctgtttg ctccttgcca gggtcaac atg gga ttg 117  
Met Gly Leu  
1  
tca cgc aaa tca tca gat gca tct gct tgc tcc tct tca gaa ata tct 165  
Ser Arg Lys Ser Ser Asp Ala Ser Ala Cys Ser Ser Ser Glu Ile Ser  
5 10 15  
gtg aaa gag ttt cta gcc aaa gcc aaa gaa gac ttt ttg aaa aaa tgg 213  
Val Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp  
20 25 30 35  
gag aat cca act cag aat aat gcc gga ctt gaa gat ttt gaa agg aaa 261  
Glu Asn Pro Thr Gln Asn Asn Ala Gly Leu Glu Asp Phe Glu Arg Lys  
40 45 50  
aaa acc ctt gga aca ggt tca ttt gga aga gtc atg ttg gta aaa cac 309  
Lys Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His  
55 60 65  
aaa  
Lys 312

<210> 817  
<211> 371  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 110..370

<400> 817  
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gggagcctgg gtgtgcgtgt ggagtccgga ctcgtgkabb acgatcgcg atg aac acg 118  
Met Asn Thr  
1  
gtc ggg acc tgg aga ctg ttg cag tkg aat agg gca gct act ggg aag 166  
Val Gly Thr Trp Arg Leu Leu Gln Xaa Asn Arg Ala Ala Thr Gly Lys  
5 10 15  
atg gag atg gag atg gag cag gtg ttt gag atg aag gtc aaa gaa aaa 214  
Met Glu Met Glu Met Glu Gln Val Phe Glu Met Lys Val Lys Glu Lys  
20 25 30 35  
gtt caa aaa ctg aag gac tct gaa gct gag ctc cag cgn cgc cat gag 262  
Val Gln Lys Leu Lys Asp Ser Glu Ala Glu Leu Gln Arg Arg His Glu  
40 45 50  
caa atg aaa aag aat ttg gaa gca cag cac aaa gaa ttg gag gaa aaa 310  
Gln Met Lys Lys Asn Leu Glu Ala Gln His Lys Glu Leu Glu Glu Lys  
55 60 65  
cgt cgt cag tkc gag gat gag aaa gca aac tgg gaa gct caa caa cgt 358  
Arg Arg Gln Xaa Glu Asp Glu Lys Ala Asn Trp Glu Ala Gln Gln Arg  
70 75 80  
att tta gaa caa c  
Ile Leu Glu Gln 371  
85

<210> 818

<211> 568  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 28..567

<400> 818  
 aaagtaaagc ggaggcagcg ggggaag atg gcg gcg gcc gtt cca cag cgg gcg 54  
 Met Ala Ala Ala Val Pro Gln Arg Ala  
 1 5  
 tgg acc gtg gag cag ctg cgc agt gag cag ctg ccc aag aag gac att 102  
 Trp Thr Val Glu Gln Leu Arg Ser Glu Gln Leu Pro Lys Lys Asp Ile  
 10 15 20 25  
 atc aag ttt ctg cag gaa cac ggt tca gat tcg gct gga gtg cag trg 150  
 Ile Lys Phe Leu Gln Glu His Gly Ser Asp Ser Ala Gly Val Gln Xaa  
 30 35 40  
 cgc gat ctc ggc tca ctg caa cct ccg cct ccc ggg ttc aaa cga ttc 198  
 Arg Asp Leu Gly Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe  
 45 50 55  
 tcc tgc ctc tgc ctc tcg agt agc tgg gac tac agg cgc gtg cca cca 246  
 Ser Cys Leu Cys Leu Ser Ser Ser Trp Asp Tyr Arg Arg Val Pro Pro  
 60 65 70  
 cgc cag trt ctt gca gaa cat aaa tta tta gga aac att aaa aat gtg 294  
 Arg Gln Xaa Leu Ala Glu His Lys Leu Leu Gly Asn Ile Lys Asn Val  
 75 80 85  
 gcc aag aca gct aac aag gac cac ttg gtt aca gcc tat aac cat ctt 342  
 Ala Lys Thr Ala Asn Lys Asp His Leu Val Thr Ala Tyr Asn His Leu  
 90 95 100 105  
 ttt gaa act aag cgt ttt aag ggt act gaa agt ata agt aaa gtg tct 390  
 Phe Glu Thr Lys Arg Phe Lys Gly Thr Glu Ser Ile Ser Lys Val Ser  
 110 115 120  
 gag caa gta aaa aat gtg aag ctt aat gaa gat aaa ccc aaa gaa acc 438  
 Glu Gln Val Lys Asn Val Lys Leu Asn Glu Asp Lys Pro Lys Glu Thr  
 125 130 135  
 aag tct gaa gag acc ctg gat gag ggt cca cca aaa tat act aaa tct 486  
 Lys Ser Glu Glu Thr Leu Asp Glu Gly Pro Pro Lys Tyr Thr Lys Ser  
 140 145 150  
 gtt mtg aaa aag gga gat aaa cca act ttc cca aaa agg gag atg ttg 534  
 Val Xaa Lys Lys Gly Asp Lys Pro Thr Phe Pro Lys Arg Glu Met Leu  
 155 160 165  
 ttc act gct ggt ata cag gra cac tac aag atg g 568  
 Phe Thr Ala Gly Ile Gln Xaa His Tyr Lys Met  
 170 175 180

<210> 819  
 <211> 489  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 138..488

<400> 819

ggctgggtttg gatccgggtc agtcgggkgc cgagatttgg gagagacgct ctgaactgac 60  
tgccccgcat caccggagcg tcccagctgc gaggagtgtg aacaggaaca tcgataagta 120  
gtgtaaaaac ttgcaca atg aaa tcc gaa gcc aag gat gga gag gag gag 170  
Met Lys Ser Glu Ala Lys Asp Gly Glu Glu Glu  
1 5 10  
agt cta cag act gct ttc aaa aaa tta aga gtg gat gca tca ggg tct 218  
Ser Leu Gln Thr Ala Phe Lys Lys Leu Arg Val Asp Ala Ser Gly Ser  
15 20 25  
gta gca tct ctg tct gtt gga gaa ggc aca ggt gtc aga gca cca gtc 266  
Val Ala Ser Leu Ser Val Gly Glu Gly Thr Gly Val Arg Ala Pro Val  
30 35 40  
aga aca gca aca gat gat acc aaa cct aaa acc aca tgt gca tct aaa 314  
Arg Thr Ala Thr Asp Asp Thr Lys Pro Lys Thr Thr Cys Ala Ser Lys  
45 50 55  
gac agt tgg cac ggg tct aca agg aag tct tca cga gga gca gtg aga 362  
Asp Ser Trp His Gly Ser Thr Arg Lys Ser Ser Arg Gly Ala Val Arg  
60 65 70 75  
act cag cgt cgt cga cgt tct aag tct cct gtc ctt cat cct cca aag 410  
Thr Gln Arg Arg Arg Arg Ser Lys Ser Pro Val Leu His Pro Pro Lys  
80 85 90  
ttt ata cat tgc agt aca ata gcg tct tct tcc agc agt caa ctc aag 458  
Phe Ile His Cys Ser Thr Ile Ala Ser Ser Ser Ser Ser Gln Leu Lys  
95 100 105  
cac aaa ags cag act gnc tca cct gat ggc a 489  
His Lys Xaa Gln Thr Xaa Ser Pro Asp Gly  
110 115

<210> 820

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 25..471

<400> 820

gaggggacgg ggtccgactc agaa atg gcg gcc tcc atg ttc tac ggc agg 51  
Met Ala Ala Ser Met Phe Tyr Gly Arg  
1 5  
cta gtg gcc gtg gcc acc ctt cgg aac cac cgg cct cgg acg gcc cag 99  
Leu Val Ala Val Ala Thr Leu Arg Asn His Arg Pro Arg Thr Ala Gln  
10 15 20 25  
cgg gct gct gct cag gtt ctg gga agt tct gga ttg ttt aat aac cat 147  
Arg Ala Ala Ala Gln Val Leu Gly Ser Ser Gly Leu Phe Asn Asn His  
30 35 40  
gga ctc caa gta cag cag caa cag caa agg aat ctc tca cta cat gaa 195  
Gly Leu Gln Val Gln Gln Gln Gln Arg Asn Leu Ser Leu His Glu  
45 50 55



tac atg agt atg gaa tta ttg caa gaa gct ggt gtc tcc gtt ccc aaa	243
Tyr Met Ser Met Glu Leu Leu Gln Glu Ala Gly Val Ser Val Pro Lys	
60 65 70	
gga tat gtg gca aag tca cca gat gaa gct tat gca att gcc aaa aaa	291
Gly Tyr Val Ala Lys Ser Pro Asp Glu Ala Tyr Ala Ile Ala Lys Lys	
75 80 85	
tta ggt tca aaa gat gtc gtg ata aag gca cag gtt tta gct ggt ggt	339
Leu Gly Ser Lys Asp Val Val Ile Lys Ala Gln Val Leu Ala Gly Gly	
90 95 100 105	
aga gga aaa gga aca ttt gaa agt ggc ctc aaa gga gga gtg aag ata	387
Arg Gly Lys Gly Thr Phe Glu Ser Gly Leu Lys Gly Gly Val Lys Ile	
110 115 120	
gtt ttc tct cca gaa gaa gca aaa gct gtt tct tca caa atg att ggg	435
Val Phe Ser Pro Glu Glu Ala Lys Ala Val Ser Ser Gln Met Ile Gly	
125 130 135	
aaa aaa ttg ttt acc aag caa acg gga gaa agg gca	471
Lys Lys Leu Phe Thr Lys Gln Thr Gly Glu Arg Ala	
140 145	

<210> 821  
 <211> 504  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 163..504

<400> 821	
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gccccgctc ctccccgcc cagcgaastc tctgaccacc ctcttttcta gagttctgcc	120
tcgcttcccg gcgcggtcgc agccctcagc ccacttagga ta atg gcg aca gct	174
Met Ala Thr Ala	
1	
gag gta ctg aac att ggt aaa aaa tta tat gag ggt aaa aca aaa gaa	222
Glu Val Leu Asn Ile Gly Lys Lys Leu Tyr Glu Gly Lys Thr Lys Glu	
5 10 15 20	
gtc tac gaa ttg tta gac agt cca gga aaa gtc ctc ctg cag tcc aag	270
Val Tyr Glu Leu Leu Asp Ser Pro Gly Lys Val Leu Leu Gln Ser Lys	
25 30 35	
gac cag att aca gca gga aat gca gct aga aaa aac cac ctg gaa gga	318
Asp Gln Ile Thr Ala Gly Asn Ala Ala Arg Lys Asn His Leu Glu Gly	
40 45 50	
aaa gct gca atc tca aat aaa atc acc agt tgt att ttt cag tta tta	366
Lys Ala Ala Ile Ser Asn Lys Ile Thr Ser Cys Ile Phe Gln Leu Leu	
55 60 65	
cag gaa gca ggt att aaa act gcc ttc acc aga aaa tgt ggg gag acw	414
Gln Glu Ala Gly Ile Lys Thr Ala Phe Thr Arg Lys Cys Gly Glu Thr	
70 75 80	
kct ttc att gca ccg cag tgt gaa atg att cca att gaa tgg gtt tgc	462
Xaa Phe Ile Ala Pro Gln Cys Glu Met Ile Pro Ile Glu Trp Val Cys	
85 90 95 100	
aga aga ata gca act ggt tct ttt ctc aaa aga aat cct ggt	504

Arg Arg Ile Ala Thr Gly Ser Phe Leu Lys Arg Asn Pro Gly  
 105 110

<210> 822  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 42..380

<400> 822  
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 Met Arg Asn Ser Tyr  
 1 5  
 aga ttt ctg gca tcc tct ctc tca gtt gtc gtt tct ctc ctg cta att 104  
 Arg Phe Leu Ala Ser Ser Leu Ser Val Val Ser Leu Leu Leu Ile  
 10 15 20  
 cct gaa gat gtc tgt gaa aaa att att gga gga aat gaa gta act cct 152  
 Pro Glu Asp Val Cys Glu Lys Ile Ile Gly Gly Asn Glu Val Thr Pro  
 25 30 35  
 cat tca aga ccc tac atg gtc cta ctt agt ctt gac aga aaa acc atc 200  
 His Ser Arg Pro Tyr Met Val Leu Leu Ser Leu Asp Arg Lys Thr Ile  
 40 45 50  
 tgt gct ggg gct ttg att gca aaa gac tgg gtg ttg act gca gct cac 248  
 Cys Ala Gly Ala Leu Ile Ala Lys Asp Trp Val Leu Thr Ala Ala His  
 55 60 65  
 tgt aac ttg aac aaa agg tcc cag gtc att ctt ggg gct cac tca ata 296  
 Cys Asn Leu Asn Lys Arg Ser Gln Val Ile Leu Gly Ala His Ser Ile  
 70 75 80 85  
 acc agg gaa gag cca aca aaa cag ata atg ctt gtt aag aaa gag ttt 344  
 Thr Arg Glu Glu Pro Thr Lys Gln Ile Met Leu Val Lys Lys Glu Phe  
 90 95 100  
 ccc tat cca tgc tat gac cca gcc aca cgc gaa ggt g 381  
 Pro Tyr Pro Cys Tyr Asp Pro Ala Thr Arg Glu Gly  
 105 110

<210> 823  
 <211> 661  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 381..659

<400> 823  
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 ctgagagcgg gccgaggaga ttggcgacgg tgctgccgtg ttttcgttg cgggtgcctg 120  
 ggctgggtggg aacagccgcc cgaaggaagc accatgattt cggccgcgca gttgttgat 180  
 gagttaatgg gccgggaccg aaacctagcc ccggacgaga agcgcasaac gtgcggtggg 240

**SECRET**

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 189..392

<400> 825  
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gtctgccgtg gacagcgaas tgctgcggtt cctgagccgg agggcgagtg cctgtgaaga 120  
aaacggggta ttgccctgag gcttatattc tgcctcagtt gtcttttctt gaaatattat 180  
aatcaga atg tct gca cag tca gtg gaa gaa gat tca ata ctt atc atc 230  
Met Ser Ala Gln Ser Val Glu Glu Asp Ser Ile Leu Ile Ile  
1 5 10  
cca act cca gat gaa gag gaa aaa att ctg aga gtg aag ttg gag gag 278  
Pro Thr Pro Asp Glu Glu Glu Lys Ile Leu Arg Val Lys Leu Glu Glu  
15 20 25 30  
gat cct gat ggc gaa gag gga tca agt atc ccc tgg aac cat ctc cca 326  
Asp Pro Asp Gly Glu Glu Gly Ser Ser Ile Pro Trp Asn His Leu Pro  
35 40 45  
gac cca gag att ttc cga cag cga ttc agg cag ttt gga tac cag gat 374  
Asp Pro Glu Ile Phe Arg Gln Arg Phe Arg Gln Phe Gly Tyr Gln Asp  
50 55 60  
tca mmt ggg ccc cgt gag g 393  
Ser Xaa Gly Pro Arg Glu  
65

<210> 826  
<211> 445  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 34..444

<400> 826  
gcattctggg gaaggagcag caccaaattcc aag atg gcg gcc agc agg agg ctg 54  
Met Ala Ala Ser Arg Arg Leu  
1 5  
atg aag gag ctt gaa gaa atc cgc aaa tgt ggg atg aaa aac ttc cgt 102  
Met Lys Glu Leu Glu Glu Ile Arg Lys Cys Gly Met Lys Asn Phe Arg  
10 15 20  
aac atc cag gtt gat gaa gct aat tta ttg act tgg caa ggg ctt att 150  
Asn Ile Gln Val Asp Glu Ala Asn Leu Leu Thr Trp Gln Gly Leu Ile  
25 30 35  
gtt cct gac aac cct cca tat gat aag gga gcc ttc aga atc gaa atc 198  
Val Pro Asp Asn Pro Pro Tyr Asp Lys Gly Ala Phe Arg Ile Glu Ile  
40 45 50 55  
aac ttt cca gca gag tac cca ttc aaa cca ccg aag atc aca ttt aaa 246  
Asn Phe Pro Ala Glu Tyr Pro Phe Lys Pro Pro Lys Ile Thr Phe Lys  
60 65 70

aca aag atc tat cac cca aac atc gac gaa aag gcn nag gtc tgt ctg 294  
 Thr Lys Ile Tyr His Pro Asn Ile Asp Glu Lys Ala Xaa Val Cys Leu  
 75 80 85  
 cca gta att agt gcc gaa aac tgg aag cca gca acc aaa acc gac caa 342  
 Pro Val Ile Ser Ala Glu Asn Trp Lys Pro Ala Thr Lys Thr Asp Gln  
 90 95 100  
 ggt aag aca tgt gcc tgt gtc ttc ctc gga agg ggt ctw tgg ggg tgc 390  
 Gly Lys Thr Cys Ala Cys Val Phe Leu Gly Arg Gly Leu Trp Gly Cys  
 105 110 115  
 tgc tct ggg gtg ggg gct tct ggt acc aga tca gac aga atc cag aga 438  
 Cys Ser Gly Val Gly Ala Ser Gly Thr Arg Ser Asp Arg Ile Gln Arg  
 120 125 130 135  
 atc ttt c 445  
 Ile Phe  
  
 <210> 827  
 <211> 459  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> 219..458  
  
 <400> 827  
 agccagctag tcaagtgact ctaagaaggg ccattttccc ttgttgtctt tgaaaatact 60  
 tcattttctt agcatttcag gagattataa catcctgtat ttcagtttct gagagcttac 120  
 tgactgattt ccctattcaa aacaatcctc atttcttaca tttctgaaga tctcaagatc 180  
 tggactactg ttgaaaaaat ttccagttag gctcactt atg tct gta aag atg gga 236  
 Met Ser Val Lys Met Gly  
 1 5  
 aaa aaa tac aag aac att gtt cta cta aaa gga tta gag gtc atc aat 284  
 Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val Ile Asn  
 10 15 20  
 gat tat cat ttt aga atg gtt aag tcc tta ctg agc aac gat tta aaa 332  
 Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp Leu Lys  
 25 30 35  
 ctt aat tta aaa atg aga gaa gag tat gac aaa att cag att gct gac 380  
 Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile Ala Asp  
 40 45 50  
 ttg atg gaa gaa aag ttc cga ggt gat gct ggt ttg ggc aaa cta ata 428  
 Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys Leu Ile  
 55 60 65 70  
 aaa att ttc gaa gat ata cca acg ctt gaa g 459  
 Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu  
 75 80  
  
 <210> 828  
 <211> 504  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>

<221> CDS  
<222> 264..503

<400> 828

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ctcaaccaag	gccttttttc	cttggtatct	ttgcagatac	ttcattttct	tagcgtttct	120
ggagattaca	acatcctgcg	gttccgtttc	tggaacttt	actgatttat	ctccccctc	180
acacaaataa	gcattgattc	ctgcatttct	gaagatctca	agatctggac	tactgttgaa	240
aaaatttcca	gtgaggctca	ctt atg tct gta aag atg gga aaa aaa tac aag				293
		Met Ser Val Lys Met Gly Lys Lys Tyr Lys				
		1	5	10		
aac att gtt cta cta aaa gga tta gag gtc atc aat gat tat cat ttt						341
Asn Ile Val Leu Leu Lys Gly Leu Glu Val Ile Asn Asp Tyr His Phe						
	15	20	25			
aga atg gtt aag tcc tta ctg agc aac gat tta aaa ctt aat tta aaa						389
Arg Met Val Lys Ser Leu Leu Ser Asn Asp Leu Lys Leu Asn Leu Lys						
	30	35	40			
atg aga gaa gag tat gac aaa att cag att gct gac ttg atg gaa gaa						437
Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile Ala Asp Leu Met Glu Glu						
	45	50	55			
aag ttc cga ggt gat gct ggt ttg ggc aaa cta ata aaa att ttc gaa						485
Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys Leu Ile Lys Ile Phe Glu						
	60	65	70			
gat ata cca acg ctt gaa g						504
Asp Ile Pro Thr Leu Glu						
	75	80				

<210> 829  
<211> 640  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 400..639

<400> 829

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aaaatacact	gctgagcaga	ggattaaaca	gactcctcac	actaccggaa	gttcagtgca	120
ttttccagga	ttttcaaggc	ttcgatgctg	tcagtgtgag	agtcactat	ccacgtttgt	180
ttatccagga	ataatgcaga	aaatctgagc	attcgtgaat	ctaactattg	agatacttca	240
ttttcttagc	gtttctggag	attacaacat	cctgcgggttc	cgtttctggg	aactttactg	300
atttatctcc	cccctcacac	aaataagcat	tgattcctgc	atttctgaag	atctcaagat	360
ctggactact	gttgaaaaaa	tttccagtga	ggctcactt	atg tct gta aag atg		414
				Met Ser Val Lys Met		
				1	5	
gga aaa aaa tac aag aac att gtt cta cta aaa gga tta gag gtc atc						462
Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val Ile						
	10	15	20			
aat gat tat cat ttt aga atg gtt aag tcc tta ctg agc aac gat tta						510
Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp Leu						
	25	30	35			

aaa ctt aat tta aaa atg aga gaa gag tat gac aaa att cag att gct 558  
 Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile Ala  
           40                          45                          50  
 gac ttg atg gaa gaa aag ttc cga ggt gat gct ggt ttg ggc aaa cta 606  
 Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys Leu  
           55                          60                          65  
 ata aaa att ttc gaa gat ata cca acg ctt gaa g 640  
 Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu  
           70                          75                          80

<210> 830  
 <211> 283  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 10..282

<400> 830  
 gaggattct atg atg gaa tac ctg aag att gca caa gat cta gaa atg tat 51  
           Met Met Glu Tyr Leu Lys Ile Ala Gln Asp Leu Glu Met Tyr  
           1                          5                          10  
 gga gtc aac tat ttt gaa ata aaa aat aaa gga act gaa ttg tgg 99  
 Gly Val Asn Tyr Phe Glu Ile Lys Asn Lys Lys Gly Thr Glu Leu Trp  
           15                          20                          25                          30  
 cta ggt gtt gat gct ttg ggt ctg aat att tat gag cat gac gac aag 147  
 Leu Gly Val Asp Ala Leu Gly Leu Asn Ile Tyr Glu His Asp Asp Lys  
                           35                          40                          45  
 tta aca cct aaa att ggt ttt ccc tgg agt gaa atc aga aat att tca 195  
 Leu Thr Pro Lys Ile Gly Phe Pro Trp Ser Glu Ile Arg Asn Ile Ser  
           50                          55                          60  
 ttt aat gac aaa aaa ttt gtt ata aag cca atc gac aaa aag gca cct 243  
 Phe Asn Asp Lys Lys Phe Val Ile Lys Pro Ile Asp Lys Lys Ala Pro  
           65                          70                          75  
 gat ttt gtg ttt tat gca cct cgt ctg aga atc aat aag c 283  
 Asp Phe Val Phe Tyr Ala Pro Arg Leu Arg Ile Asn Lys  
           80                          85                          90

<210> 831  
 <211> 430  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 125..430

<400> 831  
 atcatcactt ccggttaaccc cgccggccgc cagctccagg agggagaatg ggagaggggc 60  
 aakgaggga cgaagtgaag attgcgtcac grnsgcacat aaagacgtac gaagccgtcg 120  
 ccaa atg aca acg gca aca cga caa gaa gtc ctt ggc ctc tac cgc agc 169

Met Thr Thr Ala Thr Arg Gln Glu Val Leu Gly Leu Tyr Arg Ser  
 1 5 10 15  
 att ttc agg ctt gcg agg aaa tgg cag gcg aca tca ggg cag atg gaa 217  
 Ile Phe Arg Leu Ala Arg Lys Trp Gln Ala Thr Ser Gly Gln Met Glu  
 20 25 30  
 gac acc atc aaa gaa aaa cag tac ata cta aat gaa gcc aga acg ctg 265  
 Asp Thr Ile Lys Glu Lys Gln Tyr Ile Leu Asn Glu Ala Arg Thr Leu  
 35 40 45  
 ttc cgg aaa aac aaa aat ctc acg gac aca gac cta att aaa cag tgt 313  
 Phe Arg Lys Asn Lys Asn Leu Thr Asp Thr Asp Leu Ile Lys Gln Cys  
 50 55 60  
 ata gat gaa tgc aca gcc agg att gaw att gga ctg cat tac aag att 361  
 Ile Asp Glu Cys Thr Ala Arg Ile Xaa Ile Gly Leu His Tyr Lys Ile  
 65 70 75  
 cct tac cca ngg cca att cat ctg cct cca atg ggc ctt acc cca ctc 409  
 Pro Tyr Pro Xaa Pro Ile His Leu Pro Pro Met Gly Leu Thr Pro Leu  
 80 85 90 95  
 cga ggc cgg gga ctt cga agc 430  
 Arg Gly Arg Gly Leu Arg Ser  
 100

<210> 832  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 76..384

<400> 832  
 tttagagat tggcttggat tctgtcggat ggacttgggg ctagctgcgg cggggctgga 60  
 ggaggccaga taacc atg tca gcc aca gtt gta gat gca gty aat gct gca 111  
 Met Ser Ala Thr Val Val Asp Ala Val Asn Ala Ala  
 1 5 10  
 ccc cta tcg ggg tcc aaa gaa atg agt ttg gaa gaa cca aag aag atg 159  
 Pro Leu Ser Gly Ser Lys Glu Met Ser Leu Glu Glu Pro Lys Lys Met  
 15 20 25  
 acc aga gag gac tgg aga aag aag gag cta gaa gaa cag cga aaa 207  
 Thr Arg Glu Asp Trp Arg Lys Lys Lys Glu Leu Glu Glu Gln Arg Lys  
 30 35 40  
 ttg ggc aat gct cct gca gaa gtt gat gaa gaa gga aaa gac atc aac 255  
 Leu Gly Asn Ala Pro Ala Glu Val Asp Glu Glu Gly Lys Asp Ile Asn  
 45 50 55 60  
 ccc cat att cct cag tat att tct tca gtg cca tgg tat att gat cct 303  
 Pro His Ile Pro Gln Tyr Ile Ser Ser Val Pro Trp Tyr Ile Asp Pro  
 65 70 75  
 tca aaa aga cct act tta aaa cac cag aga cca caa cca gaa aaa caa 351  
 Ser Lys Arg Pro Thr Leu Lys His Gln Arg Pro Gln Pro Glu Lys Gln  
 80 85 90  
 aag cag ttc agc tca tct gga gaa tgg tac aag 384  
 Lys Gln Phe Ser Ser Ser Gly Glu Trp Tyr Lys  
 95 100



<210> 833  
 <211> 487  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 235..486

<400> 833  
 attttttccg tttccgtacg gaagcaaagg agccaagacc atggcgaaas cggggataag 60  
 agcggcagca gcgggaagaa aagtctaaaa cggaaagccg ctgccgaaga acttcaggag 120  
 gctgcaggcg ctggggatgg ggcgacggaa aacgggggtcc aacccccgaa agcggctgcc 180  
 tttccgccag gcttttagcat ttcggagatt aaaaacaaac agcggcgaca ctta atg 237  
 Met

1  
 ttc acg cgg tgg aaa cag cag cag cgg aag gaa aag ttg gca gct aag 285  
 Phe Thr Arg Trp Lys Gln Gln Gln Arg Lys Glu Lys Leu Ala Ala Lys  
 5 10 15  
 aaa aaa ctt aaa aaa gaa aga gag gct ctt ggc gat aag gct cca cca 333  
 Lys Lys Leu Lys Lys Glu Arg Glu Ala Leu Gly Asp Lys Ala Pro Pro  
 20 25 30  
 aag cct gta ccc aag acc att gac aac cag cga gtg tat gat gaa acc 381  
 Lys Pro Val Pro Lys Thr Ile Asp Asn Gln Arg Val Tyr Asp Glu Thr  
 35 40 45  
 aca gta gac cct aat gat gaa gag gtc gct tat gat gaa gct aca gat 429  
 Thr Val Asp Pro Asn Asp Glu Glu Val Ala Tyr Asp Glu Ala Thr Asp  
 50 55 60 65  
 gaa ttt gct tct tac ttc aac aaa cag act tct ccc aag att ctc atc 477  
 Glu Phe Ala Ser Tyr Phe Asn Lys Gln Thr Ser Pro Lys Ile Leu Ile  
 70 75 80  
 aca aca tca g  
 Thr Thr Ser 487

<210> 834  
 <211> 389  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 59..388

<400> 834  
 tttttttttt cctctwaccc ccccttctgg akyggttggtg cgatcagatc gatctaag 58  
 atg gcg act gtc gaa ccg gaa acc acc cct act cct aat ccc ccg act 106  
 Met Ala Thr Val Glu Pro Glu Thr Thr Pro Thr Pro Asn Pro Pro Thr  
 1 5 10 15  
 aca gaa gag gag aaa acg gaa tct aat cag gag gtt gct aac cca gaa 154  
 Thr Glu Glu Glu Lys Thr Glu Ser Asn Gln Glu Val Ala Asn Pro Glu  
 20 25 30

cac tat att aaa cat ccc cta cag aac aga tgg gca ctc tgg ttt ttt 202  
 His Tyr Ile Lys His Pro Leu Gln Asn Arg Trp Ala Leu Trp Phe Phe  
 35 40 45  
 aaa aat gat aaa agc aaa act tgg caa gca aac ctg cgg ctg atc tcc 250  
 Lys Asn Asp Lys Ser Lys Thr Trp Gln Ala Asn Leu Arg Leu Ile Ser  
 50 55 60  
 aag ttt gat act gtt gaa gac ttt tgg gct ctg tac aac cat atc cag 298  
 Lys Phe Asp Thr Val Glu Asp Phe Trp Ala Leu Tyr Asn His Ile Gln  
 65 70 75 80  
 ttg tct agt aat tta atg cct ggc tgt gac tac tca ctt ttt aag gat 346  
 Leu Ser Ser Asn Leu Met Pro Gly Cys Asp Tyr Ser Leu Phe Lys Asp  
 85 90 95  
 ggt att gag cct atg tgg gaa gat gag aaa aac aaa cgg gga g 389  
 Gly Ile Glu Pro Met Trp Glu Asp Glu Lys Asn Lys Arg Gly  
 100 105 110

<210> 835  
 <211> 299  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 117..299

<400> 835  
 gatgcgaact ggggccacgg cagccatcgc gctttgcagt tgggtctcct ggtgtacggc 60  
 caacgccaa taggggattg cgttccctcc agtcgcagac cctatcagat ttggat atg 119  
 Met  
 1  
 tcc ttc ata ttt gat tgg att tac agt ggt ttc agc agt gtg cta cag 167  
 Ser Phe Ile Phe Asp Trp Ile Tyr Ser Gly Phe Ser Ser Val Leu Gln  
 5 10 15  
 ttt tta gga tta tat aag aaa act ggt aaa ctg gta ttt ctt gga ttg 215  
 Phe Leu Gly Leu Tyr Lys Lys Thr Gly Lys Leu Val Phe Leu Gly Leu  
 20 25 30  
 gat aat gca gga aaa aca aca ttg cta cac atg cta aaa gat gac aga 263  
 Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp Arg  
 35 40 45  
 ctt gga caa cat gtc cca aca tta cat ccc act tcc 299  
 Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser  
 50 55 60

<210> 836  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 124..405

<400> 836

tagagagccc	cggagccg	gcgggagagg	aacgcgcasc	agccttgggg	agcccaggcc	60
cggcagccat	ggcgggtgga	gggtggccgca	gccattgctg	gctatgtgtt	tagagataag	120
gtg atg tca	gag ttt aat	aac aac ttc	cgg cag cag	atg gag aat	tac	168
Met Ser Glu	Phe Asn Asn	Asn Phe Arg	Gln Gln Met	Glu Asn Tyr		
1	5	10	15			
ccg aaa aac	aac cac act	gct tgc atc	ctg gac agg	atg cag gca	gat	216
Pro Lys Asn	Asn His Thr	Ala Ser Ile	Leu Asp Arg	Met Gln Ala	Asp	
	20	25	30			
ttt aag tgc	tgt ggg gct	gct aac tac	aca gat tgg	gag aaa atc	cct	264
Phe Lys Cys	Cys Gly Ala	Ala Asn Tyr	Thr Asp Trp	Glu Lys Ile	Pro	
	35	40	45			
tcc atg tgc	aag aac cga	gtc ccc gac	tcc tgc tgc	att aat gtt	act	312
Ser Met Ser	Lys Asn Arg	Val Pro Asp	Ser Cys Cys	Ile Asn Val	Thr	
	50	55	60			
gtg ggc tgt	ggg att aat	ttc aac gag	aag gcg atc	cat aag gag	ggc	360
Val Gly Cys	Gly Ile Asn	Phe Asn Glu	Lys Ala Ile	His Lys Glu	Gly	
	65	70	75			
tgt gtg gag	aag att ggg	ggc tgg ctg	agg aaa aat	gtg ctg gtg	gt	407
Cys Val Glu	Lys Ile Gly	Gly Trp Leu	Arg Lys Asn	Val Leu Val		
80	85	90				

<210> 837

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 101..457

<400> 837

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ggagagaaaag	gaggttccat	aggcagttct	taccaagaag	atg tgc att	cca ttc	115
				Met Ser Ile	Pro Phe	
				1	5	
tcc aac acc	cac tac cga	att cca caa	gga ttt ggg	aat ctt ctt	gaa	163
Ser Asn Thr	His Tyr Arg	Ile Pro Gln	Gly Phe Gly	Asn Leu Leu	Glu	
	10	15	20			
ggg ctg aca	cgc gag att	ctg aga gag	caa ccg gac	aat ata cca	gct	211
Gly Leu Thr	Arg Glu Ile	Leu Arg Glu	Gln Pro Asp	Asn Ile Pro	Ala	
	25	30	35			
ttt gca gca	gcc tat ttt	gag agc ctt	cta gag aaa	aga gag aaa	acc	259
Phe Ala Ala	Ala Tyr Phe	Glu Ser Leu	Leu Glu Lys	Arg Glu Lys	Thr	
	40	45	50			
aac ttt gat	cca gca gaa	tgg ggg agt	aag gta gaa	gac cgc ttc	tat	307
Asn Phe Asp	Pro Ala Glu	Trp Gly Ser	Lys Val Glu	Asp Arg Phe	Tyr	
	55	60	65			
aac aat cat	gca ttc gag	gag cww gaa	cca cct gag	aaa agt gat	cct	355
Asn Asn His	Ala Phe Glu	Glu Xaa Glu	Pro Pro Glu	Lys Ser Asp	Pro	
	70	75	80	85		
aaa caa gaa	gag tct cag	ata tct ggg	aag gag gaa	gag aca tca	gtc	403
Lys Gln Glu	Glu Ser Gln	Ile Ser Gly	Lys Glu Glu	Glu Thr Ser	Val	

	90		95		100	
acc atc tta gac tct tct gag gaa gat aag gaa aaa gaa gag gtt gct						451
Thr Ile Leu Asp Ser Ser Glu Glu Asp Lys Glu Lys Glu Glu Val Ala						
	105		110		115	
gct gtc aa						459
Ala Val						

<210> 838  
 <211> 316  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 8..316

<400> 838	
attatac atg act gga aaa gta atg gca agc aag act tca gag ctg agc	49
Met Thr Gly Lys Val Met Ala Ser Lys Thr Ser Glu Leu Ser	
1 5 10	
tat ctt gat att ttt atc cag tgt gtg ggg tgt tac aca tgc atc aca	97
Tyr Leu Asp Ile Phe Ile Gln Cys Val Gly Cys Tyr Thr Cys Ile Thr	
15 20 25 30	
gct ata ata gag cta tca cat gga tct ttt gaa aaa caa gat aga gat	145
Ala Ile Ile Glu Leu Ser His Gly Ser Phe Glu Lys Gln Asp Arg Asp	
35 40 45	
gtt tta aag gct tct ggg ttt gat ttc tta gtc aga tgc tgt ggt act	193
Val Leu Lys Ala Ser Gly Phe Asp Phe Leu Val Arg Cys Cys Gly Thr	
50 55 60	
tgg cat tta aca act aga att gtg gtc tgc aaa gaa aaa act tct aga	241
Trp His Leu Thr Thr Arg Ile Val Val Cys Lys Glu Lys Thr Ser Arg	
65 70 75	
aaa aga caa caa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	289
Lys Arg Gln Gln Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys	
80 85 90	
aaa aaa aaa aaa aaa aaa aaa aaa aaa	316
Lys Lys Lys Lys Lys Lys Lys Lys Lys	
95 100	

<210> 839  
 <211> 223  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 62..223

<400> 839	
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c atg cct aca aca cag cag tcc cct cag gat gag cag gaa aag ctc ttg	109
Met Pro Thr Thr Gln Gln Ser Pro Gln Asp Glu Gln Glu Lys Leu Leu	

1	5	10	15	
gat gaa gcc ata cag gct gtg aag gtc cag tca ttc caa atg aag aga	157			
Asp Glu Ala Ile Gln Ala Val Lys Val Gln Ser Phe Gln Met Lys Arg				
20 25 30				
tgc ctg gac aaa aac aag ctt atg gat gct cta aaa cat gct tct aat	205			
Cys Leu Asp Lys Asn Lys Leu Met Asp Ala Leu Lys His Ala Ser Asn				
35 40 45				
atg ctt ggt gaa ctc cgg	223			
Met Leu Gly Glu Leu Arg				
50				

<210> 840  
 <211> 601  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 142..600

<400> 840	
agtgagtcgc ggcgcgcgcgc actggtggtt gggtcagtgcc cgcgcgcgcga tcggtcgtta	60
cgcgcgagcg ctggtggcct tcaggtctga cgcgcgcgggt cagccctggt tcgccggctt	120
ctgggtcttt gaacagccgc g atg tcg atc ttc acc ccc acc aac cag atc	171
Met Ser Ile Phe Thr Pro Thr Asn Gln Ile	
1 5 10	
cgc cta acc aat gtg gcc gtg gta cgg atg aag cgt gcc ggg aag cgc	219
Arg Leu Thr Asn Val Ala Val Val Arg Met Lys Arg Ala Gly Lys Arg	
15 20 25	
ttc gaa atc gcc tgc tac aaa aac aag gtc gtc ggc tgg cgg agc ggc	267
Phe Glu Ile Ala Cys Tyr Lys Asn Lys Val Val Gly Trp Arg Ser Gly	
30 35 40	
gtg gaa aaa gac ctc gat gaa gtt ctg cag acc cac tca gtg ttt gta	315
Val Glu Lys Asp Leu Asp Glu Val Leu Gln Thr His Ser Val Phe Val	
45 50 55	
aat gtt tct aaa ggt cag gtt gcc aaa aag gaa gat ctc atc agt gcg	363
Asn Val Ser Lys Gly Gln Val Ala Lys Lys Glu Asp Leu Ile Ser Ala	
60 65 70	
ttt gga aca gat gac caa act gaa atc tgt aag cag att ttg act aaa	411
Phe Gly Thr Asp Asp Gln Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys	
75 80 85 90	
gga gaa gtt caa gta tca gat aaa gaa aga cac aca caa ctg gag cag	459
Gly Glu Val Gln Val Ser Asp Lys Glu Arg His Thr Gln Leu Glu Gln	
95 100 105	
atg ttt agg gac att gca act att gtg gca gac aaa tgt gtg aat cct	507
Met Phe Arg Asp Ile Ala Thr Ile Val Ala Asp Lys Cys Val Asn Pro	
110 115 120	
gaa aca aag aga cca tac acc gtg atc ctt att gag aga gcc atg aag	555
Glu Thr Lys Arg Pro Tyr Thr Val Ile Leu Ile Glu Arg Ala Met Lys	
125 130 135	
gac atc cac tat tcg gtg aaa acc aac aag agt aca aaa cag cag g	601
Asp Ile His Tyr Ser Val Lys Thr Asn Lys Ser Thr Lys Gln Gln	
140 145 150	

001 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 10

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**SECRET**

**SECRET**

**SECRET**

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gga atg tac cca tct cag atg aat ggc tac gga tca tca cct acc ttt      148
Gly Met Tyr Pro Ser Gln Met Asn Gly Tyr Gly Ser Ser Pro Thr Phe
  25                      30                      35
tcc cag acg gac aga gaa cat ggt tca aaa aca agt gca aag gcc ctt      196
Ser Gln Thr Asp Arg Glu His Gly Ser Lys Thr Ser Ala Lys Ala Leu
  40                      45                      50                      55
tat gaa caa agg aag aat tat gca cgg gac agt gtc agc agt gtg tca      244
Tyr Glu Gln Arg Lys Asn Tyr Ala Arg Asp Ser Val Ser Ser Val Ser
                      60                      65                      70
gat ata tct caa tac cgt gtt gaa cac ttg act acc ttt gtc ctg gat      292
Asp Ile Ser Gln Tyr Arg Val Glu His Leu Thr Thr Phe Val Leu Asp
                      75                      80                      85
cgg aaa gat gct atg atc act gtt gat gat gga ata agg aaa ttg aaa      340
Arg Lys Asp Ala Met Ile Thr Val Asp Asp Gly Ile Arg Lys Leu Lys
  90                      95                      100
ttg ctt gat gcc aag ggc aaa gtg tgg act caa gat atg att ctt caa      388
Leu Leu Asp Ala Lys Gly Lys Val Trp Thr Gln Asp Met Ile Leu Gln
  105                      110                      115
gtg gat gac aga gct gtg agc ctg att gat tta gaa tca aag aat gaa      436
Val Asp Asp Arg Ala Val Ser Leu Ile Asp Leu Glu Ser Lys Asn Glu
  120                      125                      130                      135
ctg gag aat ttt cct tta aac aca atc cag cac tgc caa gct gtg atg      484
Leu Glu Asn Phe Pro Leu Asn Thr Ile Gln His Cys Gln Ala Val Met
                      140                      145                      150
cat tca tgc agc tat gat tca gtt ctt gca ctg gtg tgc aaa gag cca      532
His Ser Cys Ser Tyr Asp Ser Val Leu Ala Leu Val Cys Lys Glu Pro
                      155                      160                      165
acc cag aac aag cca gat ctt cat ctc ttc cag tgt gat gag gtt aag      580
Thr Gln Asn Lys Pro Asp Leu His Leu Phe Gln Cys Asp Glu Val Lys
                      170                      175                      180
gca aac cta att agt gaa gat att gaa agt gca atc agt gac agt aaa      628
Ala Asn Leu Ile Ser Glu Asp Ile Glu Ser Ala Ile Ser Asp Ser Lys
  185                      190                      195
gga ggg aaa
Gly Gly Lys
200

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<210> 843  
 <211> 590  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 294..590

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atggctgcct gcccttggc agctgtcttt atggaccagt aggcagagcg aaattgacgc      120
tgacaagact tttgcatctt ggaagggact gtaatctact gtagtgaaga acagagcctc      180
tcaatcagac ggggtgaaat aagagacgga ggggagtcca aaagaaaagg aagaggagga      240
aaaacaagtg tgtgttgggg ggaacagggg gaaaagcatt tttggtggat ggt atg      296
                                         Met

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1

aag cca gcc atg gaa act gca gcc gag gaa aat act gaa caa agc caa	344
Lys Pro Ala Met Glu Thr Ala Ala Glu Glu Asn Thr Glu Gln Ser Gln	
5 10 15	
gag aga aaa ggc tgc ttt gaa tgc tgc atc aag tgt ctg gga gga gtc	392
Glu Arg Lys Gly Cys Phe Glu Cys Cys Ile Lys Cys Leu Gly Gly Val	
20 25 30	
ccc tac gcc tcc ctg gtg gcc acc atc ctc tgc ttc tcc ggg gtg gcc	440
Pro Tyr Ala Ser Leu Val Ala Thr Ile Leu Cys Phe Ser Gly Val Ala	
35 40 45	
tta ttc tgc ggc tgt ggg cat gtg gct ctc gca ggc acc gtg gcg att	488
Leu Phe Cys Gly Cys Gly His Val Ala Leu Ala Gly Thr Val Ala Ile	
50 55 60 65	
ctt gag caa cac ttc tcc acc aac gcc agt kac cat gcc ttg ctg agc	536
Leu Glu Gln His Phe Ser Thr Asn Ala Ser Xaa His Ala Leu Leu Ser	
70 75 80	
gag gtg ata caa ctg atg cag tat gtc atc tat gga att gcg tct ttt	584
Glu Val Ile Gln Leu Met Gln Tyr Val Ile Tyr Gly Ile Ala Ser Phe	
85 90 95	
tct tct	590
Ser Ser	

&lt;210&gt; 844

&lt;211&gt; 455

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 29..454

&lt;400&gt; 844

acccgggagg cggsgccagc gaggcaag atg gag tta gtg cag gtc ctg aaa	52
Met Glu Leu Val Gln Val Leu Lys	
1 5	
cgc ggg ctg cag cag atc acc ggc cac ggc ggt ctc cga ggc tat cta	100
Arg Gly Leu Gln Gln Ile Thr Gly His Gly Gly Leu Arg Gly Tyr Leu	
10 15 20	
cgg gtt ttt ttc agg aca aat gat gcg aag gtt ggt aca tta gtg ggg	148
Arg Val Phe Phe Arg Thr Asn Asp Ala Lys Val Gly Thr Leu Val Gly	
25 30 35 40	
gaa gac aaa tat gga aac aaa tac tat gaa gac aac aag caa ttt ttt	196
Glu Asp Lys Tyr Gly Asn Lys Tyr Tyr Glu Asp Asn Lys Gln Phe Phe	
45 50 55	
ggc cgt cac cga tgg gtt gta tat act act gaa atg aat ggc aaa aac	244
Gly Arg His Arg Trp Val Val Tyr Thr Thr Glu Met Asn Gly Lys Asn	
60 65 70	
aca ttc tgg gat gtg gat gga agc atg gtg cct cct gaa tgg cat cgt	292
Thr Phe Trp Asp Val Asp Gly Ser Met Val Pro Pro Glu Trp His Arg	
75 80 85	
tgg ctt cac agt atg act gat gat cct cca aca aca aaa cca ctt act	340
Trp Leu His Ser Met Thr Asp Asp Pro Pro Thr Thr Lys Pro Leu Thr	
90 95 100	



**06-07-2018**

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<220>  
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<222> 124..351
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<210> 846
<211> 283
<212> DNA
<213> Homo sapiens
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accttgcttc ctgcttcgcc tccgcgcctc ggcgtatggg acagagcccc cgatccgcc 60
gcaccacctg aggatccaga aaccgcccc a gcg atg gaa gag gat cag gag ctg 114
                               Met Glu Glu Asp Gln Glu Leu
                               1           5

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gag aga aaa ata tct gga ttg aag acc tca atg gct gaa ggc gag agg	162
Glu Arg Lys Ile Ser Gly Leu Lys Thr Ser Met Ala Glu Gly Glu Arg	
10 15 20	
aag aca gcc ctg gaa atg gtc cag gca gct gga aca gat aga cac tgt	210
Lys Thr Ala Leu Glu Met Val Gln Ala Ala Gly Thr Asp Arg His Cys	
25 30 35	
gtg aca ttt gta ttg cac gag gaa gac cat acc cta gga aat tct cta	258
Val Thr Phe Val Leu His Glu Glu Asp His Thr Leu Gly Asn Ser Leu	
40 45 50 55	
cgt tac atg atc atg awg aac ccg g	283
Arg Tyr Met Ile Met Xaa Asn Pro	
60	

<210> 847  
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 <212> DNA  
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<220>  
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<400> 847	
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cgcagcttag gagctgaaga tcgcggactt agcgttgccg cgtccgagtc cggccatcag	120
tggtctgcaga tccggaggcc aggagctcaa ccacccttct tcggaacagg gccggcctgc	180
tgctgtgccc tcgacgtctg gtgctgttat ctactccggg gcctaggctg gctccggggg	240
cggcttagga gaaggccgcc ggcgag atg ttc aaa aac acg ttc cag agc ggc	293
Met Phe Lys Asn Thr Phe Gln Ser Gly	
1 5	
ttc ctc tcc atc ctc tac agc atc ggc agc aag cct ctg caa atc tgg	341
Phe Leu Ser Ile Leu Tyr Ser Ile Gly Ser Lys Pro Leu Gln Ile Trp	
10 15 20 25	
gac aaa aag gta cgg aat ggc cac atc aaa aga atc act gat aat gac	389
Asp Lys Lys Val Arg Asn Gly His Ile Lys Arg Ile Thr Asp Asn Asp	
30 35 40	
atc cag tcc ctg gtg cta gag att gaa ggg aca aat gta agc acc aca	437
Ile Gln Ser Leu Val Leu Glu Ile Glu Gly Thr Asn Val Ser Thr Thr	
45 50 55	
tat atc asa tgc cct gca	455
Tyr Ile Xaa Cys Pro Ala	
60	

<210> 848  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 22..351

00400"022400

&lt;400&gt; 848

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gctcatttgt aggctgaact a atg act gcc gcc ata aga aga cag aga gaa      51
                        Met Thr Ala Ala Ile Arg Arg Gln Arg Glu
                        1      5      10
ctg agt atc ctc cca aag gtg aca ctg gaa gca atg aac acc aca gtg      99
Leu Ser Ile Leu Pro Lys Val Thr Leu Glu Ala Met Asn Thr Thr Val
                        15      20      25
atg caa ggc ttc aac aga tct gag cgg tgc ccc aga gac act cgg ata      147
Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile
                        30      35      40
gta cag ctg gta ttc cca gcc ctc tac aca gtg gtt ttc ttg acc ggc      195
Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val Val Phe Leu Thr Gly
                        45      50      55
atc ctg ctg aat act ttg gct ctg tgg gtg ttt gtt cac atc ccc agc      243
Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val His Ile Pro Ser
                        60      65      70
tcc tcc acc ttc atc atc tac ctc aaa aac act ttg gtg gcc gac ttg      291
Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu
75      80      85      90
ata atg aca cct gta ggt ctg ctt cat gcc ctt ttg atg gca gga ggg      339
Ile Met Thr Pro Val Gly Leu Leu His Ala Leu Leu Met Ala Gly Gly
                        95      100      105
agc tgt cct gat      351
Ser Cys Pro Asp
                        110

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&lt;210&gt; 849

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 115..462

&lt;400&gt; 849

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atattaccgc gtaggctaac cagtgcgctt aatagctgta ggtccagtgt aagagttccg      60
ctattcggtc tcacacctac agtggactac ccgatttttc gcttctcttc aggg atg      117
                        Met
                        1
agt cat gtg gtg gtg aaa aat gac cct gaa ctg gac cag cag ctt gct      165
Ser His Val Val Val Lys Asn Asp Pro Glu Leu Asp Gln Gln Leu Ala
                        5      10      15
aat ctg gac ctg aac tct gaa aaa cag agt gga gga gca agt aca gcg      213
Asn Leu Asp Leu Asn Ser Glu Lys Gln Ser Gly Gly Ala Ser Thr Ala
                        20      25      30
agc aaa ggg cgc tat ata cct cct cac tta agg aac aga gaa gca tct      261
Ser Lys Gly Arg Tyr Ile Pro Pro His Leu Arg Asn Arg Glu Ala Ser
35      40      45
aaa gga ttc cat gat aaa gac agt tca ggt tgg agt tgc agc aaa gat      309
Lys Gly Phe His Asp Lys Asp Ser Ser Gly Trp Ser Cys Ser Lys Asp
50      55      60      65
aag gat gca tat agc agt ttt ggg tct cga gat tct aga gga aag cct      357

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Lys	Asp	Ala	Tyr	Ser	Ser	Phe	Gly	Ser	Arg	Asp	Ser	Arg	Gly	Lys	Pro	
				70				75					80			
ggt	tat	ttc	agt	gaa	cgt	gga	agt	gga	tca	agg	gga	aga	ttt	gat	gat	405
Gly	Tyr	Phe	Ser	Glu	Arg	Gly	Ser	Gly	Ser	Arg	Gly	Arg	Phe	Asp	Asp	
			85				90					95				
cgt	gga	cgg	ntg	act	atg	atg	gta	ttg	gca	atc	gtg	raa	gac	ctg	gct	453
Arg	Gly	Arg	Xaa	Thr	Met	Met	Val	Leu	Ala	Ile	Val	Xaa	Asp	Leu	Ala	
		100					105					110				
ttg	gca	gat	t													463
Leu	Ala	Asp														
		115														

<210> 850  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 205..552

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taggccttag	gtgggttcgt	gcgccttcta	cctcgctgtt	tcggttttcc	tggtcctcg											120	
gcccttttct	cccctgttgc	agctgggagc	ggacgaagcg	cgaastggga	ttttttactg											180	
tctcctgaag	aatttaacac	aaac	atg	gat	atc	aga	cca	aat	cat	aca	att					231	
			Met	Asp	Ile	Arg	Pro	Asn	His	Thr	Ile						
			1			5											
tat	atc	aac	aat	atg	aat	gac	aaa	att	aaa	aag	gaa	gaa	ttg	aag	aga	279	
Tyr	Ile	Asn	Asn	Met	Asn	Asp	Lys	Ile	Lys	Lys	Glu	Glu	Leu	Lys	Arg		
10				15					20				25				
tcc	cta	tat	gcc	ctg	ttt	tct	cag	ttt	ggt	cat	gtg	gtg	gac	att	gtg	327	
Ser	Leu	Tyr	Ala	Leu	Phe	Ser	Gln	Phe	Gly	His	Val	Val	Asp	Ile	Val		
			30					35					40				
gct	tta	aag	acc	atg	aag	atg	agg	ggg	cag	gcc	ttt	gtc	ata	ttt	aag	375	
Ala	Leu	Lys	Thr	Met	Lys	Met	Arg	Gly	Gln	Ala	Phe	Val	Ile	Phe	Lys		
		45					50				55						
gaa	ctg	ggc	tca	tcc	aca	aat	gcc	ttg	aga	cag	cta	caa	gga	ttt	cca	423	
Glu	Leu	Gly	Ser	Ser	Thr	Asn	Ala	Leu	Arg	Gln	Leu	Gln	Gly	Phe	Pro		
		60					65				70						
ttt	tat	ggt	aaa	cca	atg	cga	ata	cag	tat	gca	aaa	aca	gat	tcg	gat	471	
Phe	Tyr	Gly	Lys	Pro	Met	Arg	Ile	Gln	Tyr	Ala	Lys	Thr	Asp	Ser	Asp		
		75				80				85							
ata	ata	tca	aaa	atg	cgt	gga	act	ttt	gct	gac	aaa	gaa	aag	aaa	aaa	519	
Ile	Ile	Ser	Lys	Met	Arg	Gly	Thr	Phe	Ala	Asp	Lys	Glu	Lys	Lys	Lys		
		90			95				100						105		
gaa	aag	aaa	aaa	gcc	aaa	act	gtg	gaa	cag	act						552	
Glu	Lys	Lys	Lys	Ala	Lys	Thr	Val	Glu	Gln	Thr							
				110					115								

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<213> Homo sapiens

<220>

<221> CDS

<222> 106..453

<400> 851

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                               Met Asp Ile Arg
                               1
cca aat cat aca att tat atc aac aat atg aat gac aaa att aaa aag      165
Pro Asn His Thr Ile Tyr Ile Asn Asn Met Asn Asp Lys Ile Lys Lys
5                               10                               15                               20
gaa gaa ttg aag aga tcc cta tat gcc ctg ttt tct cag ttt ggt cat      213
Glu Glu Leu Lys Arg Ser Leu Tyr Ala Leu Phe Ser Gln Phe Gly His
                               25                               30                               35
gtg gtg gac att gtg gct tta aag acc atg aag atg agg ggg cag gcc      261
Val Val Asp Ile Val Ala Leu Lys Thr Met Lys Met Arg Gly Gln Ala
                               40                               45                               50
ttt gtc ata ttt aag gaa ctg ggc tca tcc aca aat gcc ttg aga cag      309
Phe Val Ile Phe Lys Glu Leu Gly Ser Ser Thr Asn Ala Leu Arg Gln
                               55                               60                               65
cta caa gga ttt cca ttt tat ggt aaa cca atg cga ata cag tat gca      357
Leu Gln Gly Phe Pro Phe Tyr Gly Lys Pro Met Arg Ile Gln Tyr Ala
                               70                               75                               80
aaa aca gat tcg gat ata ata tca aaa atg cgt gga act ttt gct gac      405
Lys Thr Asp Ser Asp Ile Ile Ser Lys Met Arg Gly Thr Phe Ala Asp
85                               90                               95                               100
aaa gaa aag aaa aaa gaa aag aaa aaa gcc aaa act gtg gaa cag act      453
Lys Glu Lys Lys Lys Glu Lys Lys Lys Ala Lys Thr Val Glu Gln Thr
                               105                               110                               115

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<210> 852

<211> 441

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 47..439

<400> 852

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                               1
tta gtg ctg gat aat gga gct tac aac gcc aaa atc ggt tac agc cat      103
Leu Val Leu Asp Asn Gly Ala Tyr Asn Ala Lys Ile Gly Tyr Ser His
5                               10                               15
gaa aat gtg tcg gtt att cct aat tgt cag ttc cgg tca aaa aca gca      151
Glu Asn Val Ser Val Ile Pro Asn Cys Gln Phe Arg Ser Lys Thr Ala
20                               25                               30                               35

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cgt ctt aaa act ttt act gcc aac cag ata gat gaa ata aaa gac cct	199
Arg Leu Lys Thr Phe Thr Ala Asn Gln Ile Asp Glu Ile Lys Asp Pro	
40 45 50	
tct gga ctc ttt tac atc ctc cct ttt caa aag ggc tac ttg gtg aat	247
Ser Gly Leu Phe Tyr Ile Leu Pro Phe Gln Lys Gly Tyr Leu Val Asn	
55 60 65	
tgg gat gtt cag aga cag gtt tgg gat tac ctt ttt gga aaa gaa atg	295
Trp Asp Val Gln Arg Gln Val Trp Asp Tyr Leu Phe Gly Lys Glu Met	
70 75 80	
tat cag gtt gat ttt tta gat act aat att att atc act gaa cca tac	343
Tyr Gln Val Asp Phe Leu Asp Thr Asn Ile Ile Ile Thr Glu Pro Tyr	
85 90 95	
ttt aac ttc act tca att caa gaa tca atg aat gar att cta ttt gaa	391
Phe Asn Phe Thr Ser Ile Gln Glu Ser Met Asn Glu Ile Leu Phe Glu	
100 105 110 115	
gaa tac cag ttt caa gca gta tta aga gta aat gct ggg gct ctc agt	439
Glu Tyr Gln Phe Gln Ala Val Leu Arg Val Asn Ala Gly Ala Leu Ser	
120 125 130	
gc	441
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Met Thr Thr	
1	
tta gtg ctg gat aat gga gct tac aac gcc aaa atc ggt tac agc cat	103
Leu Val Leu Asp Asn Gly Ala Tyr Asn Ala Lys Ile Gly Tyr Ser His	
5 10 15	
gaa aat gtg tcg gtt att cct aat tgt cag ttc cgg tca aaa aca gca	151
Glu Asn Val Ser Val Ile Pro Asn Cys Gln Phe Arg Ser Lys Thr Ala	
20 25 30 35	
cgt ctt aaa act ttt act gcc aac cag ata gat gaa ata aaa gac cct	199
Arg Leu Lys Thr Phe Thr Ala Asn Gln Ile Asp Glu Ile Lys Asp Pro	
40 45 50	
tct gga ctc ttt tac atc ctc cct ttt caa aag gtt gat ttt tta gat	247
Ser Gly Leu Phe Tyr Ile Leu Pro Phe Gln Lys Val Asp Phe Leu Asp	
55 60 65	
act aat att att atc act gaa cca tac ttt aac ttc act tca att caa	295
Thr Asn Ile Ile Ile Thr Glu Pro Tyr Phe Asn Phe Thr Ser Ile Gln	
70 75 80	
gaa tca atg aat gar att cta ttt gaa gaa tac cag ttt caa gca gta	343
Glu Ser Met Asn Glu Ile Leu Phe Glu Glu Tyr Gln Phe Gln Ala Val	
85 90 95	
tta aga gta aat gct ggg gct ctc agt gc	372
Leu Arg Val Asn Ala Gly Ala Leu Ser	

100

105

<210> 854  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 110..355

<400> 854  
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 cagcactgga ggcaatgttt ctataaatca aagaagagac agtgtgaga atg tca gcc 118  
 Met Ser Ala  
 1  
 ctc aac tgg aag ccg ttt gtg tac ggg ggg ctg gcc tcc atc act gct 166  
 Leu Asn Trp Lys Pro Phe Val Tyr Gly Gly Leu Ala Ser Ile Thr Ala  
 5 10 15  
 gag tgy ggt aca ttt cca att gat tta acc aag aca cgg ctg cag att 214  
 Glu Cys Gly Thr Phe Pro Ile Asp Leu Thr Lys Thr Arg Leu Gln Ile  
 20 25 30 35  
 caa ggc cag acg aat gat gca aaa ttt aag gaa att aga tac cgk nga 262  
 Gln Gly Gln Thr Asn Asp Ala Lys Phe Lys Glu Ile Arg Tyr Arg Xaa  
 40 45 50  
 atg ttg cac gca tta gtg agg ata ggc aga gaa gan ggg gct gaa agc 310  
 Met Leu His Ala Leu Val Arg Ile Gly Arg Glu Xaa Gly Ala Glu Ser  
 55 60 65  
 act cta ctg ggg gat tgc ccc cgc gat gtt acg cca ggc atc cta 355  
 Thr Leu Leu Gly Asp Cys Pro Arg Asp Val Thr Pro Gly Ile Leu  
 70 75 80

<210> 855  
 <211> 317  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 16..315

<400> 855  
 aacactctcc tgaag atg ggc tac cat ttt gag ctt ccg ggt ccc aga atg 51  
 Met Gly Tyr His Phe Glu Leu Pro Gly Pro Arg Met  
 1 5 10  
 gtg gtc act aat ctg ctg acc agg aat cag gat aaa caa agg cag aaa 99  
 Val Val Thr Asn Leu Leu Thr Arg Asn Gln Asp Lys Gln Arg Gln Lys  
 15 20 25  
 cga cag gaa gag caa aaa cag cag caa ctg aag gaa cag aag aag ctg 147  
 Arg Gln Glu Glu Gln Lys Gln Gln Gln Leu Lys Glu Gln Lys Lys Leu  
 30 35 40  
 ata gcc atg tta gag aat ggg ttg ggg ctg ccc cct ggg atg wrg gag 195

Ile	Ala	Met	Leu	Glu	Asn	Gly	Leu	Gly	Leu	Pro	Pro	Gly	Met	Xaa	Glu	
45					50				55						60	
ctg	ttg	gga	gga	ccc	aag	cca	gat	tcc	aga	atg	cag	gaa	ttc	ttc	cag	243
Leu	Leu	Gly	Gly	Pro	Lys	Pro	Asp	Ser	Arg	Met	Gln	Glu	Phe	Phe	Gln	
				65				70						75		
cca	ccg	cca	cct	cgg	cct	ccc	aac	ccc	caa	aat	gtc	ccc	ttt	agt	caa	291
Pro	Pro	Pro	Pro	Arg	Pro	Pro	Asn	Pro	Gln	Asn	Val	Pro	Phe	Ser	Gln	
			80					85					90			
cgc	agt	nga	atg	atg	aaa	aag	cca	tc								317
Arg	Ser	Xaa	Met	Met	Lys	Lys	Pro									
		95					100									

<210> 856  
 <211> 469  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 98..469

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agatgaatgc ggctgttaag acctgcaata atccaga atg gct act ctg atc tat	115
	Met Ala Thr Leu Ile Tyr
	1 5
ggt gat aag gaa aat gga gaa cca ggc acc cgt gtg gtt gct aag gat	163
Val Asp Lys Glu Asn Gly Glu Pro Gly Thr Arg Val Val Ala Lys Asp	
	10 15 20
ggg ctg aag ctg ggg tct gga cct tca atc aaa gcc tta gat ggg aga	211
Gly Leu Lys Leu Gly Ser Gly Pro Ser Ile Lys Ala Leu Asp Gly Arg	
	25 30 35
tct caa gtt tca aca cca cgt ttt ggc aaa acg ttc gat gcc cca cca	259
Ser Gln Val Ser Thr Pro Arg Phe Gly Lys Thr Phe Asp Ala Pro Pro	
	40 45 50
gcc tta cct aaa gct act aga aag gct ttg gga act gtc aac aga gct	307
Ala Leu Pro Lys Ala Thr Arg Lys Ala Leu Gly Thr Val Asn Arg Ala	
	55 60 65 70
aca gaa aag tct gta aag acc aag gga ccc ctc aaa caa aaa cag cca	355
Thr Glu Lys Ser Val Lys Thr Lys Gly Pro Leu Lys Gln Lys Gln Pro	
	75 80 85
agc ttt tct gcc aaa aag atg act gag aag act gtt aaa gca aaa agc	403
Ser Phe Ser Ala Lys Lys Met Thr Glu Lys Thr Val Lys Ala Lys Ser	
	90 95 100
tct gtt cct gcc tca gat gak gct atc cag aaa tng aaa att ctt tcc	451
Ser Val Pro Ala Ser Asp Xaa Ala Ile Gln Lys Xaa Lys Ile Leu Ser	
	105 110 115
ctt caa tcc tct aga ctt	469
Leu Gln Ser Ser Arg Leu	
	120

<210> 857  
 <211> 385



<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 125..385

<400> 857  
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gcacaacagg ctgctctggg attctcttca gccaatcttc attgctcaag tgtctgaagc 120  
agcc atg gca gaa gta cct gag ctc gcc agt gaa atg atg gct tat tac 169  
Met Ala Glu Val Pro Glu Leu Ala Ser Glu Met Met Ala Tyr Tyr  
1 5 10 15  
agt ggc aat gag gat gac ttg ttc ttt gaa gct gat ggc cct aaa cag 217  
Ser Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln  
20 25 30  
atg aag tgc tcc ttc cag gac ctg gac ctc tgc cct ctg gat ggc ggc 265  
Met Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly  
35 40 45  
atc cag cta cga atc tcc gac cac cac tac agc aag ggc ttc agg cag 313  
Ile Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln  
50 55 60  
gcc gcg tca gtt gtt gtg gcc atg gac aag ctg agg aag atg ctg gtt 361  
Ala Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val  
65 70 75  
ccc tgc cca cag acc ttc cag gag 385  
Pro Cys Pro Gln Thr Phe Gln Glu  
80 85

<210> 858  
<211> 371  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 126..371

<400> 858  
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cttttcaaga ggaaggatga aaactctaca taggaacacg atgtgaatgg aagaaacctg 120  
tcatt atg caa ata gta cgg tat tcc gaa cag aca cta aaa ata gct gtc 170  
Met Gln Ile Val Arg Tyr Ser Glu Gln Thr Leu Lys Ile Ala Val  
1 5 10 15  
atc tca aag aat cca gtg ctt gtg tca cag tat gag aaa gta gat gct 218  
Ile Ser Lys Asn Pro Val Leu Val Ser Gln Tyr Glu Lys Val Asp Ala  
20 25 30  
ggg gaa cag cgt tta atg aat gaa gca ttc cag cca gcc agt gat ctc 266  
Gly Glu Gln Arg Leu Met Asn Glu Ala Phe Gln Pro Ala Ser Asp Leu  
35 40 45  
ttt gga cct tgc att ctc cat cag att gga tca cct ccc acc ctg agg 314  
Phe Gly Pro Cys Ile Leu His Gln Ile Gly Ser Pro Pro Thr Leu Arg

50	55	60	
ccc ccc aag act ttg aac agt tct tca gtc atc ctt aca gaa aga tac			362
Pro Pro Lys Thr Leu Asn Ser Ser Ser Val Ile Leu Thr Glu Arg Tyr			
65	70	75	
cct ctc cag			371
Pro Leu Gln			
80			

<210> 859  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 192..422

<400> 859	
gcacgcgcgt gagggatgtc gcggtctccc tagattaggc ttgggaggca aggggaggcc	60
tcctgacttt tctcactgcc ttcgttaata taaagatgaa ggcacactcc acaacttcct	120
tctggccagg cccagacatg tctgtccttg tgagataaaa gcttccatgg gagccttcct	180
tcctaatacaa g atg caa ata gta cgg tat tcc gaa cag aca cta aaa ata	230
Met Gln Ile Val Arg Tyr Ser Glu Gln Thr Leu Lys Ile	
1 5 10	
gct gtc atc tca aag aat cca gtg ctt gtg tca cag tat gag aaa gta	278
Ala Val Ile Ser Lys Asn Pro Val Leu Val Ser Gln Tyr Glu Lys Val	
15 20 25	
gat gct ggg gaa cag cgt tta atg aat gaa gca ttc cag cca gcc agt	326
Asp Ala Gly Glu Gln Arg Leu Met Asn Glu Ala Phe Gln Pro Ala Ser	
30 35 40 45	
gat ctc ttt gga cct tgc att ctc cat cag att gga tca cct ccc acc	374
Asp Leu Phe Gly Pro Cys Ile Leu His Gln Ile Gly Ser Pro Pro Thr	
50 55 60	
ctg agg ccc ccc aag act ttg aac agt tct tca gtc atc ctt aca gaa	422
Leu Arg Pro Pro Lys Thr Leu Asn Ser Ser Ser Val Ile Leu Thr Glu	
65 70 75	
ag	424

<210> 860  
 <211> 323  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 53..322

<400> 860	
acaagcctct tgatgcataa aaacagctgg gctcccttgg agacagagcg cc atg gga	58
Met Gly	
1	
aac cgg gtc tgc tgc gga gga agc tgg agc tgc cca tca act ttc cag	106

Asn	Arg	Val	Cys	Cys	Gly	Gly	Ser	Trp	Ser	Cys	Pro	Ser	Thr	Phe	Gln	
	5						10					15				
aag	aaa	aag	aaa	aga	gga	agc	caa	aca	aga	cgg	aca	ctg	aag	ccg	cag	154
Lys	Lys	Lys	Lys	Arg	Gly	Ser	Gln	Thr	Arg	Arg	Thr	Leu	Lys	Pro	Gln	
	20					25					30					
cca	caa	cag	ctg	cag	cag	aat	ctc	cca	aag	ggc	cat	gaa	aca	aca	gga	202
Pro	Gln	Gln	Leu	Gln	Gln	Asn	Leu	Pro	Lys	Gly	His	Glu	Thr	Thr	Gly	
	35				40					45					50	
cat	acg	tat	gaa	cgg	gtg	tta	cag	cag	caa	ggg	tct	caa	gag	agg	agt	250
His	Thr	Tyr	Glu	Arg	Val	Leu	Gln	Gln	Gln	Gly	Ser	Gln	Glu	Arg	Ser	
				55				60					65			
cca	ggc	ntc	atg	tcg	gaa	gac	agc	aac	tta	cat	tat	gct	gac	att	caa	298
Pro	Gly	Xaa	Met	Ser	Glu	Asp	Ser	Asn	Leu	His	Tyr	Ala	Asp	Ile	Gln	
		70					75						80			
gtg	tgc	agc	cgt	ccc	cat	gcg	cgg	g								323
Val	Cys	Ser	Arg	Pro	His	Ala	Arg									
		85					90									

<210> 861  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 87..410

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 acttgcaaaa acagcttgca aggaaa atg aag ctt cct att ttc ata gca gat 113  
 Met Lys Leu Pro Ile Phe Ile Ala Asp  
 1 5  
 gca ttc aca gca aga gca ttt cgt ggg aat cct gct gct gtt tgc ctc 161  
 Ala Phe Thr Ala Arg Ala Phe Arg Gly Asn Pro Ala Ala Val Cys Leu  
 10 15 20 25  
 cta gaa aat gaa ttg gat gaa gac atg cat cag aaa att gca agg gag 209  
 Leu Glu Asn Glu Leu Asp Glu Asp Met His Gln Lys Ile Ala Arg Glu  
 30 35 40  
 atg aac ctc tct gaa act gct ttt atc cga aaa ctg cac ccg aca gac 257  
 Met Asn Leu Ser Glu Thr Ala Phe Ile Arg Lys Leu His Pro Thr Asp  
 45 50 55  
 aac ttt gca cnn rgt tcc tgc ttt gga ctg aga tgg ttt aca cca gcg 305  
 Asn Phe Ala Xaa Xaa Ser Cys Phe Gly Leu Arg Trp Phe Thr Pro Ala  
 60 65 70  
 agt gag gtc cca ctc tgt ggc cat gcc amc ctg gct tct gca gct gtg 353  
 Ser Glu Val Pro Leu Cys Gly His Ala Xaa Leu Ala Ser Ala Ala Val  
 75 80 85  
 ctg ttt cac aaa ata aaa arc atg aat agc acg ctc acg ttt gtc act 401  
 Leu Phe His Lys Ile Lys Xaa Met Asn Ser Thr Leu Thr Phe Val Thr  
 90 95 100 105  
 ctg agt gga ga 412  
 Leu Ser Gly



60	65	70	
gaa ata aag agt gaa gaa gtt	cca gcn ntt ggg gta gca tct ccg ccc		411
Glu Ile Lys Ser Glu Glu Val	Pro Ala Xaa Gly Val Ala Ser Pro Pro		
75	80	85	

<210> 864  
 <211> 457  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 41..457

<400> 864	
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	Met Phe Ser Arg Ala
	1 5
ggt gtc gct ggg ctg tgc gcc tgg acc ttg cag ccg caa tgg att caa	103
Gly Val Ala Gly Leu Ser Ala Trp Thr Leu Gln Pro Gln Trp Ile Gln	
10 15 20	
ggt cga aat atg gca act ttg aaa gat atc acc agg aga cta aag tcc	151
Val Arg Asn Met Ala Thr Leu Lys Asp Ile Thr Arg Arg Leu Lys Ser	
25 30 35	
atc aaa aac atc cag aaa att acc aag tct atg aaa atg gta gcg gca	199
Ile Lys Asn Ile Gln Lys Ile Thr Lys Ser Met Lys Met Val Ala Ala	
40 45 50	
gca aaa tat gcc cga gct gag aga gag ctg aaa cca gct cga ata tat	247
Ala Lys Tyr Ala Arg Ala Glu Arg Glu Leu Lys Pro Ala Arg Ile Tyr	
55 60 65	
gga ttg gga tct tta gct ctg tat gaa aaa gct gat atc aag ggg cct	295
Gly Leu Gly Ser Leu Ala Leu Tyr Glu Lys Ala Asp Ile Lys Gly Pro	
70 75 80 85	
gaa gac aag aag aaa cac ctc ctt att ggt gtg tcc tca gat cga gga	343
Glu Asp Lys Lys Lys His Leu Leu Ile Gly Val Ser Ser Asp Arg Gly	
90 95 100	
ctg tgt ggt gct att cat tcc tcc att gct aaa cag atg aaa agc gag	391
Leu Cys Gly Ala Ile His Ser Ser Ile Ala Lys Gln Met Lys Ser Glu	
105 110 115	
ggt gct aca cta aca gca gct ggg aaa gaa gtt ntg ctt gtt gga att	439
Val Ala Thr Leu Thr Ala Ala Gly Lys Glu Val Xaa Leu Val Gly Ile	
120 125 130	
ggt gac ctc ttc tcc ggg	457
Gly Asp Leu Phe Ser Gly	
135	

<210> 865  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 147..422

<400> 865

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cgctgggctg tcggcctgga ccttgacagcc gcaatgtcac caggagacta aagtccatca    120
aaaacatcca gaaaattacc aagtct atg aaa atg gta gcg gca gca aaa tat      173
                Met Lys Met Val Ala Ala Ala Lys Tyr
                  1             5

gcc cga gct gag aga gag ctg aaa cca gct cga ata tat gga ttg gga      221
Ala Arg Ala Glu Arg Glu Leu Lys Pro Ala Arg Ile Tyr Gly Leu Gly
10             15             20             25
tct tta gct ctg tat gaa aaa gct gat atc aag ggg cct gaa gac aag      269
Ser Leu Ala Leu Tyr Glu Lys Ala Asp Ile Lys Gly Pro Glu Asp Lys
                30             35             40
aag aaa cac ctg ctt att ggt gtg tcc tca gat cga gga ctg tgt ggt      317
Lys Lys His Leu Leu Ile Gly Val Ser Ser Asp Arg Gly Leu Cys Gly
                45             50             55
gct att cat tcc tcc att gct aaa cag atg aaa agc gag gtt gct aca      365
Ala Ile His Ser Ser Ile Ala Lys Gln Met Lys Ser Glu Val Ala Thr
                60             65             70
cta aca gca gct ggg aaa gaa gtt ntg ctt gtt gga att ggt gac ctg      413
Leu Thr Ala Ala Gly Lys Glu Val Xaa Leu Val Gly Ile Gly Asp Leu
                75             80             85
ttc tcc ggg
Phe Ser Gly
90

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<210> 866

<211> 330

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 155..328

<400> 866

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agatatcttg caggcactgc agaaactttc tgaagacaaa aaccttgacag aaaggggaaga    120
actcactcat aaattatcta ttatcacaac aaaa atg gac gca aat gac aaa aaa      175
                Met Asp Ala Asn Asp Lys Lys
                  1             5

ata cag gaa aag gat cgt gag ctt gaa att aaa aac atc tat agt cat      223
Ile Gln Glu Lys Asp Arg Glu Leu Glu Ile Lys Asn Ile Tyr Ser His
10             15             20
cca ata ctt aaa aat tta cat gac aca gag gac tat cca aaa gtt tct      271
Pro Ile Leu Lys Asn Leu His Asp Thr Glu Asp Tyr Pro Lys Val Ser
25             30             35
tca aca aaa tca gtc caa gca gac aga aaa att ttg cca ttc aca agt      319
Ser Thr Lys Ser Val Gln Ala Asp Arg Lys Ile Leu Pro Phe Thr Ser
40             45             50             55
atg aga cac ca

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Met Arg His

<210> 867

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 156..500

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tgaggcagcg caccgctgcc gcagggtgcg cgatgccttg aacctgggaa actatgtgaa 120  
gcaacactct ggattttgaa agacatcttt tcatac atg gga cag caa att tcg 173

Met Gly Gln Gln Ile Ser

1

5

gat cag aca cag ttg gtt att aac aag tta cca gaa aaa gta gca aaa 221  
Asp Gln Thr Gln Leu Val Ile Asn Lys Leu Pro Glu Lys Val Ala Lys

10

15

20

cat gtt mcg ttg gtt cga gag agt ggc tcc tta act tat gaa gaa ttt 269  
His Val Xaa Leu Val Arg Glu Ser Gly Ser Leu Thr Tyr Glu Glu Phe

25

30

35

cty ggg aga gta gct gag ctt aat gat gta acg gct aaa gtg gct tct 317  
Leu Gly Arg Val Ala Glu Leu Asn Asp Val Thr Ala Lys Val Ala Ser

40

45

50

ggc cag gaa aaa cat ctt ctc ttt gag gta caa cct ggg tct gat tcc 365  
Gly Gln Glu Lys His Leu Leu Phe Glu Val Gln Pro Gly Ser Asp Ser

55 60 65 70

tct gct ttt tgg aaa gtg gtt gta cgg gtg gtc tgt acc aag att aac 413  
Ser Ala Phe Trp Lys Val Val Val Arg Val Val Cys Thr Lys Ile Asn

75

80

85

aaa agc agt ggc att gtg gag gca tca cgg atc atg aat tta tac cag 461  
Lys Ser Ser Gly Ile Val Glu Ala Ser Arg Ile Met Asn Leu Tyr Gln

90

95

100

ttt att caa ctt tat aaa gat atc aca agt caa gca gca 500  
Phe Ile Gln Leu Tyr Lys Asp Ile Thr Ser Gln Ala Ala

105

110

115

<210> 868

<211> 420

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 6..419

<400> 868

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Met Pro Met Ala Gly Leu Leu Lys Gly Leu Val Arg Gln Leu Glu

1

5

10

15

cag ttc aga gtt caa caa caa gct tcc aag atg ccg ccc aaa gga aaa	98
Gln Phe Arg Val Gln Gln Gln Ala Ser Lys Met Pro Pro Lys Gly Lys	
20 25 30	
agt ggt tct gga aaa gcg ggg aaa ggg gga gca gcc tct ggg agt gac	146
Ser Gly Ser Gly Lys Ala Gly Lys Gly Gly Ala Ala Ser Gly Ser Asp	
35 40 45	
agt gct gac aag aag gct caa ggt ccc aaa ggt ggt ggc aat gca gta	194
Ser Ala Asp Lys Lys Ala Gln Gly Pro Lys Gly Gly Gly Asn Ala Val	
50 55 60	
aag gtc aga cac att cta tgt gaa aaa cat ggc aaa atc atg gaa gcc	242
Lys Val Arg His Ile Leu Cys Glu Lys His Gly Lys Ile Met Glu Ala	
65 70 75	
atg gaa aag tta aag tct ggg atg aga ttc aat gaa gtg gcc gca cag	290
Met Glu Lys Leu Lys Ser Gly Met Arg Phe Asn Glu Val Ala Ala Gln	
80 85 90 95	
tat agt gaa gat aaa gcc agg caa ggg ggt gac ttg ggt tgg atg acc	338
Tyr Ser Glu Asp Lys Ala Arg Gln Gly Gly Asp Leu Gly Trp Met Thr	
100 105 110	
aga ggg tcc atg gtg gga cca ttt caa gaa gca gca ttt gcc ttg cct	386
Arg Gly Ser Met Val Gly Pro Phe Gln Glu Ala Ala Phe Ala Leu Pro	
115 120 125	
gta agt ggg atg gat aag cct gtg ttt aca gac c	420
Val Ser Gly Met Asp Lys Pro Val Phe Thr Asp	
130 135	

<210> 869  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 6..350

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Met Pro Met Ala Gly Leu Leu Lys Gly Leu Val Arg Gln Leu Glu	
1 5 10 15	
cag ttc aga gtt caa caa caa gct tcc aag atg ccg ccc aaa gga aaa	98
Gln Phe Arg Val Gln Gln Gln Ala Ser Lys Met Pro Pro Lys Gly Lys	
20 25 30	
agt ggt tct gga aaa gcg ggg aaa ggg gga gca gcc tct ggg agt gac	146
Ser Gly Ser Gly Lys Ala Gly Lys Gly Gly Ala Ala Ser Gly Ser Asp	
35 40 45	
agt gct gac aag aag gct caa ggt ccc aaa ggt ggt ggc aat gca gta	194
Ser Ala Asp Lys Lys Ala Gln Gly Pro Lys Gly Gly Gly Asn Ala Val	
50 55 60	
aag gtc aga cac att cta tgt gaa aaa cat ggc aaa atc atg gaa gcc	242
Lys Val Arg His Ile Leu Cys Glu Lys His Gly Lys Ile Met Glu Ala	
65 70 75	
atg gaa aag tta aag tct ggg atg aga ttc aat gaa gtg gcc gca cag	290
Met Glu Lys Leu Lys Ser Gly Met Arg Phe Asn Glu Val Ala Ala Gln	
80 85 90 95	



tat agt gaa gat aaa gcc agg caa ggg att ccc agc ctg cag caa cat 338  
 Tyr Ser Glu Asp Lys Ala Arg Gln Gly Ile Pro Ser Leu Gln Gln His  
                   100                  105                  110  
 gct ggt cac caw rg 352  
 Ala Gly His Xaa  
                   115

<210> 870  
 <211> 307  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 133..306

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 catggcaaaa tc atg gaa gcc atg gaa aag tta aag tct ggg atg aga ttc 171  
                   Met Glu Ala Met Glu Lys Leu Lys Ser Gly Met Arg Phe  
                   1                  5                  10  
 aat gaa gtg gcc gca cag tat agt gaa gat aaa gcc agg caa ggg agg 219  
 Asn Glu Val Ala Ala Gln Tyr Ser Glu Asp Lys Ala Arg Gln Gly Arg  
                   15                  20                  25  
 atg cag caa caa ggc acc atc ttg gaa gca gag agc agc cct cac cag 267  
 Met Gln Gln Gln Gly Thr Ile Leu Glu Ala Glu Ser Ser Pro His Gln  
                   30                  35                  40                  45  
 ata cca atc ctg ctg gca cct tca tct tgg act ctt cag c 307  
 Ile Pro Ile Leu Leu Ala Pro Ser Ser Trp Thr Leu Gln  
                   50                  55

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 3..197

<400> 871  
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                   Met Leu Phe Pro Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys  
                   1                  5                  10                  15  
 cag ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc 95  
 Gln Pro Tyr Gly Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly  
                   20                  25                  30  
 ttt tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag aaa 143  
 Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys  
                   35                  40                  45  
 aga agg gga aga aga tca acg aag aaa aga agg aga agg gga aga aaa 191

004220" 666T560

Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys  
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gaa ggg 197  
 Glu Gly  
 65

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 75..449

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 gctgaagaga gaag atg gcg ctt gac gga cca gag cag atg gag ctg gag 110  
                   Met Ala Leu Asp Gly Pro Glu Gln Met Glu Leu Glu  
                   1                  5                  10  
 gag ggg aag gca ggc agc gga ctc cgc caa tat tat ctg tcc aag att 158  
 Glu Gly Lys Ala Gly Ser Gly Leu Arg Gln Tyr Tyr Leu Ser Lys Ile  
                   15                  20                  25  
 gaa gaa ctc cag ctg att gtg aat gat aag agc caa aac ctc cgg agg 206  
 Glu Glu Leu Gln Leu Ile Val Asn Asp Lys Ser Gln Asn Leu Arg Arg  
                   30                  35                  40  
 ctg cag gca cag agg aac gaa cta aat gct aaa gtt cgc cta ttg cgg 254  
 Leu Gln Ala Gln Arg Asn Glu Leu Asn Ala Lys Val Arg Leu Leu Arg  
                   45                  50                  55                  60  
 gag gag cta cag ctg ctg cag gag cag ggc tcc tat gtg ggg gaa gta 302  
 Glu Glu Leu Gln Leu Leu Gln Glu Gln Gly Ser Tyr Val Gly Glu Val  
                   65                  70                  75  
 gtc cgg gcc atg gat aag aag aaa gtg ttg gtc aag gta cat cct gaa 350  
 Val Arg Ala Met Asp Lys Lys Lys Val Leu Val Lys Val His Pro Glu  
                   80                  85                  90  
 ggt aaa ttt gtt gta gac gtg gac aaa aac att gac atc aat gat gtg 398  
 Gly Lys Phe Val Val Asp Val Asp Lys Asn Ile Asp Ile Asn Asp Val  
                   95                  100                  105  
 aca ccc aat tgc cgg gtg gct cta agg aat gac agc tac act ctg cac 446  
 Thr Pro Asn Cys Arg Val Ala Leu Arg Asn Asp Ser Tyr Thr Leu His  
                   110                  115                  120  
 aag 449  
 Lys  
 125

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 117..647

<400> 873

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actcgccgcc gacgacctgt ctgcgcgagc gcacgcnttg ccgcccgcgc gcagaa atg 119  
Met

ctt cgg tta ccc aca gtc ttt cgc cag atg aga ccg gtg tcc agg gta 1  
Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg Val 167  
5 10 15

ctg gct cct cat ctc act cgg gct tat gcc aaa gat gta aaa ttt ggt 215  
Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly  
20 25 30

gca gat gcc cga gcc tta atg ctt caa ggt gta gac ctt tta gcc gat 263  
Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala Asp  
35 40 45

gct gtg gcc gtt aca atg ggg cca aag gga aga aca gtg att att gag 311  
Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile Glu  
50 55 60 65

cag agt tgg gga agt ccc aaa gta aca aaa gat ggt gtg act gtt gca 359  
Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala  
70 75 80

aag tca att gac tta aaa gat aaa tac aar aac att gga gct aaa ctt 407  
Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu  
85 90 95

gtt caa gat gtt gcc aat aac aca aat gaa gaa gct ggg gat ggc act 455  
Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr  
100 105 110

acc act gct act gta ctg gca cgc tct ata gcc aag gaa ggc ttc gag 503  
Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu  
115 120 125

aag att agc aaa ggt gct aat cca gtg gaa atc agg aga ggt gtg atg 551  
Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val Met  
130 135 140 145

tta gct gtt gat gct gta att gct gaa ctt aaa aag cag tct aaa cct 599  
Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro  
150 155 160

gtg acc acc cct gaa gaa att gca cag gtt gct acg att tct gca aac 647  
Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn  
165 170 175

gg 649

<210> 874

<211> 652

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 19..651

<400> 874

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agc act ggc ccc aca gag cca tgg tcc atc cga gag aag cta tgt tta												99
Ser Thr Gly Pro Thr Glu Pro Trp Ser Ile Arg Glu Lys Leu Cys Leu												
	15				20					25		
gca tct tct gtc atg aga agt ggc gat caa aat tgg gta tca gtt agc												147
Ala Ser Ser Val Met Arg Ser Gly Asp Gln Asn Trp Val Ser Val Ser												
	30				35					40		
aga gca atc aag ccc ttt gca gaa cct ggc cgc cct cca gac tgg ttc												195
Arg Ala Ile Lys Pro Phe Ala Glu Pro Gly Arg Pro Pro Asp Trp Phe												
	45				50					55		
tct caa aaa cat tgt gct tcc cag tac tcg gag ctt tta gag acc act												243
Ser Gln Lys His Cys Ala Ser Gln Tyr Ser Glu Leu Leu Glu Thr Thr												
	60				65					70		75
gag aca cca aaa cgg aaa cga ggt gaa aag gga gaa gtg gtg gaa act												291
Glu Thr Pro Lys Arg Lys Arg Gly Glu Lys Gly Glu Val Val Glu Thr												
	80									85		90
gtt gaa gat gtt att gtt cgg aaa ttg act gct gag cga gtt gaa gaa												339
Val Glu Asp Val Ile Val Arg Lys Leu Thr Ala Glu Arg Val Glu Glu												
	95									100		105
cta aag aaa gtg ata aag gaa acc cag gag aga tat aga cgg cta aag												387
Leu Lys Lys Val Ile Lys Glu Thr Gln Glu Arg Tyr Arg Arg Leu Lys												
	110				115					120		
aga gat gca gaa cta att caa gct gga cac atg gac agc aga ctg gat												435
Arg Asp Ala Glu Leu Ile Gln Ala Gly His Met Asp Ser Arg Leu Asp												
	125				130					135		
gag ctt tgc aat gac att gca acg aaa aag aaa ttg gaa gaa gag gag												483
Glu Leu Cys Asn Asp Ile Ala Thr Lys Lys Lys Leu Glu Glu Glu Glu												
	140				145					150		155
gct gaa gta aag agg aag gct aca gat gct gca tac cag gct cgt caa												531
Ala Glu Val Lys Arg Lys Ala Thr Asp Ala Ala Tyr Gln Ala Arg Gln												
	160									165		170
gca gta aaa aca ccc ccc cgg agg tta ccc act gtg atg gtt cgc tct												579
Ala Val Lys Thr Pro Pro Arg Arg Leu Pro Thr Val Met Val Arg Ser												
	175									180		185
cct ata gat tct gcc tcc cca gga ggt gat tat cca ctt ggg gac ttg												627
Pro Ile Asp Ser Ala Ser Pro Gly Asp Tyr Pro Leu Gly Asp Leu												
	190				195					200		
act cca acc act atg gaa gag gct a												652
Thr Pro Thr Thr Met Glu Glu Ala												
	205				210							

<210> 875  
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 <212> DNA  
 <213> Homo sapiens

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 <221> CDS  
 <222> 549..782

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cccacagagc catgggccat ccgagagaag ctatgttttag catcttctgt catgagaagt 120
ggcgatcaaaa attgggggtg gtcttactct gtcaccagg ctggagtgca gtggcgcgat 180
ttgggctcac tgcagcctct tgacttctct gggtcaagg atcctcctac ctcagctgcc 240
caagtagctg ggaccacagg ccgcaggtat cagttagcag agcaatcaag ccctttgcag 300
aacctggccg ccctccagac tggttctctc aaaaacattg tgcttcccag tactcggagc 360
ttttagagac cactgagaca ccaaaacgga aacgaggtga aaagggagaa gtggtggaaa 420
ctggtgaaga tggtattgtt cggaaattga ctgctgagcg agttgaagaa ctaaagaaag 480
tgataaagga aaccaggag agatatagac ggctaaagag agatgcagaa ctaattcaag 540
ctggacac atg gac agc aga ctg gat gag ctt tgc aat gac att gca acg 590
Met Asp Ser Arg Leu Asp Glu Leu Cys Asn Asp Ile Ala Thr

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1 5 10
aaa aag aaa ttg gaa gaa gag gag gct gaa gta aag agg aag gct aca 638
Lys Lys Lys Leu Glu Glu Glu Glu Ala Glu Val Lys Arg Lys Ala Thr
15 20 25 30
gat gct gca tac cag gct cgt caa gca gta aaa aca ccc ccc cgg agg 686
Asp Ala Ala Tyr Gln Ala Arg Gln Ala Val Lys Thr Pro Pro Arg Arg
35 40 45
tta ccc act gtg atg gtt cgc tct cct ata gat tct gcc tcc cca gga 734
Leu Pro Thr Val Met Val Arg Ser Pro Ile Asp Ser Ala Ser Pro Gly
50 55 60
ggg gat tat cca ctt ggg gac ttg act cca acc act atg gaa gag gct a 783
Gly Asp Tyr Pro Leu Gly Asp Leu Thr Pro Thr Thr Met Glu Glu Ala
65 70 75

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<210> 876  
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<213> Homo sapiens

<220>  
<221> CDS  
<222> 45..413

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Met Asn Leu Gly
1
gat ggt tta aag ctt gaa act gaa tta ctg gat gga aaa acc aag cta 104
Asp Gly Leu Lys Leu Glu Thr Glu Leu Leu Asp Gly Lys Thr Lys Leu
5 10 15 20
ata ttg tct cca tat gaa cat aaa tca aaa att tct gtg aag atg gga 152
Ile Leu Ser Pro Tyr Glu His Lys Ser Lys Ile Ser Val Lys Met Gly
25 30 35
aat aag gcc aag att gca aaa tgt cct tta aga aca aaa act ggg cac 200
Asn Lys Ala Lys Ile Ala Lys Cys Pro Leu Arg Thr Lys Thr Gly His
40 45 50
att cta aaa tca aca caa gat act tgt att ggg agt gaa aaa ctt ttg 248
Ile Leu Lys Ser Thr Gln Asp Thr Cys Ile Gly Ser Glu Lys Leu Leu
55 60 65
caa aag aag cca gtt ggt tca gaa aca tca cag gca aaa ggt gaa aaa 296
Gln Lys Lys Pro Val Gly Ser Glu Thr Ser Gln Ala Lys Gly Glu Lys
70 75 80
aat gga atg act ttt tca tcc act aag gat tta tgt aaa caa tgt ata 344

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Asn Gly Met Thr Phe Ser Ser Thr Lys Asp Leu Cys Lys Gln Cys Ile  
 85 90 95 100  
 gat aaa gac tgt ctt cat atc cag aaa gag att tca cct gca act cct 392  
 Asp Lys Asp Cys Leu His Ile Gln Lys Glu Ile Ser Pro Ala Thr Pro  
 105 110 115  
 aat atg cag aag act aga aac a 414  
 Asn Met Gln Lys Thr Arg Asn  
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<210> 877  
 <211> 511  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 134..511

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 ttcgccgtag catctttcgc agcggaccga agagaagaaa agtaggccag agccgaactc 120  
 tcttctgccc aag atg tct att ggt gtg ccg att aaa gta ctg cat gag 169  
 Met Ser Ile Gly Val Pro Ile Lys Val Leu His Glu  
 1 5 10  
 gcc gag ggc cac att gtg aca tgt gag acg aac acc ggt gag gta tat 217  
 Ala Glu Gly His Ile Val Thr Cys Glu Thr Asn Thr Gly Glu Val Tyr  
 15 20 25  
 cgg ggg aag ctc att gaa gca gag gac aac atg aac tgc cag atg tcc 265  
 Arg Gly Lys Leu Ile Glu Ala Glu Asp Asn Met Asn Cys Gln Met Ser  
 30 35 40  
 aac atc aca gtc aca tac aga gat ggc cga gtg gca cag ctg gag cag 313  
 Asn Ile Thr Val Thr Tyr Arg Asp Gly Arg Val Ala Gln Leu Glu Gln  
 45 50 55 60  
 gta tac atc cgt ggc agc aaa atc cgc ttt ctg att ttg cct gac atg 361  
 Val Tyr Ile Arg Gly Ser Lys Ile Arg Phe Leu Ile Leu Pro Asp Met  
 65 70 75  
 ctg aag aac gca ccc atg tta aag agc atg aaa aat aaa aac caa ggc 409  
 Leu Lys Asn Ala Pro Met Leu Lys Ser Met Lys Asn Lys Asn Gln Gly  
 80 85 90  
 tca ggg gct ggc cga gga aaa gct gcc att ctc aag gcc caa gtg gcc 457  
 Ser Gly Ala Gly Arg Gly Lys Ala Ala Ile Leu Lys Ala Gln Val Ala  
 95 100 105  
 gca aga gga aga gga cgt gga atg gga snt gga aac atc ttt caa aag 505  
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 110 115 120  
 cga aga 511  
 Arg Arg  
 125

<210> 878  
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 <212> DNA  
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<220>  
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 <222> 167..433

<400> 878

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tattctgttt gtaagccttt ctgatgtgcc attattgctg ctgtgtttcc tgttttatgt      120
aggtggtagc cctcggagag taccagatgg gactgtgggtt actgtc atg gcg ggt      175
                                     Met Ala Gly
                                     1
aac gat gaa aat tat tct gct gag ctc cgg aat gcc tct gct gtw atg      223
Asn Asp Glu Asn Tyr Ser Ala Glu Leu Arg Asn Ala Ser Ala Val Met
   5                                     10                                     15
aaa aac caa gta gca agg ttc aac gat ctg aga ttt gtg ggc cgg agt      271
Lys Asn Gln Val Ala Arg Phe Asn Asp Leu Arg Phe Val Gly Arg Ser
20                                     25                                     30                                     35
gga cga ggc aag agt ttc acc ttg acc ata acc gtc ttc aca aat cct      319
Gly Arg Gly Lys Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro
                                     40                                     45                                     50
ccc caa gta gct acc tat cac aga gca att aaa gtt aca gta gat gga      367
Pro Gln Val Ala Thr Tyr His Arg Ala Ile Lys Val Thr Val Asp Gly
                                     55                                     60                                     65
cct cgg gaa ccc aga agg cac aga cag aag ctt gat gac tct aaa cct      415
Pro Arg Glu Pro Arg Arg His Arg Gln Lys Leu Asp Asp Ser Lys Pro
                                     70                                     75                                     80
agt ttg ttc tct gac cgc ct      435
Ser Leu Phe Ser Asp Arg
   85

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<210> 879  
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 <212> DNA  
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<220>  
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 <222> 147..311

<400> 879

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actgggcttg cgaggaaacc gcctcggagc tgcagccgaa gscaaggaat cactgaagat      120
cggcgaggga ggacagggggg ttcattc atg ggt ggc ttt ttc tca agt ata ttt      173
                                     Met Gly Gly Phe Phe Ser Ser Ile Phe
                                     1                                     5
tcc agt ctg ttt gga act cgg gaa atg aga att tta att ttg gga tta      221
Ser Ser Leu Phe Gly Thr Arg Glu Met Arg Ile Leu Ile Leu Gly Leu
10                                     15                                     20                                     25
gat gga gca gga aaa acc aca att ttg tac aga tta caa gtg gga gaa      269
Asp Gly Ala Gly Lys Thr Thr Ile Leu Tyr Arg Leu Gln Val Gly Glu
                                     30                                     35                                     40
gtt gtt act act ata cct acc att gga ttt aat gta gag acg g      312

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Val Val Thr Thr Ile Pro Thr Ile Gly Phe Asn Val Glu Thr  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 25..369

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Met Glu Ser Gly Lys Met Ala Pro Pro  
1 5  
aag aac gct ccg aga gat gcc ttg gtg atg gca cag atc ctg aag gat 99  
Lys Asn Ala Pro Arg Asp Ala Leu Val Met Ala Gln Ile Leu Lys Asp  
10 15 20 25  
atg gga atc aca gag tat gaa cca agg gtt ata aat caa atg ttg gaa 147  
Met Gly Ile Thr Glu Tyr Glu Pro Arg Val Ile Asn Gln Met Leu Glu  
30 35 40  
ttt gct ttc cgt tat gtg act aca att ctg gat gat gca aaa att tat 195  
Phe Ala Phe Arg Tyr Val Thr Thr Ile Leu Asp Asp Ala Lys Ile Tyr  
45 50 55  
tcg agc cat gct aag aaa cct aat gtt gat gca gat gat gtg aga ctg 243  
Ser Ser His Ala Lys Lys Pro Asn Val Asp Ala Asp Asp Val Arg Leu  
60 65 70  
gca atc cag tgt cgt gct gac caa tct ttt acc tct cct ccc cca aga 291  
Ala Ile Gln Cys Arg Ala Asp Gln Ser Phe Thr Ser Pro Pro Pro Arg  
75 80 85  
gat ttt tta ctg gat atc gca agg cag aaa aat caa acc cct ttg cca 339  
Asp Phe Leu Leu Asp Ile Ala Arg Gln Lys Asn Gln Thr Pro Leu Pro  
90 95 100 105  
ctg att aag cca tat gca gga cct aga ctg c 370  
Leu Ile Lys Pro Tyr Ala Gly Pro Arg Leu  
110 115

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<212> DNA  
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<221> CDS  
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caaagaactt gcgtcaaaat caggactgaa atacattaat gtgggtgatt tagctcgaga 180  
agtctgatca tcggatatc atg gag tct ggc aag acg gct tct ccc aag agc 232



	Met	Glu	Ser	Gly	Lys	Thr	Ala	Ser	Pro	Lys	Ser	
	1			5					10			
atg ccg aaa gat gca cag atg atg gca caa atc ctg aag gat atg ggg												280
Met Pro Lys Asp Ala Gln Met Met Ala Gln Ile Leu Lys Asp Met Gly												
	15			20					25			
att aca gaa tat gag cca aga gtt ata aat cag atg ttg gag ttt gcc												328
Ile Thr Glu Tyr Glu Pro Arg Val Ile Asn Gln Met Leu Glu Phe Ala												
	30			35					40			
ttc cga kat gtg acc aca att cta gat gat gca aaa att tat tca agc												376
Phe Arg Xaa Val Thr Thr Ile Leu Asp Asp Ala Lys Ile Tyr Ser Ser												
	45			50					55			
cat gct aag aaa gct act gtt gat gca gat gat gtg cga wtg gca atc												424
His Ala Lys Lys Ala Thr Val Asp Ala Asp Asp Val Arg Xaa Ala Ile												
	60			65					70			75
cag twc cgc gct gat cag tct ttt a												449
Gln Xaa Arg Ala Asp Gln Ser Phe												
	80											

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 <212> DNA  
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 <222> 315..545

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caaagaactt gcgtcaaaat caggactgaa atacattaat gtgggtgatt tagctcgaga	180
agtctgatca tcggatawca tggagtckgg caagatggcg cctcccaaga acgctccgag	240
agatgccttg gtgatggcac agatcctgaa ggatatggga atcacagagt atgaaccaag	300
ggttataaan tcaa atg ttg gaa ttt gct ttc cgt tat gtg act aca att	350
Met Leu Glu Phe Ala Phe Arg Tyr Val Thr Thr Ile	
	1 5 10
ctg gat gat gca aaa att tat tcg agc cat gct aag aaa cct aat gtt	398
Leu Asp Asp Ala Lys Ile Tyr Ser Ser His Ala Lys Lys Pro Asn Val	
	15 20 25
gat gca gat gat gtg aga ctg gca atc cag tgt cgt gct gac caa tct	446
Asp Ala Asp Asp Val Arg Leu Ala Ile Gln Cys Arg Ala Asp Gln Ser	
	30 35 40
ttt acc tct cct ccc cca aga gat ttt tta ctg gat atc gca agg cag	494
Phe Thr Ser Pro Pro Pro Arg Asp Phe Leu Leu Asp Ile Ala Arg Gln	
	45 50 55 60
aaa aat caa acc cct ttg cca ctg att aag cca tat gca gga cct aga	542
Lys Asn Gln Thr Pro Leu Pro Leu Ile Lys Pro Tyr Ala Gly Pro Arg	
	65 70 75
ctg c	546
Leu	

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<212> DNA  
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gcgattttct attttgtaca tacattattt tgtatatact gtat atg atg act tca 116  
Met Met Thr Ser  
1  
gtg agc agt gac cat tgt cga ggt gct cag gaa aaa cca cag att tca 164  
Val Ser Ser Asp His Cys Arg Gly Ala Gln Glu Lys Pro Gln Ile Ser  
5 10 15 20  
gca gca caa tca acg caa cca cag aaa caa gtg gta cag gca aca gct 212  
Ala Ala Gln Ser Thr Gln Pro Gln Lys Gln Val Val Gln Ala Thr Ala  
25 30 35  
gaa cag atg cgt ctc gct caa gtg atc ttt gat aag aat gat tca gat 260  
Glu Gln Met Arg Leu Ala Gln Val Ile Phe Asp Lys Asn Asp Ser Asp  
40 45 50  
ttt gaa gct aaa gtt aag cag ctt atg gaa gtg aca g 297  
Phe Glu Ala Lys Val Lys Gln Leu Met Glu Val Thr  
55 60

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<211> 500  
<212> DNA  
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<220>  
<221> CDS  
<222> 299..499

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ccagtcattc tgcttgctga tcaagaacac ttaacagctt caggctttcc tgatactttg 120  
acgaaggtaa ttgggactcc catcaagtct ccacacagct agcagccacs yggggcactt 180  
ctccagcata tgtaagtga actcagaagg caacattccc tgaacatast cttccaccag 240  
aatctcctct acagattttt gctgsscctt ttaccagtgg ctgaatctac tttctctt 298  
atg gat cgc tta cac ctg aga cga act aca gaa cag cac gta cca gag 346  
Met Asp Arg Leu His Leu Arg Arg Thr Thr Glu Gln His Val Pro Glu  
1 5 10 15  
gtg gaa gtc caa gtc aaa cgc aga agg act gcc tca ctg agc aac caa 394  
Val Glu Val Gln Val Lys Arg Arg Arg Thr Ala Ser Leu Ser Asn Gln  
20 25 30  
gag tgt cag ttg tac ccg agg cgt tct cag cag cag caa gta cct gtg 442  
Glu Cys Gln Leu Tyr Pro Arg Arg Ser Gln Gln Gln Gln Val Pro Val  
35 40 45  
gtg gat ttc cag gct gaa ctg agg cag gca ttc tta gct gag aca cca 490  
Val Asp Phe Gln Ala Glu Leu Arg Gln Ala Phe Leu Ala Glu Thr Pro  
50 55 60

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Arg Gly Gly  
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Met  
1  
cag ctg gag cac tgc ctt tct cct tct atc atg ctc tcc aag aaa ttt 167  
Gln Leu Glu His Cys Leu Ser Pro Ser Ile Met Leu Ser Lys Lys Phe  
5 10 15  
ctc aat gtg agc agc agc tac cca cat tca ggc gga tcc gag ctt gtc 215  
Leu Asn Val Ser Ser Ser Tyr Pro His Ser Gly Gly Ser Glu Leu Val  
20 25 30  
ttg cac gat cat ccc att atc tcg acc act gac aac ctg gag aga agt 263  
Leu His Asp His Pro Ile Ile Ser Thr Thr Asp Asn Leu Glu Arg Ser  
35 40 45  
tca cct ttg aaa aaa att acc agg ggg atg acg aat cag tca gat aca 311  
Ser Pro Leu Lys Lys Ile Thr Arg Gly Met Thr Asn Gln Ser Asp Thr  
50 55 60 65  
gac aat ttt cct gac tcc aag gac tca cca ggg gac gtc cag aga agt 359  
Asp Asn Phe Pro Asp Ser Lys Asp Ser Pro Gly Asp Val Gln Arg Ser  
70 75 80  
aaa ctc tct cct gtc ttg gac ggg gtc tc 388  
Lys Leu Ser Pro Val Leu Asp Gly Val  
85 90

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accagcggcg ac atg acg ggg tac act ccg gat gag aaa ctg cgg ctg cag 171  
Met Thr Gly Tyr Thr Pro Asp Glu Lys Leu Arg Leu Gln  
1 5 10

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cag ctg cga gag ctg aga agg cga tgg ctg aag gac cag gag ctg agc	219
Gln Leu Arg Glu Leu Arg Arg Arg Trp Leu Lys Asp Gln Glu Leu Ser	
15 20 25	
cct cgg gag ccg gtg ctg ccc cca cag aag atg ggg cct atg gag aaa	267
Pro Arg Glu Pro Val Leu Pro Pro Gln Lys Met Gly Pro Met Glu Lys	
30 35 40 45	
ttc tgg aat aaa ttt ttg gag aat aaa tcc cct tgg agg aaa atg gtc	315
Phe Trp Asn Lys Phe Leu Glu Asn Lys Ser Pro Trp Arg Lys Met Val	
50 55 60	
cat ggg gta tac aaa aag agt atc ttt gtt ttc act cat gta ctt gta	363
His Gly Val Tyr Lys Lys Ser Ile Phe Val Phe Thr His Val Leu Val	
65 70 75	
cct gtc tgg att att cat tat tac atg aag tat cat gtt tct gaa aaa	411
Pro Val Trp Ile Ile His Tyr Tyr Met Lys Tyr His Val Ser Glu Lys	
80 85 90	
cca tat ggc ata gtt gaa aag aag tcc aga ata ttc cct ggt gat aca	459
Pro Tyr Gly Ile Val Glu Lys Lys Ser Arg Ile Phe Pro Gly Asp Thr	
95 100 105	
att ctg g	
Ile Leu	466
110	
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tg atg ttt agt ttg agg ttc att tgt gtc aaa cag aac tct gtg tac	107
Met Phe Ser Leu Arg Phe Ile Cys Val Lys Gln Asn Ser Val Tyr	
1 5 10 15	
tgg tgt tca gtt cca agg gaa ggc tgg cac tcc atg gag gtt agc aaa	155
Trp Cys Ser Val Pro Arg Glu Gly Trp His Ser Met Glu Val Ser Lys	
20 25 30	
aac cat cat tat gcc aac cat cag gaa tac gat cca gac act tgt gcc	203
Asn His His Tyr Ala Asn His Gln Glu Tyr Asp Pro Asp Thr Cys Ala	
35 40 45	
cgc tgt atc tca gta cga gag tct cca agg aaa aca caa cac agt cag	251
Arg Cys Ile Ser Val Arg Glu Ser Pro Arg Lys Thr Gln His Ser Gln	
50 55 60	
gta gtc gag gga gca ata gtt aca cag aga aga gac aga gca aga tca	299
Val Val Glu Gly Ala Ile Val Thr Gln Arg Arg Asp Arg Ala Arg Ser	
65 70 75	
gtt tca gta gtg cgt atg ggt ccc ctg tgt cca ggg gtc cct cgt ggc	347
Val Ser Val Val Arg Met Gly Pro Leu Cys Pro Gly Val Pro Arg Gly	
80 85 90 95	
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105

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                                   Met Ala Lys Gly Asp Pro
                                   1                               5
aag aaa cca aag ggc aag atg tcc gct tat gcc ttc ttt gtg cag aca      162
Lys Lys Pro Lys Gly Lys Met Ser Ala Tyr Ala Phe Phe Val Gln Thr
                                   10                               15                               20
tgc aga gaa gaa cat aag aag aaa aac cca gag gtc cct gtc aat ttt      210
Cys Arg Glu Glu His Lys Lys Lys Asn Pro Glu Val Pro Val Asn Phe

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gcg gaa ttt tcc aag aag tgc tct gag agg tgg aag acg atg tcc ggg			258
Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Gly			
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aaa gag aaa tct aaa ttt gat gaa atg gca aag gca gat aaa gtg cgc			306
Lys Glu Lys Ser Lys Phe Asp Glu Met Ala Lys Ala Asp Lys Val Arg			
55	60	65	70
tat gat cgg gaa atg aag gat tat gga cca gct aag gga ggc aag aag			354
Tyr Asp Arg Glu Met Lys Asp Tyr Gly Pro Ala Lys Gly Gly Lys Lys			
75	80	85	
aag aag gat cct aat gct ccc aaa agg cca ccg tct gga ttc ttc ctg			402
Lys Lys Asp Pro Asn Ala Pro Lys Arg Pro Pro Ser Gly Phe Phe Leu			
90	95	100	
ttc tgt tca gaa ttc cgc ccc aag atc aaa tcc aca aac ccc ggc atc			450
Phe Cys Ser Glu Phe Arg Pro Lys Ile Lys Ser Thr Asn Pro Gly Ile			
105	110	115	
tct att gga gac gg			464
Ser Ile Gly Asp			
120			

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gccttcactg gatcttcagc ctgttaaaca agaaaacgaa aaacccttc cagaaaac	178
atg gat gca ttt gaa aaa gtg aga aca aaa tta gaa aca cag cca caa	226
Met Asp Ala Phe Glu Lys Val Arg Thr Lys Leu Glu Thr Gln Pro Gln	
1	5
gaa gaa tat gaa atc atc aat gtg gaa gtt aaa cat ggt ggt ttt gtt	274
Glu Glu Tyr Glu Ile Ile Asn Val Glu Val Lys His Gly Gly Phe Val	
20	25
tat tac caa gaa ggt tgt tgc ttg gtt cgt tcc aaa gat gaa gaa gca	322
Tyr Tyr Gln Glu Gly Cys Cys Leu Val Arg Ser Lys Asp Glu Glu Ala	
35	40
gac agt gat aat tat gaa gtt tta ttc aat ttg gag gaa ctt aag tta	370
Asp Ser Asp Asn Tyr Glu Val Leu Phe Asn Leu Glu Glu Leu Lys Leu	
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gac cag ccc ttc att gat tgt atc aga gt	399
Asp Gln Pro Phe Ile Asp Cys Ile Arg	
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tgcttcact	ggtttgtgtc	cagagccgga	ctgattctct	caatttgca	tcttcagcct	180
gttaaacaag	aaaacgaaaa	accccttcca	gaaaac	atg	gat gca ttt gaa aaa	234
				Met Asp Ala Phe Glu Lys		
				1	5	
gtg aga aca	aaa tta gaa	aca cag cca	caa gaa gaa	tat gaa	atc atc	282
Val Arg Thr	Lys Leu Glu	Thr Gln Pro	Gln Glu Glu	Tyr Glu	Ile Ile	
	10	15	20			
aat gtg gaa	gtt aaa cat	ggt ggt ttt	gtt tat tac	caa gaa	ggt tgt	330
Asn Val Glu	Val Lys His	Gly Gly Phe	Val Tyr Tyr	Gln Glu	Gly Cys	
	25	30	35			
tgc ttg gtt	cgt tcc aaa	gat gaa gaa	gca gac aat	gat aat	tat gaa	378
Cys Leu Val	Arg Ser Lys	Asp Glu Glu	Ala Asp Asn	Asp Asn	Tyr Glu	
	40	45	50			
gtt tta ttc	aat ttg gag	gaa ctt aag	tta gac cag	ccc ttc	att gat	426
Val Leu Phe	Asn Leu Glu	Glu Glu Leu	Lys Leu Asp	Gln Pro	Phe Ile Asp	
55	60	65	70			
gta tca gag	ttg ctc cag	atg aaa a				451
Val Ser Glu	Leu Leu Gln	Met Lys				
	75					

<210> 892  
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 <212> DNA  
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<220>  
 <221> CDS  
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ggctttcaag	tctgtggttg	tgggcactaa	cccagacaag	aaaaggaaag	acctgcagta	180
tcggtgcagg	aaaggcaaag	aagggaacat	ctcaac	atg gaa	aag ctc tac aaa	234
				Met Glu Lys Leu Tyr Lys		
				1	5	
gaa aat gaa	gga aag cca	gag aat gaa	aga aac cta	gaa agt	gag gga	282
Glu Asn Glu	Gly Lys Pro	Glu Asn Glu	Arg Asn Leu	Glu Ser	Glu Gly	
	10	15	20			
aag cca gag	gat gag gga	agt aca gaa	gat gaa gga	aag tca	gac gag	330
Lys Pro Glu	Asp Glu Gly	Ser Thr Glu	Asp Glu Gly	Lys Ser	Asp Glu	
	25	30	35			
gaa gaa aag	ccg gac atg	gag ggg aag	aca gaa tgc	gag gga	aag cga	378
Glu Glu Lys	Pro Asp Met	Glu Gly Lys	Thr Glu Cys	Glu Gly	Lys Arg	

40		45		50		
gag gat gag gga gan cca ggt gat gag gga caa ctg gaa gat gan gga						426
Glu Asp Glu Gly Xaa Pro Gly Asp Glu Gly Gln Leu Glu Asp Xaa Gly						
55		60		65		70
aac cag gaa aag cag ggc aag tct gaa ggt gag gmc aag cca caa agt						474
Asn Gln Glu Lys Gln Gly Lys Ser Glu Gly Glu Xaa Lys Pro Gln Ser						
	75		80		85	
gag ggc aag cca gcc tcc ca						494
Glu Gly Lys Pro Ala Ser						
	90					

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 <212> DNA  
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Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp	
1 5 10 15	
agc aaa ggc ttt gat gaa tac atg aag gag cta ggt gag gca ccc ggc	155
Ser Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Glu Ala Pro Gly	
	20 25 30
ctg gca gcg cct gca acg tgg cgt gtt gtg cgg tcg tct gtc cct agg	203
Leu Ala Ala Pro Ala Thr Trp Arg Val Val Arg Ser Ser Val Pro Arg	
	35 40 45
tcc ccg tca gcg tgc cag att ctg ggg cag gag atg ctc ggc ggc cta	251
Ser Pro Ser Ala Cys Gln Ile Leu Gly Gln Glu Met Leu Gly Gly Leu	
	50 55 60
ccc cca tcc cct ccc a	
Pro Pro Ser Pro Pro	267
	65

<210> 894  
 <211> 454  
 <212> DNA  
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<220>  
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Met Ser Asp Gln Gln Leu Asp Cys Ala Leu Asp Leu Met Arg Arg	
1 5 10 15	



ctg cct ccc cag caa atc gag aaa aac ctc agc gac ctg atc gas stg	157
Leu Pro Pro Gln Gln Ile Glu Lys Asn Leu Ser Asp Leu Ile Xaa Xaa	
20 25 30	
gtc ccc agt cta tgt gag gat ctc ctg tct tct gtt gac cag cca ctg	205
Val Pro Ser Leu Cys Glu Asp Leu Leu Ser Ser Val Asp Gln Pro Leu	
35 40 45	
aaa att gcc aga gac aag gtg gtg gga aag gat tac ctt ttg tgt gac	253
Lys Ile Ala Arg Asp Lys Val Val Gly Lys Asp Tyr Leu Leu Cys Asp	
50 55 60	
tac aac aga gat ggg gac tcc tat agg tca cca tgg agt aac aag tat	301
Tyr Asn Arg Asp Gly Asp Ser Tyr Arg Ser Pro Trp Ser Asn Lys Tyr	
65 70 75	
gac cct ccc ttg gag gat ggg gcc atg ccg tca gct cgg ctg aga aag	349
Asp Pro Pro Leu Glu Asp Gly Ala Met Pro Ser Ala Arg Leu Arg Lys	
80 85 90 95	
ctg gag gtg gaa gcc aac aat gcc ttt gac cag tat cga gac ctg tat	397
Leu Glu Val Glu Ala Asn Asn Ala Phe Asp Gln Tyr Arg Asp Leu Tyr	
100 105 110	
ttt gaa ggt ggc gtc tca tct gtc tac ctc tgg gat ctg gat cat ggc	445
Phe Glu Gly Gly Val Ser Ser Val Tyr Leu Trp Asp Leu Asp His Gly	
115 120 125	
ttt gct gga	454
Phe Ala Gly	
130	

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 <212> DNA  
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Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser	
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gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa	149
Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys	
25 30 35	
ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta	197
Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu	
40 45 50	
ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga	245
Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg	
55 60 65 70	
cag tcg gaa gat gac gat tca gag act gaa aaa cct gag gct gat gac	293
Gln Ser Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp	
75 80 85	

cca aag gat aat aca gaa gca gaa aag cga gac ccc ca 331  
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<220>  
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 Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser  
 10 15 20

gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa 149  
 Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys  
 25 30 35

ggc gga ttg gta tct gat gcc tat ggg gag gat acc aat ccg cta tat 197  
 Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Thr Asn Pro Leu Tyr  
 40 45 50

cca gcc ttg tct ctg cca ccg cc 220  
 Pro Ala Leu Ser Leu Pro Pro  
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 atttggagtt cttacaac atg gca gac att gac aac aaa gaa cag tct gaa 171  
 Met Ala Asp Ile Asp Asn Lys Glu Gln Ser Glu  
 1 5 10

ctt gat caa gat ttg gat gat gtt gaa gaa gta gaa gaa gag gaa act 219  
 Leu Asp Gln Asp Leu Asp Asp Val Glu Glu Val Glu Glu Glu Glu Thr  
 15 20 25

ggt gaa gaa aca aaa ctc aaa gca cgt cag cta act gtt cag atg atg 267  
 Gly Glu Glu Thr Lys Leu Lys Ala Arg Gln Leu Thr Val Gln Met Met  
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caa aat cct cag att ctt gca gcc ctt caa gaa aga ctt gat ggt ctg 315

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Val	Glu	Thr	Pro	Thr	Gly	Tyr	Ile	Glu	Ser	Leu	Pro	Arg	Val	Val	Lys	
60					65					70					75	
aga	cga	gtg	aat	gct	ctc	aaa	aac	ctg	caa	gtt	aaa	tgt	gca	cag	ata	411
Arg	Arg	Val	Asn	Ala	Leu	Lys	Asn	Leu	Gln	Val	Lys	Cys	Ala	Gln	Ile	
			80						85				90			
gaa	gcc	aaa	ttc	tat	gag	gaa	gtc	atg	akc	ttg	aaa	gga	agt	atg	ctg	459
Glu	Ala	Lys	Phe	Tyr	Glu	Glu	Val	Met	Xaa	Leu	Lys	Gly	Ser	Met	Leu	
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						1											
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Asn	Pro	Trp	Asp	Pro	Ala	Ser	Ala	Pro	Asn	Gly	Ala	Gly	Leu	Val	Leu		
5				10					15					20			
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Gly	His	Phe	Ile	Ala	Ser	Gly	Met	Val	Asn	Gln	Glu	Met	Leu	Asn	Met		
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Ser	Lys	Lys	Thr	Val	Ser	Cys	Phe	Val	Asn	Phe	Thr	Arg	Leu	Gln	Gln		
			40					45					50				
atc	aca	aat	att	caa	gct	gaa	atc	tac	cag	aaa	aac	ctg	gaa	att	gaa	248	
Ile	Thr	Asn	Ile	Gln	Ala	Glu	Ile	Tyr	Gln	Lys	Asn	Leu	Glu	Ile	Glu		
		55				60						65					
ctc	ctg	aaa	cta	gaa	aaa	gat	aca	gca	gat	gtt	gtt	cat	cct	ttc	ttt	296	
Leu	Leu	Lys	Leu	Glu	Lys	Asp	Thr	Ala	Asp	Val	Val	His	Pro	Phe	Phe		
		70				75				80							
ttg	gag	atg	aag	tct	tgc	tat	gtt	gcc	cag	gct	ggg	ctc	gaa	ctc	atg	344	
Leu	Glu	Met	Lys	Ser	Cys	Tyr	Val	Ala	Gln	Ala	Gly	Leu	Glu	Leu	Met		
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gcc																347	
Ala																	

<210> 899  
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                               Met Ser Gly Lys
                               1
gca aat gct tcc aag aaa aac gct caa cag tta aaa aga aat cca aag      162
Ala Asn Ala Ser Lys Lys Asn Ala Gln Gln Leu Lys Arg Asn Pro Lys
5                               10                               15                               20
aga aaa aag gat aat gag gaa gtt gtg ttg tca gag aat aag gtt aga      210
Arg Lys Lys Asp Asn Glu Glu Val Val Leu Ser Glu Asn Lys Val Arg
                               25                               30                               35
aac aca gtg aaa aat aaa aat cat ctg aaa gat ctg tct tct gaa      258
Asn Thr Val Lys Lys Asn Lys Asn His Leu Lys Asp Leu Ser Ser Glu
                               40                               45                               50
gga caa aca aag cac act aac cta aaw cac gga aag aca gca gcc agc      306
Gly Gln Thr Lys His Thr Asn Leu Xaa His Gly Lys Thr Ala Ala Ser
                               55                               60                               65
aag aga aaa acc tgg caa cct ctg tca aag agt acc aga gac cat ttg      354
Lys Arg Lys Thr Trp Gln Pro Leu Ser Lys Ser Thr Arg Asp His Leu
                               70                               75                               80
caa act atg atg gaa tca gta ata atg aca att ttr ngf aac agt att      402
Gln Thr Met Met Glu Ser Val Ile Met Thr Ile Leu Xaa Asn Ser Ile
85                               90                               95                               100
ana gaa aaa gaa gam ata cra tac cat ctc aac ttc ctg aag aaa aga t      451
Xaa Glu Lys Glu Xaa Ile Xaa Tyr His Leu Asn Phe Leu Lys Lys Arg
                               105                               110                               115

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<210> 900  
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 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 37..420

<400> 900

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                               Met Ala Asp Gly Lys Ala
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gga gac gag aag cct gaa aag tcg cag cga gct gga gcc gcc ggn aga      102
Gly Asp Glu Lys Pro Glu Lys Ser Gln Arg Ala Gly Ala Ala Gly Arg
                               10                               15                               20
cct gaa gaa gaa gca gaa aaa cct gtg aaa act aag act gtt tct tcc      150
Pro Glu Glu Glu Ala Glu Lys Pro Val Lys Thr Lys Thr Val Ser Ser
                               25                               30                               35
agt aat gga ggg gaa agt tcc agt cgc agc gct gag aag cga tca gct      198

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Ser	Asn	Gly	Gly	Glu	Ser	Ser	Ser	Arg	Ser	Ala	Glu	Lys	Arg	Ser	Ala	
40						45				50						
gaa	gaa	gaa	gct	gcc	gac	ctc	cca	aca	aag	cct	aca	aag	atc	tcc	aag	246
Glu	Glu	Glu	Ala	Ala	Asp	Leu	Pro	Thr	Lys	Pro	Thr	Lys	Ile	Ser	Lys	
55					60				65					70		
ttt	gga	ttt	gcc	ata	ggt	agt	cag	acg	aca	aag	aaa	gca	tca	gcc	ata	294
Phe	Gly	Phe	Ala	Ile	Gly	Ser	Gln	Thr	Thr	Lys	Lys	Ala	Ser	Ala	Ile	
			75					80					85			
tcc	atc	rnn	ctt	gga	tca	agt	aag	nct	aaa	gaa	act	gtt	cca	act	ctt	342
Ser	Ile	Xaa	Leu	Gly	Ser	Ser	Lys	Xaa	Lys	Glu	Thr	Val	Pro	Thr	Leu	
			90				95					100				
gct	cca	aaa	act	ctt	tca	gta	gca	gca	gct	ttt	rnt	gaa	gat	gaa	ggt	390
Ala	Pro	Lys	Thr	Leu	Ser	Val	Ala	Ala	Ala	Phe	Xaa	Glu	Asp	Glu	Gly	
		105				110					115					
agt	gaa	cca	gag	gaa	atg	cct	cca	gaa	gca	aa						422
Ser	Glu	Pro	Glu	Glu	Met	Pro	Pro	Glu	Ala							
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gcttgtggac	ggtgtaggcc	gctgcaggcc	acc atg aac	cgg ctt ccg	gat gac											114
			Met Asn Arg	Leu Pro Asp	Asp											
			1		5											
tac gac	ccc tac	gcg gtt	gaa gag	cct agc	gac gag	gag ccg	gct ttg									162
Tyr Asp	Pro Tyr	Ala Val	Glu Glu	Pro Ser	Asp Glu	Glu Pro	Ala Leu									
	10		15		20											
agc agg	tgg gct	ccc gcc	cca nmc	tgg ccc	ccg agg	att tgg	gtc gag									210
Ser Arg	Trp Ala	Pro Ala	Pro Xaa	Trp Pro	Pro Arg	Ile Trp	Val Glu									
	25		30		35											
gcc tgg	ctt tgg	tcg cct	cca ttc	gtt gcg	cct gcc	gag cct	acg cag									258
Ala Trp	Leu Trp	Ser Pro	Pro Phe	Val Ala	Pro Ala	Glu Pro	Thr Gln									
	40		45		50		55									
acc cta	gcg gct	cgg gag	cct gtc	gtg cct	gtt act	tgt gcg	aas caa									306
Thr Leu	Ala Ala	Arg Glu	Pro Val	Val Pro	Val Thr	Cys Ala	Xaa Gln									
		60		65		70										
agg gct	ttc ctg	atg ggg	tcg cgc	agt ccc	gga g											340
Arg Ala	Phe Leu	Met Gly	Ser Arg	Ser Pro	Gly											
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<220>  
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<222> 94..447

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Met Asn Arg Leu Pro Asp Asp  
1 5  
tac gac ccc tac gcg gtt gaa gag cct agc gac gag gag ccg gct ttg 162  
Tyr Asp Pro Tyr Ala Val Glu Glu Pro Ser Asp Glu Glu Pro Ala Leu  
10 15 20  
agc agc tct gag gat gaa gtg gat gtg ctt tta cat gga act cct gac 210  
Ser Ser Ser Glu Asp Glu Val Asp Val Leu Leu His Gly Thr Pro Asp  
25 30 35  
caa aaa cga aaa ctc atc aga gaa tgt ctt acc gga gaa agt gaa tca 258  
Gln Lys Arg Lys Leu Ile Arg Glu Cys Leu Thr Gly Glu Ser Glu Ser  
40 45 50 55  
tct agt gaa gat gaa ttt gaa aag gag atg gaa gct gaa tta aat tct 306  
Ser Ser Glu Asp Glu Phe Glu Lys Glu Met Glu Ala Glu Leu Asn Ser  
60 65 70  
acc atg aaa aca atg gag gac aag tta tcc tct ctg gga act gga tct 354  
Thr Met Lys Thr Met Glu Asp Lys Leu Ser Ser Leu Gly Thr Gly Ser  
75 80 85  
tcc tca gga aat gga aaa gtt gca aca gct ccg aca agg tac tac gat 402  
Ser Ser Gly Asn Gly Lys Val Ala Thr Ala Pro Thr Arg Tyr Tyr Asp  
90 95 100  
gat ata tat ntt gat tct gat tcc gag gat gaa gac aga gca gta 447  
Asp Ile Tyr Xaa Asp Ser Asp Ser Glu Asp Glu Asp Arg Ala Val  
105 110 115

<210> 903  
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tcccgaactgt aaacataggg gatatgtgtt cacttagcat ggacttctgg gaggggcca 180  
ggaagggcgg tctggagttt tattgaatag agcagtgtgt attcggtctgc ctgcctgccc 240  
gctgcttgct tctctggctg tgcctctgct taaagaaatc agtccttctt ttccgactta 300  
gtcctcgagg agaagtttca gactacaagg tatcattgga acatttcaag atcatcaaat 360  
caaattccac agggattggg gaccaaccag aaggctcaga catctgattg ctgacctgtc 420  
cagacatcat ctggtctccc tgaacctgaa atcacacc atg gat gat ttt gag cgt 476  
Met Asp Asp Phe Glu Arg  
1 5  
cgc aga gaa ctt aga agg caa aag agg gag gag atg cga ctc gaa gca 524

Arg	Arg	Glu	Leu	Arg	Arg	Gln	Lys	Arg	Glu	Glu	Met	Arg	Leu	Glu	Ala		
			10					15					20				
gaa	aga	atc	gcc	tac	cag	agg	aat	gac	gat	gat	gaa	gag	gag	gca	gcc		572
Glu	Arg	Ile	Ala	Tyr	Gln	Arg	Asn	Asp	Asp	Asp	Glu	Glu	Glu	Ala	Ala		
		25					30				35						
cgg	gaa	cgg	cgc	cgc	cga	gcc	cga	cag	gaa	cgg	ctg	cgg	cag	aag	cag		620
Arg	Glu	Arg	Arg	Arg	Arg	Ala	Arg	Gln	Glu	Arg	Leu	Arg	Gln	Lys	Gln		
	40					45				50							
gag	gaa	gaa	tcc	ttg	gna	cag	gtg	acc	gac	cag	gtg	gag	gtg	aat	gcc		668
Glu	Glu	Glu	Ser	Leu	Xaa	Gln	Val	Thr	Asp	Gln	Val	Glu	Val	Asn	Ala		
55					60					65				70			
cag	aac	agt	gtg	cct	gac	gag	gag	gcc	aag	aca	acc	a					705
Gln	Asn	Ser	Val	Pro	Asp	Glu	Glu	Ala	Lys	Thr	Thr						
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		Met	Ala	Ala	Gln	Gly	Glu	Pro	Gln	Val	Gln	Phe	Lys				
		1				5				10							
ctt	gta	ttg	gtt	ggt	gat	ggt	ggt	act	gga	aaa	acg	acc	ttc	gtg	aaa		159
Leu	Val	Leu	Val	Gly	Asp	Gly	Gly	Thr	Gly	Lys	Thr	Thr	Phe	Val	Lys		
		15				20					25						
cgt	cat	ttg	act	ggt	gaa	ttt	gag	aag	aag	tat	gta	gcc	acc	ttg	ggt		207
Arg	His	Leu	Thr	Gly	Glu	Phe	Glu	Lys	Lys	Tyr	Val	Ala	Thr	Leu	Gly		
	30				35					40							
gtt	gag	gtt	cat	ccc	cta	gtg	ttc	cac	acc	aac	aga	gga	cct	att	aag		255
Val	Glu	Val	His	Pro	Leu	Val	Phe	His	Thr	Asn	Arg	Gly	Pro	Ile	Lys		
45				50					55					60			
ttc	aat	gta	tgg	gac	aca	gcc	ggc	cag	gag	aaa	ttc	ggt	gga	ctg	aga		303
Phe	Asn	Val	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Lys	Phe	Gly	Gly	Leu	Arg		
			65				70					75					
gat	ggc	tat	tat	atc	ctc	acg	caa	gca	acc								333
Asp	Gly	Tyr	Tyr	Ile	Leu	Thr	Gln	Ala	Thr								
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 <222> 76..504

<400> 905

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ggaaggaacg ccgcg atg gct gcg cag gga gag ccc cag gtc cag ttc aaa 111
      Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys
      1          5          10
ctt gta ttg gtt ggt gat ggt ggt act gga aaa acg acc ttc gtg aaa 159
Leu Val Leu Val Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys
      15          20          25
cgt cat ttg act ggt gaa ttt gag aag aag tat gta gcc acc ttg ggt 207
Arg His Leu Thr Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly
      30          35          40
gtt gag gtt cat ccc cta gtg ttc cac acc aac aga gga cct att aag 255
Val Glu Val His Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys
      45          50          55          60
ttc aat gta tgg gac aca gcc ggc cag gag aaa ttc ggt gga ctg aga 303
Phe Asn Val Trp Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg
      65          70          75
gat ggc tat tat atc caa gcc cag tgt gcc atc ata atg ttt gat gta 351
Asp Gly Tyr Tyr Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val
      80          85          90
aca tcg aga gtt act tac aag aat gtg cct aac tgg cat aga gat ctg 399
Thr Ser Arg Val Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu
      95          100          105
gta cga gtg tgt gaa aac atc ccc att gtg ttg tgt ggc aac aaa gtg 447
Val Arg Val Cys Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val
      110          115          120
gat att aag gac agg aaa gtg aag gcg aaa tcc att gtc ttc cac cga 495
Asp Ile Lys Asp Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg
      125          130          135          140
aag aag aat 504
Lys Lys Asn

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<210> 906

<211> 267

<212> DNA

<213> Homo sapiens

<220>

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<222> 108..266

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      Met Ala Asp
      1
aaa cca gac atg ggg gaa atc gcc agc ttc gat aag gcc aag ctg naa 164
Lys Pro Asp Met Gly Glu Ile Ala Ser Phe Asp Lys Ala Lys Leu Xaa
      5          10          15
gaa aaa cgg aga cgc agg aga aga aca ccc tgc cga cca aag aga cca 212
Glu Lys Arg Arg Arg Arg Arg Arg Thr Pro Cys Arg Pro Lys Arg Pro

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20	25	30	35	
ttg agc agg aga agc	gga gtg aaa ttt cct	aag atc ctg gtc	aat ggt	260
Leu Ser Arg Arg Ser	Gly Val Lys Phe Pro	Lys Ile Leu Val	Asn Gly	
	40	45	50	
ctc gtg c				267
Leu Val				

<210> 907  
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 <222> 108..281

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	Met Ala Asp
	1
aaa cca gac atg ggg gaa atc gcc agc ttc gat aag gcc aag ctg aag	164
Lys Pro Asp Met Gly Glu Ile Ala Ser Phe Asp Lys Ala Lys Leu Lys	
5 10 15	
aaa acg gag acg cag gag aag aac acc ctg ccg acc aaa gag agt gag	212
Lys Thr Glu Thr Gln Glu Lys Asn Thr Leu Pro Thr Lys Glu Ser Glu	
20 25 30 35	
tgt gcc tcg gtc tcc cgc gcc cca gcc cag ccc ctc acc ctg ctc ttc	260
Cys Ala Ser Val Ser Arg Ala Pro Ala Gln Pro Leu Thr Leu Leu Phe	
40 45 50	
ctt gca aac cca ctc ctc cac cc	283
Leu Ala Asn Pro Leu Leu His	
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<220>  
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gcgagtctcg tgctgtgtcg gacctgcagc ccctggcctt ccgccacc atg gag tac	117
	Met Glu Tyr
	1
ctc atc ggt atc caa ggc ccc gac tat gtt ctt gtc gcc tcc gac cgg	165
Leu Ile Gly Ile Gln Gly Pro Asp Tyr Val Leu Val Ala Ser Asp Arg	
5 10 15	
gtg gcc gcc agc aat att gtc cag atg aag gac gat cat gac aag atg	213

Val	Ala	Ala	Ser	Asn	Ile	Val	Gln	Met	Lys	Asp	Asp	His	Asp	Lys	Met		
20					25					30					35		
ttt	aag	atg	agt	gaa	aag	ata	tta	ctc	ctg	tgt	gtt	gga	gag	gct	gga		261
Phe	Lys	Met	Ser	Glu	Lys	Ile	Leu	Leu	Leu	Cys	Val	Gly	Glu	Ala	Gly		
				40				45					50				
gac	act	gta	cag	ttt	gca	gaa	tat	att	cag	aaa	aac	gtg	caa	ctt	tat		309
Asp	Thr	Val	Gln	Phe	Ala	Glu	Tyr	Ile	Gln	Lys	Asn	Val	Gln	Leu	Tyr		
			55				60					65					
aag	atg	cga	aat	gga	tat	gaa	ttg	tct	ccc	acg	gca	gca	gct	aac	ttc		357
Lys	Met	Arg	Asn	Gly	Tyr	Glu	Leu	Ser	Pro	Thr	Ala	Ala	Ala	Asn	Phe		
		70				75					80						
aca	cgc	cga	aac	ctg	gct	gac	tgt	ctt	cgg	agt	cgg	acc	cca	tat	cat		405
Thr	Arg	Arg	Asn	Leu	Ala	Asp	Cys	Leu	Arg	Ser	Arg	Thr	Pro	Tyr	His		
	85				90				95								
gtg	aac	ctc	ctc	ctg	gct	ggc	tat	gat	gag	cat	gaa	ggg	cca	gcg	ctg		453
Val	Asn	Leu	Leu	Leu	Ala	Gly	Tyr	Asp	Glu	His	Glu	Gly	Pro	Ala	Leu		
100				105					110					115			
tat	tac	atg	gac	tac	ctg	gca	gcc	ttg	gcc	aag	gcc	ctt	ttg	cag	ccc		501
Tyr	Tyr	Met	Asp	Tyr	Leu	Ala	Ala	Leu	Ala	Lys	Ala	Leu	Leu	Gln	Pro		
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Thr	Ala	Met															

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					Met Glu Tyr												
					1												
ctc atc ggt atc caa ggc ccc gac tat gnt ctt gtc gcc tcc gac cgg																165	
Leu Ile Gly Ile Gln Gly Pro Asp Tyr Xaa Leu Val Ala Ser Asp Arg																	
5				10				15									
gtg gcc gcc agc aat att gtc cas ktg aag gac gga tat gaa ttg tct																213	
Val Ala Ala Ser Asn Ile Val Xaa Xaa Lys Asp Gly Tyr Glu Leu Ser																	
20				25				30								35	
ccc acg gca gca gct aac ttc aca cgc cga aac ctg gct gac tgt ctt																261	
Pro Thr Ala Ala Ala Asn Phe Thr Arg Arg Asn Leu Ala Asp Cys Leu																	
			40				45					50					
cgg agt cgg rcc cca tat cat gtg aac ctc ctc ctg gct gsc tat gat																309	
Arg Ser Arg Xaa Pro Tyr His Val Asn Leu Leu Leu Ala Xaa Tyr Asp																	
			55				60					65					
gag cat gaa ggg cca gcg ctg tat tac atg gac tac ctg gca gcc ttg																357	
Glu His Glu Gly Pro Ala Leu Tyr Tyr Met Asp Tyr Leu Ala Ala Leu																	
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gcc aag gcc ctt ttg cag ccc acg gct atg g																388	

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<213> Homo sapiens

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tccctcccca caaagatagg tggcgcgtgt ttcaggggtct ctcgtctctc tcctacagaa 180  
aagaaaaaga aaaaaatgtc attagaagag gcgtaacacg tcagtccgtc cccaggtttg 240  
tgtttcctgg agtggccgaa agagatcagt tctaacctgc tctgcagaat aacggctctg 300  
cctcccgaca ctcttggcga gggttttgta cagtttgctc cgggagctgt ttcttcgctt 360  
ccaccttttt ctccccaca cttcgcggct tcttcattgct ttttcttctc anccatttct 420  
ggccaaaact acaaacaaga cttcgcagat cgagcctgcg tgctgccgaa gcagggcgcc 480  
gagtccatgc gaactgccat ctgatccgct cttatca atg aag cag ccg atc atg 535  
Met Lys Gln Pro Ile Met  
1 5  
gcg gat ggc ccc cgg tgc aag agg cgc aaa caa gcc aat ccc agg agg 583  
Ala Asp Gly Pro Arg Cys Lys Arg Arg Lys Gln Ala Asn Pro Arg Arg  
10 15 20  
aaa aac ggt aag aag cag ccc gaa cca aac ttt tcc ggg cca cta cgc 631  
Lys Asn Gly Lys Lys Gln Pro Glu Pro Asn Phe Ser Gly Pro Leu Arg  
25 30 35  
ggc tcg aga ccc agg gag aag gag ggg gaa agg gaa agg aac cga ggc 679  
Gly Ser Arg Pro Arg Glu Lys Glu Gly Glu Arg Glu Arg Asn Arg Gly  
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681

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<212> DNA  
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<220>  
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Met Val His Ala Glu Ala Phe Ser Arg Pro Leu  
1 5 10  
agt cgg aat gaa gtt gtt ggt tta att ttc cgt ttg aca ata ttt ggt 159  
Ser Arg Asn Glu Val Val Gly Leu Ile Phe Arg Leu Thr Ile Phe Gly  
15 20 25

gca gtg aca tac ttt act atc aaa tgg atg gta gat gca att gat cca 207  
Ala Val Thr Tyr Phe Thr Ile Lys Trp Met Val Asp Ala Ile Asp Pro  
30 35 40  
acc aga aag caa aaa gta gaa gct cag aaa cag gca gaa aaa cta atg 255  
Thr Arg Lys Gln Lys Val Glu Ala Gln Lys Gln Ala Glu Lys Leu Met  
45 50 55  
aag caa att gga gtg aaa aat gtg aag ctc tca gaa tat gaa atg agt 303  
Lys Gln Ile Gly Val Lys Asn Val Lys Leu Ser Glu Tyr Glu Met Ser  
60 65 70 75  
att gct gct cat ctt gta gac cct ctt aat atg cat gtt act tgg agt 351  
Ile Ala Ala His Leu Val Asp Pro Leu Asn Met His Val Thr Trp Ser  
80 85 90  
gat ata gca ggt tta gat gat gtc att acg gat ctg aaa gac aca gtc 399  
Asp Ile Ala Gly Leu Asp Asp Val Ile Thr Asp Leu Lys Asp Thr Val  
95 100 105  
atc tta cct atc aaa aag aaa cat ttg ttt gag aat tcc agg ctt ctg 447  
Ile Leu Pro Ile Lys Lys Lys His Leu Phe Glu Asn Ser Arg Leu Leu  
110 115 120  
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agagggtaga aaaatctgcc cttcatttaa aaattgaatg tttcact atg tat tta 176  
Met Tyr Leu  
1  
aaa agc gat tca gga tta gga gga tgg ata acc ata cca gct gta gct 224  
Lys Ser Asp Ser Gly Leu Gly Gly Trp Ile Thr Ile Pro Ala Val Ala  
5 10 15  
gat gtt cta aaa tat tct tgc att gtt tgc tgg tct tct agg gaa aag 272  
Asp Val Leu Lys Tyr Ser Cys Ile Val Cys Trp Ser Ser Arg Glu Lys  
20 25 30 35  
aat aat gtg gaa cag gac ctt aag gag aag gaa gat act att aaa cag 320  
Asn Asn Val Glu Gln Asp Leu Lys Glu Lys Glu Asp Thr Ile Lys Gln  
40 45 50  
agg aca agt gag gtt cag gat ctt caa gat gaa gtt caa agg gag aat 368  
Arg Thr Ser Glu Val Gln Asp Leu Gln Asp Glu Val Gln Arg Glu Asn  
55 60 65  
act aat ctg caa aaa cta cag gcc cag aaa cag cag gta cag gaa ctc 416  
Thr Asn Leu Gln Lys Leu Gln Ala Gln Lys Gln Gln Val Gln Glu Leu  
70 75 80  
ctt gat gaa ctg gat gag cag aaa gcc cag ctg gag gag caa ctc aag 464

Leu Asp Glu Leu Asp Glu Gln Lys Ala Gln Leu Glu Glu Gln Leu Lys  
 85 90 95

gaa gtc  
 Glu Val  
 100

470

<210> 913  
 <211> 308  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 112..306

<400> 913

accgccgctg ccggcgccgc tgctgtaggg gaccagcgcg ggtgcscaga cgaaaggcgc 60  
 tctttgccag ctgaaagtcc cacggaaaaa ctaccatctc cctgcscac c atg gca 117  
 Met Ala  
 1  
 gac gaa att gat ttc act act gga gat gcc ggg gct tcc agc ant tac 165  
 Asp Glu Ile Asp Phe Thr Thr Gly Asp Ala Gly Ala Ser Ser Xaa Tyr  
 5 10 15  
 cct atg cag tgc tgc gcc ttg cgc aaa aac ggc ttc gtg gtg ctc aaa 213  
 Pro Met Gln Cys Ser Ala Leu Arg Lys Asn Gly Phe Val Val Leu Lys  
 20 25 30  
 gga cga cca tgc aaa ata gtg gag atg tca act tcc aaa act gga aag 261  
 Gly Arg Pro Cys Lys Ile Val Glu Met Ser Thr Ser Lys Thr Gly Lys  
 35 40 45 50  
 cat ggt cat gcc aag gtt cac ctt gtc gga att gat att tty wyk ga 308  
 His Gly His Ala Lys Val His Leu Val Gly Ile Asp Ile Phe Xaa  
 55 60 65

<210> 914  
 <211> 465  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 125..463

<400> 914

acattaacgc acacatcagt tccaggcccc attccattct ctgaacatct tctgacacac 60  
 tgacagtgtc gagcagagca agaaaacggg caatgctgtg agagccattg gaagactgtc 120  
 ctct atg gca atg atc tca ggg ctc agt ggc agg aaa tcc tca aca ggc 169  
 Met Ala Met Ile Ser Gly Leu Ser Gly Arg Lys Ser Ser Thr Gly  
 1 5 10 15  
 tca cca acc agc ccg ctc aat gca gaa aaa cta gaa tct gaa gaa gat 217  
 Ser Pro Thr Ser Pro Leu Asn Ala Glu Lys Leu Glu Ser Glu Glu Asp  
 20 25 30  
 gtg tcc caa gct ttc ctt gag gct gtt gct gag gaa aag cct cat gta 265

Val	Ser	Gln	Ala	Phe	Leu	Glu	Ala	Val	Ala	Glu	Glu	Lys	Pro	His	Val	
			35					40					45			
aaa	ccc	tat	ttc	tct	aag	acc	att	cgc	gat	tta	gaa	gtt	gtg	gag	gga	313
Lys	Pro	Tyr	Phe	Ser	Lys	Thr	Ile	Arg	Asp	Leu	Glu	Val	Val	Glu	Gly	
		50					55					60				
agt	gct	gct	aga	ttt	gac	tgc	aag	att	gaa	gga	tac	cca	gac	ccc	gag	361
Ser	Ala	Ala	Arg	Phe	Asp	Cys	Lys	Ile	Glu	Gly	Tyr	Pro	Asp	Pro	Glu	
	65					70					75					
gtt	gtc	tgg	ttc	aaa	gat	gac	cag	tca	atc	agg	gag	tcc	cgc	cac	ttc	409
Val	Val	Trp	Phe	Lys	Asp	Asp	Gln	Ser	Ile	Arg	Glu	Ser	Arg	His	Phe	
80					85				90					95		
cag	ata	gac	tac	gat	gag	gac	ggg	aac	tgc	tct	tta	att	att	agt	gat	457
Gln	Ile	Asp	Tyr	Asp	Glu	Asp	Gly	Asn	Cys	Ser	Leu	Ile	Ile	Ser	Asp	
				100				105						110		
gtt	tgc	gg														465
Val	Cys															

&lt;210&gt; 915

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 91..393

&lt;400&gt; 915

gcacgccgcc	ttcgccgctg	gctccgtctg	ttggggggcg	aacacgccgc	ggtcctcgtc		60
gtgtgaagta	agaactctgc	tagagaggaa	atg gct gct tca tca tca tcc tcc				114
			Met Ala Ala Ser Ser Ser Ser Ser				
			1		5		
tca gct ggt ggg gtc agt gga agt tct gtc act gga tct ggt ttc agt							162
Ser Ala Gly Gly Val Ser Gly Ser Ser Val Thr Gly Ser Gly Phe Ser							
10		15		20			
gtc tca gac ctt gcc cca cca cgg aaa gcc ctt ttc acc tac ccc aaa							210
Val Ser Asp Leu Ala Pro Pro Arg Lys Ala Leu Phe Thr Tyr Pro Lys							
25		30		35		40	
gga gct gga gag atg tta gaa gat ggc tct gag aga ttc ctc tgc gaa							258
Gly Ala Gly Glu Met Leu Glu Asp Gly Ser Glu Arg Phe Leu Cys Glu							
	45		50		55		
tct gtt ttt agc tat caa gtg gca tcc acg ctt aaa cag gtg aaa cat							306
Ser Val Phe Ser Tyr Gln Val Ala Ser Thr Leu Lys Gln Val Lys His							
	60		65		70		
gat cag caa gtt gct cgg atg gaa aaa cta gct ggt ttg gta gaa gag							354
Asp Gln Gln Val Ala Arg Met Glu Lys Leu Ala Gly Leu Val Glu Glu							
	75		80		85		
ctg gag gct gac gag tgg cgg ttt aag ccc atc gag cag							393
Leu Glu Ala Asp Glu Trp Arg Phe Lys Pro Ile Glu Gln							
	90		95		100		

&lt;210&gt; 916

&lt;211&gt; 458

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 156..458

<400> 916

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gtggtgagcg caccactcag gctggtcctg ggggtggggc tgtaggggaa agtgctaaag 120  
ccgctgagtg aagtaagaac tctgctagag aggaa atg gct gct tca tca tca 173  
Met Ala Ala Ser Ser Ser  
1 5  
tcc tcc tca gct ggt ggg gtc agt gga agt tct gtc act gga tct ggt 221  
Ser Ser Ser Ala Gly Gly Val Ser Gly Ser Ser Val Thr Gly Ser Gly  
10 15 20  
ttc agt gtc tca gac ctt gcc cca cca cgg aaa gcc ctt ttc acc tac 269  
Phe Ser Val Ser Asp Leu Ala Pro Pro Arg Lys Ala Leu Phe Thr Tyr  
25 30 35  
ccc aaa gga gct gga gag atg tta gaa gat ggc tct gag aga ttc ctc 317  
Pro Lys Gly Ala Gly Glu Met Leu Glu Asp Gly Ser Glu Arg Phe Leu  
40 45 50  
tgc gaa tct gtt ttt agc tat caa gtg gca tcc acg ctt aaa cag gtg 365  
Cys Glu Ser Val Phe Ser Tyr Gln Val Ala Ser Thr Leu Lys Gln Val  
55 60 65 70  
aaa cat gat cag caa gtt gct cgg atg gaa aaa cta gct ggt ttg gta 413  
Lys His Asp Gln Gln Val Ala Arg Met Glu Lys Leu Ala Gly Leu Val  
75 80 85  
gaa gag ctg gag gct gac gag tgg cgg ttt aag ccc atc gag cag 458  
Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe Lys Pro Ile Glu Gln  
90 95 100

<210> 917

<211> 449

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 100..447

<400> 917

acgttttcgct tccgcctacc tcgcccaggc tgccagaccg gaagcgctcc gctgtacctg 60  
gatcctgctc ctctgggttg aaaccggggc gccgccaag atg ccg gct tac cac 114  
Met Pro Ala Tyr His  
1 5  
tct tct ctc atg gat cct gat acc aaa ctc atc gga aac atg gca ctg 162  
Ser Ser Leu Met Asp Pro Asp Thr Lys Leu Ile Gly Asn Met Ala Leu  
10 15 20  
ttg cct atc aga agt caa ttc aaa gga cct gcc ccc aga gag aca aaa 210  
Leu Pro Ile Arg Ser Gln Phe Lys Gly Pro Ala Pro Arg Glu Thr Lys  
25 30 35  
gat aca gat att gtg gat gaa gcc atc tat tac ttc aag gcc aat gtc 258

Asp Thr Asp Ile Val Asp Glu Ala Ile Tyr Tyr Phe Lys Ala Asn Val	
40 45 50	
ttc ttc aaa aac tat gaa att aag aat gaa gct gat agg acc ttg ata	306
Phe Phe Lys Asn Tyr Glu Ile Lys Asn Glu Ala Asp Arg Thr Leu Ile	
55 60 65	
tat ata act ctc tac att tct gaa tgt ctg aag aaa ctg caa aag tgc	354
Tyr Ile Thr Leu Tyr Ile Ser Glu Cys Leu Lys Lys Leu Gln Lys Cys	
70 75 80 85	
aat tcc aaa agc caa ggt gag aaa gaa atg tat acg ctg gga atc act	402
Asn Ser Lys Ser Gln Gly Glu Lys Glu Met Tyr Thr Leu Gly Ile Thr	
90 95 100	
aat ttt ccc att cct gga gag cct ggt ttt cca ctt aac gca att ta	449
Asn Phe Pro Ile Pro Gly Glu Pro Gly Phe Pro Leu Asn Ala Ile	
105 110 115	

<210> 918  
 <211> 353  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 52..351

<400> 918	
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Met Gln	
1	
tcg gat gat gtt atc tgg gat aca cta gga aac aag caa ttt tgt tcc	105
Ser Asp Asp Val Ile Trp Asp Thr Leu Gly Asn Lys Gln Phe Cys Ser	
5 10 15	
ttc aaa ata aga acc aag act cag agc ttc tgc cga aat gaa tat agc	153
Phe Lys Ile Arg Thr Lys Thr Gln Ser Phe Cys Arg Asn Glu Tyr Ser	
20 25 30	
ctg act gga ctg tgt aat cgg tca tcc tgt ccc ctg gca aat agt cag	201
Leu Thr Gly Leu Cys Asn Arg Ser Ser Cys Pro Leu Ala Asn Ser Gln	
35 40 45 50	
tat gcc act att aaa gaa gag aaa gga cag tgc tac ttg tat atg aag	249
Tyr Ala Thr Ile Lys Glu Glu Lys Gly Gln Cys Tyr Leu Tyr Met Lys	
55 60 65	
ggt ata gaa cga gcg gct ttt cct cgg cgt ctc tgg gaa cgg gtc cgg	297
Val Ile Glu Arg Ala Ala Phe Pro Arg Arg Leu Trp Glu Arg Val Arg	
70 75 80	
ctt agt aaa aac tat gag aaa gca ctg gag caa ata gat gaa aat ctg	345
Leu Ser Lys Asn Tyr Glu Lys Ala Leu Glu Gln Ile Asp Glu Asn Leu	
85 90 95	
att act gg	
Ile Thr	353
100	

<210> 919  
 <211> 449  
 <212> DNA



<213> Homo sapiens

<220>

<221> CDS

<222> 246..449

<400> 919

ggtggcggcc attttgattg gtgttgatt tattttagg agaggctcct gagcgctagg 60  
tccgcactgt ggtgactgaa cccagaagtc ggggagcagt tgtcctccgc tgcacagagg 120  
ctactctgga gctctgtgac ggcgcccagc gtgaccact cctgggcccag gatacggacc 180  
gtcgtgcccata tatctcctgg ctggtcgccc taccctcccg actctgctta aaaccacgtg 240  
gttcg atg gct gcc gcg gct acg ctg agg ctc tcc gct cag gag tct cac 290  
Met Ala Ala Ala Thr Leu Arg Leu Ser Ala Gln Glu Ser His  
1 5 10 15  
tct gtc atc cag act gga gtg cag tgg cgt gat cac agc tca cca caa 338  
Ser Val Ile Gln Thr Gly Val Gln Trp Arg Asp His Ser Ser Pro Gln  
20 25 30  
cct ccg cct aca gga gat att ttg ata cag gat ctc act cta ttc ccc 386  
Pro Pro Pro Thr Gly Asp Ile Leu Ile Gln Asp Leu Thr Leu Phe Pro  
35 40 45  
agg cta gag tgc gat ggc acc atc tgc gct gat tgc rac ctc cat ttt 434  
Arg Leu Glu Cys Asp Gly Thr Ile Ser Ala Asp Cys Xaa Leu His Phe  
50 55 60  
cca gga agg ctc ttt  
Pro Gly Arg Leu Phe 449  
65

<210> 920

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 246..425

<400> 920

ggtggcggcc attttgattg gtgttgatt tattttagg agaggctcct gagcgctrng 60  
tccgcactgt ggtgactgaa cccagaagtc ggggagcagt tgtcctccgc tgcacagagg 120  
ctactctgga gctctgtgac ggcgcccagc gtgaccact cctgggcccag gatacggacc 180  
gtcgtgcccata tatctcctgg ctggtcgccc taccctcccg actctgctta aaaccacgtg 240  
gttcg atg gct gcc gcg gct acg ctg agg ctc tcc gct cag atc ctg cac 290  
Met Ala Ala Ala Thr Leu Arg Leu Ser Ala Gln Ile Leu His  
1 5 10 15  
tgg atg gat cag cgg aca aca cac aga ccg gta atc tgg gtc aat cag 338  
Trp Met Asp Gln Arg Thr Thr His Arg Pro Val Ile Trp Val Asn Gln  
20 25 30  
ttc tgc cat ccc acc nag aac aga aaa cag cat gaa aaa ctc act tta 386  
Phe Cys His Pro Thr Xaa Asn Arg Lys Gln His Glu Lys Leu Thr Leu  
35 40 45  
acc ccc tat gaa tcc atc tcc aac cag act gat cag cac 425  
Thr Pro Tyr Glu Ser Ile Ser Asn Gln Thr Asp Gln His

50

55

60

<210> 921  
 <211> 445  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 246..443

&lt;400&gt; 921

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ggtggcggcc attttgattg gtgttgatt tatttgtagg agaggctcct gagcgctagg      60
tccgactgt ggtgactgaa cccagaagtc ggggagcagt tgcctccgc tgcacagagg      120
ctactctgga gctctgtgac ggcgccagc gtgacctact cctgggccag gatacggacc      180
gtcgtgcca tatctcctgg ctggtcgccc taccctcccg actctgctta aaaccacgtg      240
gttcg atg gct gcc gcg gct acg ctg agg ctc tcc gct cag gag tct cgc      290
Met Ala Ala Ala Ala Thr Leu Arg Leu Ser Ala Gln Glu Ser Arg
  1          5          10          15
tct gtc atc cag act gga gtg cag tgg cgt gat cac agc tca cca caa      338
Ser Val Ile Gln Thr Gly Val Gln Trp Arg Asp His Ser Ser Pro Gln
          20          25          30
cct ccg cct aca gga gat att ttg ata cag cag ctt ctt ctt ggc aca      386
Pro Pro Pro Thr Gly Asp Ile Leu Ile Gln Gln Leu Leu Leu Gly Thr
          35          40          45
atc ctg aac tgg gca gaa cgt cct tcc caa act cgc gga aga caa atg      434
Ile Leu Asn Trp Ala Glu Arg Pro Ser Gln Thr Arg Gly Arg Gln Met
          50          55          60
gct cct gtg ac
Ala Pro Val
  65

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<210> 922  
 <211> 258  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 29..256

&lt;400&gt; 922

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atttttggcc tgtcaggtcc atccggcg atg ctg ggt ctg gac gag ctc ggg      52
Met Leu Gly Leu Asp Glu Leu Gly
  1          5
agg agt ggt tgt ggc cat tgc aca cag gcg gat ctg agg ttc ggc gac      100
Arg Ser Gly Cys Gly His Cys Thr Gln Ala Asp Leu Arg Phe Gly Asp
  10          15          20
gcc gct ggt cgc gac ccg gga mag gac aam san cag aam mac cgc cga      148
Ala Ala Gly Arg Asp Pro Gly Xaa Asp Xaa Xaa Gln Xaa Xaa Arg Arg
  25          30          35          40
gcm mgc gtt ccc ccc ccg ccc aga gtc atg gcg gca gca gcc gct ctg      196

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<221> CDS  
<222> 100..507

<400> 924

ccttgacagag cggcgccgg aggagacgca cgcagctgac tttgtcttct ccgcacgact 60  
gttacagagg tctccagagc cttctctctc ctgtgcaaaa atg gca act ctt aag 114  
Met Ala Thr Leu Lys  
1 5  
gaa aaa ctc att gca cca gtt gcg gaa gaa gag gca aca gtt cca aac 162  
Glu Lys Leu Ile Ala Pro Val Ala Glu Glu Glu Ala Thr Val Pro Asn  
10 15 20  
aat aag atc act gta gtg ggt gtt gga caa gtt ggt atg gcg tgt gct 210  
Asn Lys Ile Thr Val Val Gly Val Gly Gln Val Gly Met Ala Cys Ala  
25 30 35  
atc agc att ctg gga aag tct ctg gct gat gaa ctt gct ctt gtg gat 258  
Ile Ser Ile Leu Gly Lys Ser Leu Ala Asp Glu Leu Ala Leu Val Asp  
40 45 50  
gtt ttg gaa gat aag ctt aaa gga gaa atg atg gat ctg cag cat ggg 306  
Val Leu Glu Asp Lys Leu Lys Gly Glu Met Met Asp Leu Gln His Gly  
55 60 65  
agc tta ttt ctt cag aca cct aaa att gtg gca gat aaa gat tat tct 354  
Ser Leu Phe Leu Gln Thr Pro Lys Ile Val Ala Asp Lys Asp Tyr Ser  
70 75 80 85  
gtg acc gcc aat tct aag att gta gtg gta act gca gga gtc cgt cag 402  
Val Thr Ala Asn Ser Lys Ile Val Val Val Thr Ala Gly Val Arg Gln  
90 95 100  
caa gra ggg gag agt cgg ctc aat ctg gtg cag aga aat gtt aat gtc 450  
Gln Xaa Gly Glu Ser Arg Leu Asn Leu Val Gln Arg Asn Val Asn Val  
105 110 115  
ttc aaa ttc att att cct cag atc gtc aag tac agt cct gat tgc atc 498  
Phe Lys Phe Ile Ile Pro Gln Ile Val Lys Tyr Ser Pro Asp Cys Ile  
120 125 130  
ata att gtg  
Ile Ile Val 507  
135

<210> 925  
<211> 336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 100..336

<400> 925

ccttgacagag cggcgccgg aggagacgca cgcagctgac tttgtcttct ccgcacgact 60  
gttacagagg tctccagagc cttctctctc ctgtgcaaaa atg gca act ctt aag 114  
Met Ala Thr Leu Lys  
1 5  
gaa aaa ctc att gca cca gtt gcg gaa gaa gag gca aca gtt cca aac 162  
Glu Lys Leu Ile Ala Pro Val Ala Glu Glu Xaa Ala Thr Val Pro Asn

aat aag atc act gta gtg ggt gtt	10	gga caa gtt ggt atg gcg tgt gct	15	20	
Asn Lys Ile Thr Val Val Gly Val		Gly Gln Val Gly Met Ala Cys Ala			210
25		30		35	
atc agc att ctg gga aag gta cat		ttc aag aac acc ata gat gat aga			258
Ile Ser Ile Leu Gly Lys Val His		Phe Lys Asn Thr Ile Asp Asp Arg			
40		45		50	
gaa gtt cag cat gtg tac aca gtt		tct ttg ggc acc ttg gaa ttt tat			306
Glu Val Gln His Val Tyr Thr Val		Ser Leu Gly Thr Leu Glu Phe Tyr			
55		60		65	
tat atc ttt aaa aga ttt ctt ttt		ttc ctg			336
Tyr Ile Phe Lys Arg Phe Leu Phe		Phe Leu			
70		75			

<210> 926  
 <211> 567  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 151..567

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ccaagtctcc actgccagtg tgaaatcttc		agagaagaat ttctcttttag ttctttgcaa	120
gaaggtagag ataaagacac tttttcaaaa		atg gca atg gta tca gaa ttc ctc	174
		Met Ala Met Val Ser Glu Phe Leu	
	1	5	
aag cag gcc tgg ttt att gaa aat		gaa gag cag gaa tat gtt caa act	222
Lys Gln Ala Trp Phe Ile Glu Asn		Glu Glu Gln Tyr Val Gln Thr	
10		15	
gtg aag tca tcc aaa ggt ggt ccc		gga tca gcg gtg agc ccc tat cct	270
Val Lys Ser Ser Lys Gly Gly Pro		Gly Ser Ala Val Ser Pro Tyr Pro	
25		30	
acc ttc aat cca tcc tcg gat gtc		gct gcc ttg cat aag gcc ata atg	318
Thr Phe Asn Pro Ser Ser Asp Val		Ala Ala Leu His Lys Ala Ile Met	
45		50	
gtt aaa ggt gtg gat gaa gca acc		atc att gac att cta act aag cga	366
Val Lys Gly Val Asp Glu Ala Thr		Ile Ile Asp Ile Leu Thr Lys Arg	
60		65	
aac aat gca cag cgt caa cag atc		aaa gca gca tat ctc cag gaa aca	414
Asn Asn Ala Gln Arg Gln Gln Ile		Lys Ala Ala Tyr Leu Gln Glu Thr	
75		80	
gga aag ccc ctg gat gaa aca ctg		aag aaa gcc ctt aca ggt cac ctt	462
Gly Lys Pro Leu Asp Glu Thr Leu		Lys Lys Ala Leu Thr Gly His Leu	
90		95	
gag gag gtt gtt tta gct ctg cta		aaa act cca gcg caa ttt gat gct	510
Glu Glu Val Val Leu Ala Leu Leu		Lys Thr Pro Ala Gln Phe Asp Ala	
105		110	
gat gaa ctt cgt gct gcc atg aag		ggc ctt gga act gat gaa gat act	558
Asp Glu Leu Arg Ala Ala Met Lys		Gly Leu Gly Thr Asp Glu Asp Thr	
125		130	
		135	

004220"666ET560

cta att gag  
Leu Ile Glu

567

<210> 927  
<211> 386  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 18..386

<400> 927  
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Met Ser Ala Ser Gln Asp Ser Arg Ser Arg Asp  
1 5 10  
aat ggc ccc gat ggg atg gag ccc gaa ggc gtc atc gag agt aac tgg 98  
Asn Gly Pro Asp Gly Met Glu Pro Glu Gly Val Ile Glu Ser Asn Trp  
15 20 25  
aat gag att gtt gac agc ttt gat gac atg aac ctc tcg gag tcc ctt 146  
Asn Glu Ile Val Asp Ser Phe Asp Asp Met Asn Leu Ser Glu Ser Leu  
30 35 40  
ctc cgt ggc atc tac gcc tat ggt ttt gag aag ccc tct gcc atc cag 194  
Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile Gln  
45 50 55  
cag cga gcc att cta cct tgt atc aag ggt tat gat gtg att gct caa 242  
Gln Arg Ala Ile Leu Pro Cys Ile Lys Gly Tyr Asp Val Ile Ala Gln  
60 65 70 75  
gcc caa tct ggg act ggg aaa acg gcc aca ttt gcc ata tcg att ctg 290  
Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ala Ile Ser Ile Leu  
80 85 90  
cag cag att gaa tta gat cta aaa gcc acc cag gcc ttg gtc cta gca 338  
Gln Gln Ile Glu Leu Asp Leu Lys Ala Thr Gln Ala Leu Val Leu Ala  
95 100 105  
ccc act cga gaa ttg gct cag cag gta aar agt ggc ttc tat tcc ctc 386  
Pro Thr Arg Glu Leu Ala Gln Gln Val Lys Ser Gly Phe Tyr Ser Leu  
110 115 120

<210> 928  
<211> 615  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 91..615

<400> 928  
ctttcttttc agtcgggcgc tgagtgggtt ttcggatcat gtctgggtggc tccgcggatt 60  
ataagcagag aacatggcgg cccagagggg atg gac ccc gat ggt gtc atc gag 114  
Met Asp Pro Asp Gly Val Ile Glu  
1 5

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agc aac tgg aat gag att gtt gat aac ttt gat gat atg aat tta aag      162
Ser Asn Trp Asn Glu Ile Val Asp Asn Phe Asp Asp Met Asn Leu Lys
  10                      15                      20
gag tct ctc ctt cgt ggc atc tat gct tac ggt ttt gag aag cct tcc      210
Glu Ser Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser
  25                      30                      35                      40
gct att cag cag aga gct att att ccc tgt att aaa ggg tat gat gtg      258
Ala Ile Gln Gln Arg Ala Ile Ile Pro Cys Ile Lys Gly Tyr Asp Val
                      45                      50                      55
att gct caa gct cag tca ggt act ggc aag aca gcc aca ttt gct att      306
Ile Ala Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ala Ile
                      60                      65                      70
tcc atc ctg caa cag ttg gag att gag ttc aag gag acc caa gca cta      354
Ser Ile Leu Gln Gln Leu Glu Ile Glu Phe Lys Glu Thr Gln Ala Leu
                      75                      80                      85
gta ttg gcc ccc acc aga gaa ctg gct caa cag atc caa aag gta att      402
Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile Gln Lys Val Ile
                      90                      95                      100
ctg gca ctt gga gac tat atg gga gcc act tgt cat gcc tgc att ggt      450
Leu Ala Leu Gly Asp Tyr Met Gly Ala Thr Cys His Ala Cys Ile Gly
  105                      110                      115                      120
gga aca aat gtt cga aat gaa atg caa aaa ctg cag gct gaa gca cca      498
Gly Thr Asn Val Arg Asn Glu Met Gln Lys Leu Gln Ala Glu Ala Pro
                      125                      130                      135
cat att gtt gtt ggt aca ccc ggg aga gtg ttt gat atg tta aac aga      546
His Ile Val Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Asn Arg
                      140                      145                      150
aga tac mtt tct cca aaa tgg atc aaa atg ttt gtt ttg gat gaa gca      594
Arg Tyr Xaa Ser Pro Lys Trp Ile Lys Met Phe Val Leu Asp Glu Ala
                      155                      160                      165
gat gaa atg ttg agc cgt ggt
Asp Glu Met Leu Ser Arg Gly
                      170                      175

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<210> 929  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 184..378

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<400> 929
ctttcttttc agtcgggcgc tgagtggttt ttcggatcat gtctgggtggc tccgcggatt      60
ataacagcag aacatggcgg cccagagggga atggaccccg atggtgtcat cgaggtaaga      120
aacggttgat gatcttgaag ctttggaag atccaaaagg taattctggc acttgagac      180
tat atg gga gcc act tgt cat gcc tgc att ggt gga aca aat gtt cga      228
  Met Gly Ala Thr Cys His Ala Cys Ile Gly Gly Thr Asn Val Arg
    1                      5                      10                      15
aat gaa atg caa aaa ctg cag gct gaa gca cca cat att gtt gtt ggt      276
Asn Glu Met Gln Lys Leu Gln Ala Glu Ala Pro His Ile Val Val Gly
                      20                      25                      30

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aca ccc ggg aga gtg ttt gat atg tta aac aga aga tac mtt tct cca	324
Thr Pro Gly Arg Val Phe Asp Met Leu Asn Arg Arg Tyr Xaa Ser Pro	
35 40 45	
aaa tgg atc aaa atg ttt gtt ttg gat gaa gca gat gaa atg ttg agc	372
Lys Trp Ile Lys Met Phe Val Leu Asp Glu Ala Asp Glu Met Leu Ser	
50 55 60	
cgt ggt	378
Arg Gly	
65	

<210> 930  
 <211> 203  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 17..202

<400> 930	
ctagtttcta aggatc atg tct gcg agc cag gat tcc cgg act gag cct aac	52
Met Ser Ala Ser Gln Asp Ser Arg Thr Glu Pro Asn	
1 5 10	
ccc gag gag cgg ccg cgt gag gca cca gga gcc cac ccg gcg ccg ggc	100
Pro Glu Glu Arg Pro Arg Glu Ala Pro Gly Ala His Pro Ala Pro Gly	
15 20 25	
ggg cgg gtc cat ttt gcc gca caa gcc ggg cta ttg gca aac tgc gga	148
Gly Arg Val His Phe Ala Ala Gln Ala Gly Leu Leu Ala Asn Cys Gly	
30 35 40	
tgg gca ggt cca cct tcc ttc ggg ggt gag cgg cct gag atc cag aga	196
Trp Ala Gly Pro Pro Ser Phe Gly Gly Glu Arg Pro Glu Ile Gln Arg	
45 50 55 60	
caa tgg c	203
Gln Trp	

<210> 931  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 233..388

<400> 931	
gtgctgcggc attcacgtga tctgcacggg cgcagatgta ggcaccgggc cgagtgcctg	60
ccctctgtcc ccgcggctgg gtctcgtctg ctccgggtcc tgggctccta attcttggtc	120
cagcttcttc caggtctgcg cgtctgttgt tcccagcgct ctgcgaasct gaaaaggagg	180
agcaacctgt ccagaatccc cgcaggacag gaaaaggagg ggaaatctcg ac atg gaa	238
Met Glu	
1	
aaa ctc tac agt gaa aat gaa gga atg gct tca aac caa gga aag atg	286



Lys	Leu	Tyr	Ser	Glu	Asn	Glu	Gly	Met	Ala	Ser	Asn	Gln	Gly	Lys	Met	
	5						10					15				
gaa	aat	gaa	gaa	cag	cca	caa	gac	gag	aga	aag	cca	gaa	gta	act	tgt	334
Glu	Asn	Glu	Glu	Gln	Pro	Gln	Asp	Glu	Arg	Lys	Pro	Glu	Val	Thr	Cys	
	20					25				30						
act	ctg	gaa	gac	aag	aag	tta	gaa	aac	gag	gga	aag	aca	gam	aac	aag	382
Thr	Leu	Glu	Asp	Lys	Lys	Leu	Glu	Asn	Glu	Gly	Lys	Thr	Xaa	Asn	Lys	
35					40				45					50		
cgc	aaa															388
Arg	Lys															

<210> 932  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 175..375

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ccctctgtcc	ccgcggctgg	gtctcgtctg	ctccggttcc	tgggctccta	attcttggtc		120									
cagcttcttc	caggtcagtg	tgcgggcctt	ccacgctgcc	agcggaacac	tgga atg		177									
					Met											
					1											
gcg gaa ggg gaa cgg gtc tgc gcg tct gtk gtt ccc agc gct ctg cga							225									
Ala Glu Gly Glu Arg Val Cys Ala Ser Val Val Pro Ser Ala Leu Arg																
	5					10				15						
acg ctg aaa agg agg agc aac ctg tcc aga atc ccc gca gga cag gaa							273									
Thr Leu Lys Arg Arg Ser Asn Leu Ser Arg Ile Pro Ala Gly Gln Glu																
	20					25				30						
aag gag ggg aaa tct cga cat gtt gct ccc cct ttt cgc ttt ttc cct							321									
Lys Glu Gly Lys Ser Arg His Val Ala Pro Pro Phe Arg Phe Phe Pro																
	35				40				45							
ttt tcc ggt ttt ttg ttt ttt ggt ttt ctt ttt ccc gtc ttt tct ttc							369									
Phe Ser Gly Phe Leu Phe Phe Gly Phe Leu Phe Pro Val Phe Ser Phe																
50				55					60					65		
ccc tcc																375
Pro Ser																

<210> 933  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 292..447

<400>	933															
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ccctctgtcc ccgcggtctg gtctcgtctg ctccggttcc tgggctccta attcttggtc 120
cagcttcttc caggtcagtg tgcgggcctt ccacgctgcc agcggaacac tggaatggcg 180
gaaggggaac gggctcgcgc gtctgttgtt cccagcgctc tgcgaasctg aaaaggagga 240
gcaacctgtc cagaatcccc gcaggacagg aaaaggaggg gaaatctcga c atg gaa 297
                                     Met Glu
                                     1
aaa ctc tac agt gaa aat gaa gga atg gct tca aan caa gga aag atg 345
Lys Leu Tyr Ser Glu Asn Glu Gly Met Ala Ser Xaa Gln Gly Lys Met
      5              10              15
gaa aat gaa gaa cag cca caa gac gag aga aag cca gaa gta act tgt 393
Glu Asn Glu Glu Gln Pro Gln Asp Glu Arg Lys Pro Glu Val Thr Cys
      20              25              30
act ctg gaa gac aag aag tta gaa aac gag gga aag aca gam aac aag 441
Thr Leu Glu Asp Lys Lys Leu Glu Asn Glu Gly Lys Thr Xaa Asn Lys
      35              40              45              50
cgc aaa 447
Arg Lys

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<210> 934  
 <211> 244  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 23..244

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<400> 934
tacattggca gcgtactcaa aa atg atg tcg cca ctt aaa aac tct tca gat 52
                        Met Met Ser Pro Leu Lys Asn Ser Ser Asp
                        1      5      10
gga tta act agt ctt aac caa agc aac tcc acc ttg gta gca ctc cca 100
Gly Leu Thr Ser Leu Asn Gln Ser Asn Ser Thr Leu Val Ala Leu Pro
      15              20              25
gag ggt agg cag gaa ttg tca gat ggg cag gtt aag aca ggc atc agc 148
Glu Gly Arg Gln Glu Leu Ser Asp Gly Gln Val Lys Thr Gly Ile Ser
      30              35              40
atg tcc tta ctc acc gtc att gaa aaa ttg aga gaa agg aca gac caa 196
Met Ser Leu Leu Thr Val Ile Glu Lys Leu Arg Glu Arg Thr Asp Gln
      45              50              55
aac gct tca gac gat gac att ttg aaa gag ttg cag gac aac gcc cag 244
Asn Ala Ser Asp Asp Asp Ile Leu Lys Glu Leu Gln Asp Asn Ala Gln
      60              65              70

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<210> 935  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 119..424

&lt;400&gt; 935

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attcaaagca gaaggtcgcg cttggaggaa gtggcggtt tgagtcggt ggcccaatcg      60
ctgttactac ttctctgaag ctctctcgg ctgcttgccg agacaccctg ccgccaag      118
atg cct cga att atg atc aag ggg ggc gta tgg agg aat acc gag gat      166
Met Pro Arg Ile Met Ile Lys Gly Gly Val Trp Arg Asn Thr Glu Asp
1           5           10           15
gaa att ctg aaa gca gcg gta atg aaa tat ggg aaa aat cag tgg tct      214
Glu Ile Leu Lys Ala Ala Val Met Lys Tyr Gly Lys Asn Gln Trp Ser
           20           25           30
agg att gcc tca ttg ctg cat aga aaa tca gca aag cag tgc aaa gcc      262
Arg Ile Ala Ser Leu Leu His Arg Lys Ser Ala Lys Gln Cys Lys Ala
           35           40           45
aga tgg tat gaa tgg ctg gat cca agc att aag aag aca gaa tgg tcc      310
Arg Trp Tyr Glu Trp Leu Asp Pro Ser Ile Lys Lys Thr Glu Trp Ser
           50           55           60
aga gaa gaa gag gaa aaa ctc ttg cac ttg gcc aag ttg atg cca act      358
Arg Glu Glu Glu Glu Lys Leu Leu His Leu Ala Lys Leu Met Pro Thr
65           70           75           80
cag tgg agg acc att gct cca atc att gga aga aca gcg gcc cag tgc      406
Gln Trp Arg Thr Ile Ala Pro Ile Ile Gly Arg Thr Ala Ala Gln Cys
           85           90           95
tta gaa cac tat gaa ttt      424
Leu Glu His Tyr Glu Phe
           100

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&lt;210&gt; 936

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 37..366

&lt;400&gt; 936

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aagtcgttnc gggagggaga cgcagaggcg gacaag atg gcg gcg gca gct gta      54
Met Ala Ala Ala Ala Val
1           5
cag ggc ggg aga agc ggt ggt agc gga ggc tgt agt ggg gct ggt ggt      102
Gln Gly Gly Arg Ser Gly Gly Ser Gly Gly Cys Ser Gly Ala Gly Gly
           10           15           20
gct tcc aac tgc ggg aca gga agt ggc cgt agc ggc ttg ttg gat aag      150
Ala Ser Asn Cys Gly Thr Gly Ser Gly Arg Ser Gly Leu Leu Asp Lys
           25           30           35
tgg aag ata gat gat aag cct gta aaa att gac aag tgg gat gga tca      198
Trp Lys Ile Asp Asp Lys Pro Val Lys Ile Asp Lys Trp Asp Gly Ser
           40           45           50
gct gtg aaa aac tct ttg gat gat tct gcc aaa aag gag aag agc atc      246
Ala Val Lys Asn Ser Leu Asp Asp Ser Ala Lys Lys Glu Lys Ser Ile
55           60           65           70
ttt ctc gtg gcc cac agg aaa gat cct aca gga atg gat cct gat gat      294
Phe Leu Val Ala His Arg Lys Asp Pro Thr Gly Met Asp Pro Asp Asp

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	75		80		85	
att tgg cag ctg tcc tcc agt cnk aaa agg ttt gat gac aaa tac acc						342
Ile Trp Gln Leu Ser Ser Ser Xaa Lys Arg Phe Asp Asp Lys Tyr Thr						
	90		95		100	
ttg aag ctg acc ttc atc agt agg						366
Leu Lys Leu Thr Phe Ile Ser Arg						
	105		110			

<210> 937  
 <211> 605  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 177..605

<400> 937	
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ggagaagcgg tggtagcggg ggctgtagtg gggctggtgg tgcttccaac tgcgggacag	120
gaagtggccg tagcggcttg ttggataagt ggaagataga tgataagcct gtaaaa atg	179
	Met
	1
gac aag atg gcg gcg gca gnt gta cag ggc ggg aga agc ggt ggt agc	227
Asp Lys Met Ala Ala Ala Xaa Val Gln Gly Gly Arg Ser Gly Gly Ser	
	5 10 15
gga ggc tgt agt ggg gct ggt ggt gct tcc aac tgc ggg aca gga agt	275
Gly Gly Cys Ser Gly Ala Gly Gly Ala Ser Asn Cys Gly Thr Gly Ser	
	20 25 30
ggc cgt agc ggc ttg ttg gat aag tgg aag ata gat gat aag cct gta	323
Gly Arg Ser Gly Leu Leu Asp Lys Trp Lys Ile Asp Asp Lys Pro Val	
	35 40 45
aaa att gac aag tgg gat gga tca gct gtg aaa aac tct ttg gat gat	371
Lys Ile Asp Lys Trp Asp Gly Ser Ala Val Lys Asn Ser Leu Asp Asp	
	50 55 60 65
tct gcc aaa aag gta ctt ctg gaa aaa tac aaa tat gtg gag aat ttt	419
Ser Ala Lys Lys Val Leu Leu Glu Lys Tyr Lys Tyr Val Glu Asn Phe	
	70 75 80
ggt cta att gat ggt cgc ctc acc atc tgt aca atc tcc tgt ttc ttt	467
Gly Leu Ile Asp Gly Arg Leu Thr Ile Cys Thr Ile Ser Cys Phe Phe	
	85 90 95
gcc ata gtg gct ttg att tgg gat tat atg cac ccc ttt cca gag tcc	515
Ala Ile Val Ala Leu Ile Trp Asp Tyr Met His Pro Phe Pro Glu Ser	
	100 105 110
aaa ccc gtt ttg gct ttg tgt gtc ata tcc tat ttt gtg atg atg ggg	563
Lys Pro Val Leu Ala Leu Cys Val Ile Ser Tyr Phe Val Met Met Gly	
	115 120 125
att ctg acc att tat acc tca tat aag gag aag agc atc ttt	605
Ile Leu Thr Ile Tyr Thr Ser Tyr Lys Glu Lys Ser Ile Phe	
	130 135 140

<210> 938  
 <211> 456

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 37..456

<400> 938  
aagtcgttnc gggagggaga cgcagaggcg gacaag atg gcg gcg gca gct gta 54  
Met Ala Ala Ala Ala Val  
1 5  
cag ggc ggg aga agc ggt ggt agc gga ggc tgt agt ggg gct ggt ggt 102  
Gln Gly Gly Arg Ser Gly Gly Ser Gly Gly Cys Ser Gly Ala Gly Gly  
10 15 20  
gct tcc aac tgc ggg aca gga agt ggc cgt agc ggc ttg ttg gat aag 150  
Ala Ser Asn Cys Gly Thr Gly Ser Gly Arg Ser Gly Leu Leu Asp Lys  
25 30 35  
tgg aag ata gat gat aag cct gta aaa att gac aag tgg gat gga tca 198  
Trp Lys Ile Asp Asp Lys Pro Val Lys Ile Asp Lys Trp Asp Gly Ser  
40 45 50  
gct gtg aaa aac tct ttg gat gat tct gcc aaa aag gta ctt ctg gaa 246  
Ala Val Lys Asn Ser Leu Asp Asp Ser Ala Lys Lys Val Leu Leu Glu  
55 60 65 70  
aaa tac aaa tat gtg gag aat ttt ggt cta att gat ggt cgc ctc acc 294  
Lys Tyr Lys Tyr Val Glu Asn Phe Gly Leu Ile Asp Gly Arg Leu Thr  
75 80 85  
atc tgt aca atc tcc tgt ttc ttt gcc ata gtg gct ttg att tgg gat 342  
Ile Cys Thr Ile Ser Cys Phe Phe Ala Ile Val Ala Leu Ile Trp Asp  
90 95 100  
tat atg cac ccc ttt cca gag tcc aaa ccc gtt ttg gct ttg tgt gtc 390  
Tyr Met His Pro Phe Pro Glu Ser Lys Pro Val Leu Ala Leu Cys Val  
105 110 115  
ata tcc tat ttt gtg atg atg ggg att ctg acc att tat acc tca tat 438  
Ile Ser Tyr Phe Val Met Met Gly Ile Leu Thr Ile Tyr Thr Ser Tyr  
120 125 130  
aag gag aag agc atc ttt 456  
Lys Glu Lys Ser Ile Phe  
135 140

<210> 939  
<211> 472  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 131..472

<400> 939  
aaaggsnagg gcctgactaa acctggagac tcgggtggcc gaggggcttc ataccagctg 60  
aagagcgaca agccgctggc agccgcggat ctcaccgccg ctcagggttt ttagaacttc 120  
agccataaaa atg ggc aga att ttc ctt gat cat atc ggt ggt acc cgt 169

	Met Gly Arg Ile Phe Leu Asp His Ile Gly Gly Thr Arg	
	1 5 10	
ctg ttt tct tgt gca aac tgt gat acg atc ctg acc aac cgc tca gaa		217
Leu Phe Ser Cys Ala Asn Cys Asp Thr Ile Leu Thr Asn Arg Ser Glu		
15 20 25		
ctc atc tcc act cgt ttc aca ggc gcc act ggc aga gca ttt ctt ttt		265
Leu Ile Ser Thr Arg Phe Thr Gly Ala Thr Gly Arg Ala Phe Leu Phe		
30 35 40 45		
aac aag gta gtt aac ctg cag tac agy gaa gtt caa gat cgg gtc atg		313
Asn Lys Val Val Asn Leu Gln Tyr Ser Glu Val Gln Asp Arg Val Met		
50 55 60		
ctc act ggc cgc cac atg gtt cga gat gtg agc tgc aaa aac tgc aat		361
Leu Thr Gly Arg His Met Val Arg Asp Val Ser Cys Lys Asn Cys Asn		
65 70 75		
agc aaa ctg gga tgg atc tat gag ttt gcc act gaa gac agc cag cga		409
Ser Lys Leu Gly Trp Ile Tyr Glu Phe Ala Thr Glu Asp Ser Gln Arg		
80 85 90		
tat aag gaa ggc cgc gtg atc ctg gna cgt gct cta gtt cga gag ast		457
Tyr Lys Glu Gly Arg Val Ile Leu Xaa Arg Ala Leu Val Arg Glu Xaa		
95 100 105		
gag ggc ttg agg agc		472
Glu Gly Leu Arg Ser		
110		
<210> 940		
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<212> DNA		
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<222> 90..443		
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cgggagtttt tgctacagtt ttcgccacc atg agt cgc agc tat aat gat gag		113
Met Ser Arg Ser Tyr Asn Asp Glu		
1 5		
ctg cag ttc ttg gag aag atc aat aaa aac tgc tgg agg atc aag aag		161
Leu Gln Phe Leu Glu Lys Ile Asn Lys Asn Cys Trp Arg Ile Lys Lys		
10 15 20		
ggc ttc gtg ccc aac atg cag gtt gaa ggt gtt ttc tat gtg aat gat		209
Gly Phe Val Pro Asn Met Gln Val Glu Gly Val Phe Tyr Val Asn Asp		
25 30 35 40		
gct ctg gag aaa ttg atg ttt gag gaa tta agg aat gcc tgt cga ggt		257
Ala Leu Glu Lys Leu Met Phe Glu Glu Leu Arg Asn Ala Cys Arg Gly		
45 50 55		
ggt ggt gtt ggt ggc ttc ctg cca gcc atg aaa cag att ggc aat gtg		305
Gly Gly Val Gly Gly Phe Leu Pro Ala Met Lys Gln Ile Gly Asn Val		
60 65 70		
gca gcc ctg cct gga att gtt cat cga tct att ggg ctt cct gat gtc		353
Ala Ala Leu Pro Gly Ile Val His Arg Ser Ile Gly Leu Pro Asp Val		
75 80 85		

cat tca gga tat ggg ttt gct att ggg aac atg gca gcc ttt gat atg 401  
 His Ser Gly Tyr Gly Phe Ala Ile Gly Asn Met Ala Ala Phe Asp Met  
     90                    95                    100  
 aat gac cct gaa gca gta gta tcc cca ggt ggt gtc ggg ttt g 444  
 Asn Asp Pro Glu Ala Val Val Ser Pro Gly Gly Val Gly Phe  
 105                    110                    115

<210> 941  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 202..399

<400> 941  
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 gtgacggccc gtttcagacc gccggcagct actgcaaggc aaaagccgga gtggacgtgt 120  
 cttttgaaac tgctgctctt tcacttctca ggcgtcaccc agagctcagc acccaggctg 180  
 aactctgtac catttggaag a atg gaa gct gat gca tct gtt gac atg ttt 231  
                     Met Glu Ala Asp Ala Ser Val Asp Met Phe  
                     1                    5                    10  
 tcc aaa gtc ctg gag cat cag ctg ctt cag act acc aaa ctg gtg gaa 279  
 Ser Lys Val Leu Glu His Gln Leu Leu Gln Thr Thr Lys Leu Val Glu  
                     15                    20                    25  
 gaa cat ttg gat tct gaa att caa aaa ctg gat cag atg gat gag gat 327  
 Glu His Leu Asp Ser Glu Ile Gln Lys Leu Asp Gln Met Asp Glu Asp  
                     30                    35                    40  
 gaa ttg gaa cgc ctt aaa gaa aag aga ctc cag gca cta agg aaa gct 375  
 Glu Leu Glu Arg Leu Lys Glu Lys Arg Leu Gln Ala Leu Arg Lys Ala  
                     45                    50                    55  
 caa cag cag ama caa gaa tgg ctt t 400  
 Gln Gln Gln Xaa Gln Glu Trp Leu  
     60                    65

<210> 942  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 32..400

<400> 942  
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                                     Met Ala Ala Ile Gly Arg Gly  
                                     1                    5  
 cgc tct ctg aag aac ctc cga gta cga ggg cgg aat gac agc ggc gag 100  
 Arg Ser Leu Lys Asn Leu Arg Val Arg Gly Arg Asn Asp Ser Gly Glu  
     10                    15                    20

gag aac gtc ccg ctg gat ctg acc cga gaa cct tct gat aac tta aga 148  
 Glu Asn Val Pro Leu Asp Leu Thr Arg Glu Pro Ser Asp Asn Leu Arg  
 25 30 35  
 gag att ctc caa aat gtg gcc aga ttg cag gga gta tca aat atg aga 196  
 Glu Ile Leu Gln Asn Val Ala Arg Leu Gln Gly Val Ser Asn Met Arg  
 40 45 50 55  
 aag cta ggc cat ctg aat aac ttt act aag ctt ctt tgt gat att ggc 244  
 Lys Leu Gly His Leu Asn Asn Phe Thr Lys Leu Leu Cys Asp Ile Gly  
 60 65 70  
 cac agt gaa gaa aaa ctg ggc ttt cac tat gag gat atc ata att tgt 292  
 His Ser Glu Glu Lys Leu Gly Phe His Tyr Glu Asp Ile Ile Ile Cys  
 75 80 85  
 ttg cgg tta gct tta tta aat gaa gca aaa gaa gtg cga gca gca ggg 340  
 Leu Arg Leu Ala Leu Leu Asn Glu Ala Lys Glu Val Arg Ala Ala Gly  
 90 95 100  
 cta cga gcg ctt cga tat ctc atc caa gac tcc agt att ctc cag aag 388  
 Leu Arg Ala Leu Arg Tyr Leu Ile Gln Asp Ser Ser Ile Leu Gln Lys  
 105 110 115  
 gtg cta aaa ttg a 401  
 Val Leu Lys Leu  
 120

<210> 943  
 <211> 448  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 30..446

<400> 943  
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 Met Asp Xaa Leu Val Ser Glu Cys  
 1 5  
 tcc gcg cgg ctg ctg cag cag gaa gaa gag att aaa tct ctg act gct 101  
 Ser Ala Arg Leu Leu Gln Gln Glu Glu Glu Ile Lys Ser Leu Thr Ala  
 10 15 20  
 gaa att gac cgg ttg aaa aac tgt ggc tgt tta gga gct tct cca aat 149  
 Glu Ile Asp Arg Leu Lys Asn Cys Gly Cys Leu Gly Ala Ser Pro Asn  
 25 30 35 40  
 ttg gag cag tta caa gaa gaa aat tta aaa tta aag tat cga ctg aat 197  
 Leu Glu Gln Leu Gln Glu Glu Asn Leu Lys Leu Lys Tyr Arg Leu Asn  
 45 50 55  
 att ctt cga aag agt ctt cag gca gaa agg aac aaa cca act aaa aat 245  
 Ile Leu Arg Lys Ser Leu Gln Ala Glu Arg Asn Lys Pro Thr Lys Asn  
 60 65 70  
 atg att aac att att agc cgc cta caa gag gtc ttt ggt cat gca att 293  
 Met Ile Asn Ile Ile Ser Arg Leu Gln Glu Val Phe Gly His Ala Ile  
 75 80 85  
 aag gct gca tat cca gat ttg gaa aat cct cct ctg cta gtg aca cca 341  
 Lys Ala Ala Tyr Pro Asp Leu Glu Asn Pro Pro Leu Leu Val Thr Pro  
 90 95 100





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aagtcggcgg tcggcgtggg gcrct atg ccg ggg cgg cac gtt tct cga gtc      52
                        Met Pro Gly Arg His Val Ser Arg Val
                        1                               5

cgg gca ttg tac aag cgc gtc ttg cag ctg sac cgt gtt ctg ccc ccg      100
Arg Ala Leu Tyr Lys Arg Val Leu Gln Leu Xaa Arg Val Leu Pro Pro
10                               15                               20                               25

gac ctc aaa tcc ctg ggc gac cag tac gtg aaa gac gaa ttt agg aga      148
Asp Leu Lys Ser Leu Gly Asp Gln Tyr Val Lys Asp Glu Phe Arg Arg
                        30                               35                               40

cat aag acc gtt ggt tct gac gag gca cag cgt ttc ttg caa gaa tgg      196
His Lys Thr Val Gly Ser Asp Glu Ala Gln Arg Phe Leu Gln Glu Trp
                        45                               50                               55

gag gtg tat gca aca gcg tta ttg caa cag gct aac gaa aac aga caa      244
Glu Val Tyr Ala Thr Ala Leu Leu Gln Gln Ala Asn Glu Asn Arg Gln
60                               65                               70

aat tca act gga aaa gca tgt ttt ggc acc ttc ctc cca gaa gaa aaa      292
Asn Ser Thr Gly Lys Ala Cys Phe Gly Thr Phe Leu Pro Glu Glu Lys
75                               80                               85

ctt aat gac ttt cgt gat gaa caa att gga cag ttg cag gag ctg atg      340
Leu Asn Asp Phe Arg Asp Glu Gln Ile Gly Gln Leu Gln Glu Leu Met
90                               95                               100                               105

caa gaa gcc aca aaa ccc aat agg caa ttt a      371
Gln Glu Ala Thr Lys Pro Asn Arg Gln Phe
                        110                               115

<210> 946
<211> 376
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..376

<400> 946
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aacaccttga tgggaaagggt ggctcatgga atgttttctt atcctttgaa cactcctcat      120
ttcagaagct ttgcttctgt tgcaaccaaa c atg aca ctt agc gtg ctg agc      172
                        Met Thr Leu Ser Val Leu Ser
                        1                               5

agg aag gac aag gaa aga gta att cgc aga ctg tta tta cag gcc cct      220
Arg Lys Asp Lys Glu Arg Val Ile Arg Arg Leu Leu Leu Gln Ala Pro
10                               15                               20

cca ggg gaa ttt gta aat gcc ttt gat gat ctc tgt ctg ctt atc cgt      268
Pro Gly Glu Phe Val Asn Ala Phe Asp Asp Leu Cys Leu Leu Ile Arg
25                               30                               35

gat gaa aaa ctt atg cac cac caa ggt gag tgt gca ggc cac caa cac      316
Asp Glu Lys Leu Met His His Gln Gly Glu Cys Ala Gly His Gln His
40                               45                               50                               55

tgc caa ama tat tct gta cca ctc tgc atc gat gga ant cca gta ctc      364
Cys Gln Xaa Tyr Ser Val Pro Leu Cys Ile Asp Gly Xaa Pro Val Leu
60                               65                               70

ttg tct cac cac      376

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Leu Ser His His  
75

<210> 947  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 42..467

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Met Ser Tyr Pro Ala  
1 5  
gat gat tat gag tct gag gcg gct tat gac ccc tac gct tat ccc agc 104  
Asp Asp Tyr Glu Ser Glu Ala Ala Tyr Asp Pro Tyr Ala Tyr Pro Ser  
10 15 20  
gac tat gat atg cac aca gga gat cca aag cag gac ctt gct tat gaa 152  
Asp Tyr Asp Met His Thr Gly Asp Pro Lys Gln Asp Leu Ala Tyr Glu  
25 30 35  
cgt cag tat gaa cag caa acc tat cag gtg atc cct gag gtg atc aaa 200  
Arg Gln Tyr Glu Gln Gln Thr Tyr Gln Val Ile Pro Glu Val Ile Lys  
40 45 50  
aac ttc atc cag tat ttc cac aaa act gtc tca gat ttg att gac cag 248  
Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser Asp Leu Ile Asp Gln  
55 60 65  
aaa gtg tat gag cta cag gcc agt cgt gtc tcc agt gat gtc att gac 296  
Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser Ser Asp Val Ile Asp  
70 75 80 85  
cag aag gtg tat gag atc cag gac atc tat gag aac agc tgg acc aag 344  
Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu Asn Ser Trp Thr Lys  
90 95 100  
ctg act gaa aga ttc ttc aag aat aca cct tgg ccc gag gct gaa gcc 392  
Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp Pro Glu Ala Glu Ala  
105 110 115  
att gct cca cag gtt ggc aat gat gct gtc ttc ctg att tta tac aaa 440  
Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe Leu Ile Leu Tyr Lys  
120 125 130  
gaa tta tac tac agg cac ata tat gcc aa 469  
Glu Leu Tyr Tyr Arg His Ile Tyr Ala  
135 140

<210> 948  
<211> 473  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 15..473

004220"666E1560

<400> 948  
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Met Leu Gly Ala Gln Trp Arg Arg Asn Gln Pro Ser  
1 5 10  
agg gcg gcg gag gag tgg agt caa cat atc aat gga gca agt cac agt 98  
Arg Ala Ala Glu Glu Trp Ser Gln His Ile Asn Gly Ala Ser His Ser  
15 20 25  
cgt cga tgc cag ctt ctt ctt gaa atc tac cca gaa tgg aat cct gac 146  
Arg Arg Cys Gln Leu Leu Leu Glu Ile Tyr Pro Glu Trp Asn Pro Asp  
30 35 40  
aat gat aca gga cac aca atg ggt gat cca ttc atg ttg cag cag tct 194  
Asn Asp Thr Gly His Thr Met Gly Asp Pro Phe Met Leu Gln Gln Ser  
45 50 55 60  
aca aat cca gca cca gga att ctg gga cct cca cct ccc tca ttt cat 242  
Thr Asn Pro Ala Pro Gly Ile Leu Gly Pro Pro Pro Ser Phe His  
65 70 75  
ctt ggg gga cca gca gtt gga cca aga gga aat ctg ggt gct gga aat 290  
Leu Gly Gly Pro Ala Val Gly Pro Arg Gly Asn Leu Gly Ala Gly Asn  
80 85 90  
gga aac ctg caa gga cct aga cac atg cag aaa ggc aga gtg gaa act 338  
Gly Asn Leu Gln Gly Pro Arg His Met Gln Lys Gly Arg Val Glu Thr  
95 100 105  
agc aga gtt gtt cac atc atg gat ttt caa cga ggg aaa aac ttg aga 386  
Ser Arg Val Val His Ile Met Asp Phe Gln Arg Gly Lys Asn Leu Arg  
110 115 120  
tac cag cta tta cag ctg gta gaa cca ttt gga gtc att tca aat cat 434  
Tyr Gln Leu Leu Gln Leu Val Glu Pro Phe Gly Val Ile Ser Asn His  
125 130 135 140  
ctg att cta aat aaa att aat gag gca ttt att gaa atg 473  
Leu Ile Leu Asn Lys Ile Asn Glu Ala Phe Ile Glu Met  
145 150

<210> 949  
<211> 637  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> 338..637

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aaaaacttta taaaccccc ggagcccgag cagtgtgaag aagaggcgag aacgaccccc 120  
ggaccgacca aagcccgcg gccgctgcat ccgcgtcca gcacctacgt cccgctgccg 180  
tcgccgccgc caccatgccc aagagamagg ctgaagggga tgctaaggga gataaagcaa 240  
aggtgaagga cgaaccacag agaagatccg cgagggttgc tgtggttcgt ccttcacctt 300  
tgctttatct cccttagcat cccagacgc ggagaaa atg gcg gca ggg gtc gaa 355  
Met Ala Ala Gly Val Glu  
1 5  
gcg gcg gcg gag gtg gcg gcg acg gag atc aaa atg gag gaa gag agc 403  
Ala Ala Ala Glu Val Ala Ala Thr Glu Ile Lys Met Glu Glu Glu Ser

	10		15		20	
ggc gcg ccc ggc gtg ccg agc ggc aac ggg gct ccg ggc cct aag ggt						451
Gly Ala Pro Gly Val Pro Ser Gly Asn Gly Ala Pro Gly Pro Lys Gly						
	25		30		35	
gaa gga gaa cga cct gct cag aat gag aag agg aag gag aaa aac ata						499
Glu Gly Glu Arg Pro Ala Gln Asn Glu Lys Arg Lys Glu Lys Asn Ile						
	40		45		50	
aaa aga gga ggc aat cgc ttt gag cca tat gcc aat cca act aaa aga						547
Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr Ala Asn Pro Thr Lys Arg						
	55		60		65	70
tac aga gcc ttc att aca aac ata cct ttt gat gtg aaa tgg cag tca						595
Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe Asp Val Lys Trp Gln Ser						
	75		80		85	
ctt aaa gac ctg gtt aaa gaa aaa gtt ggt gag gta aca tac						637
Leu Lys Asp Leu Val Lys Glu Lys Val Gly Glu Val Thr Tyr						
	90		95		100	

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 213..467

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gcaaggtggg aagtgaagtc agtgcctcag ttgctgatca gtgtgttttt tgtgtccaat	120
tcttttatca ccaaaaaaga gaagaaatat tgcagtgaat gaagattcct ctgcatttta	180
gcactgcttt ttcaactgta gttggctttt ga atg agg atg aca atg gaa gag	233
Met Arg Met Thr Met Glu Glu	
	1 5
atg aag aat gaa gct gag acc aca tcc atg gtt tct atg ccc ctc tat	281
Met Lys Asn Glu Ala Glu Thr Thr Ser Met Val Ser Met Pro Leu Tyr	
	10 15 20
gca gtc atg tat cct gtg ttt aat gag cta gaa cga gta aat ctg tct	329
Ala Val Met Tyr Pro Val Phe Asn Glu Leu Glu Arg Val Asn Leu Ser	
	25 30 35
gca gcc cag aca ctg aga gcc gct ttc atc aag gct gaa aaa gaa aat	377
Ala Ala Gln Thr Leu Arg Ala Ala Phe Ile Lys Ala Glu Lys Glu Asn	
	40 45 50 55
cca ggt ctc aca caa gac atc att atg aaa att tta gag aaa aaa agc	425
Pro Gly Leu Thr Gln Asp Ile Ile Met Lys Ile Leu Glu Lys Lys Ser	
	60 65 70
gtg gaa gtt aac ttc acg grg tcc ctt ctt cgt atg gca gct g	468
Val Glu Val Asn Phe Thr Xaa Ser Leu Leu Arg Met Ala Ala	
	75 80 85

<210> 951  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 287..541

<400> 951

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tgcaagggtgg gaagtgaagt cagtgcctca gttgctgctt tctcctctaa atcttgggtct    120
cttgtttgga agtgactaac agcatttttg catgagaaag ccctaaaaag atcagtgtgt      180
tttttggtgc caattctttt atcaccaaaa aagagaagaa atattgcagt gaatgaagat      240
tcctctgcat tttagcactg ctttttcaac tgtagttggc ttttga atg agg atg      295
                                     Met Arg Met

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aca atg gaa gag atg aag aat gaa gct gag acc aca tcc atg gtt tct      343
Thr Met Glu Glu Met Lys Asn Glu Ala Glu Thr Thr Ser Met Val Ser
      5              10              15
atg ccc ctc tat gca gtc atg tat cct gtg ttt aat gag cta gaa cga      391
Met Pro Leu Tyr Ala Val Met Tyr Pro Val Phe Asn Glu Leu Glu Arg
      20              25              30              35
gta aat ctg tct gca gcc cag aca ctg aga gcc gct ttc atc aag gct      439
Val Asn Leu Ser Ala Ala Gln Thr Leu Arg Ala Ala Phe Ile Lys Ala
              40              45              50
gaa aaa gaa aat cca ggt ctc aca caa gac atc att atg aaa att tta      487
Glu Lys Glu Asn Pro Gly Leu Thr Gln Asp Ile Ile Met Lys Ile Leu
              55              60              65
gag aaa aaa agc gtg gaa gtt aac ttc acg grg tcc ctt ctt cgt atg      535
Glu Lys Lys Ser Val Glu Val Asn Phe Thr Xaa Ser Leu Leu Arg Met
              70              75              80
gca gct g
Ala Ala
      85

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<210> 952  
 <211> 392  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 147..392

<400> 952

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ctattgccta gctgccagat taaccttgcc ttgaaaataa cgattgcccc ataggctatt      60
cagtgtgaagg aagacaaaaa ttccttgga acctactagt gggtttgcc tccagatttg      120
gtagacgcaa aaagcaaagg gggaac atg ggc aaa gga aga ttt gat gar aaa      173
                                     Met Gly Lys Gly Arg Phe Asp Glu Lys
                                     1              5
gaa aat gtg tcc aac tgc atc cag ttg aaa act tca gtt att aag ggt      221
Glu Asn Val Ser Asn Cys Ile Gln Leu Lys Thr Ser Val Ile Lys Gly
      10              15              20              25
att aag aat caa ttg ata gag caa ttt cca ggt att gaa cca tgg ctt      269
Ile Lys Asn Gln Leu Ile Glu Gln Phe Pro Gly Ile Glu Pro Trp Leu

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	30		35		40	
aat caa atc atg cct aag aaa gat cct gtc aaa ata gtc cga tgc cat						317
Asn Gln Ile Met Pro Lys Lys Asp Pro Val Lys Ile Val Arg Cys His						
	45		50		55	
gaa cat ata gaa atc ctt aca gta aat gga gwr tta ctc ttt ttt aga						365
Glu His Ile Glu Ile Leu Thr Val Asn Gly Xaa Leu Leu Phe Phe Arg						
	60		65		70	
caa aga gaa ggg cct ttt tat cca acc						392
Gln Arg Glu Gly Pro Phe Tyr Pro Thr						
	75		80			

<210> 953  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 266..547

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tacgtggagt ccagaggagc ggaagtagtc agatttgact gagagccgtw aagcgcggy	120
gggytcwsgt ntttccggat aacgactaca gtcgccactg tcagtgccgg ccttcctcgt	180
gtgaggggat ctgccggacc cctgcaaatt caatttcttt cccattccgg gcccttcct	240
atcgtcgccc ccttcacctt ggatc atg ttc aag aaa ttt gat gaa aaa gaa	292
	Met Phe Lys Lys Phe Asp Glu Lys Glu
	1 5
aat gtg tcc aac tgc atc cag ttg aaa act tca gtt att aag ggt att	340
Asn Val Ser Asn Cys Ile Gln Leu Lys Thr Ser Val Ile Lys Gly Ile	
	10 15 20 25
aag aat caa ttg ata gag caa ttt cca ggt att gaa cca tgg ctt aat	388
Lys Asn Gln Leu Ile Glu Gln Phe Pro Gly Ile Glu Pro Trp Leu Asn	
	30 35 40
caa atc atg cct aag aaa gat cct gtc aaa ata gtc cga tgc cat gaa	436
Gln Ile Met Pro Lys Lys Asp Pro Val Lys Ile Val Arg Cys His Glu	
	45 50 55
cat ata gaa atc ctt aca gta aat gga gaa tta ctc ttt ttt aga caa	484
His Ile Glu Ile Leu Thr Val Asn Gly Glu Leu Leu Phe Phe Arg Gln	
	60 65 70
aga gaa ggg cct ttt tat cca acc cta aga tta ctt cac aaa tat cct	532
Arg Glu Gly Pro Phe Tyr Pro Thr Leu Arg Leu Leu His Lys Tyr Pro	
	75 80 85
ttt atc ctg cca cac	547
Phe Ile Leu Pro His	
	90

<210> 954  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 227..526

<400> 954

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tacatggcca atttagtaac agcaagcaaa accaaaatga gcaaaggaga ggatcccaat      120
aatcccagat ctataaagcg gattttctcaa gggggtagag rtaacmmcct agctattgct      180
aaatgtgata tcactcagtt gaaaaagaaa caatcagaag tgagca atg gga gcc      235
                                   Met Gly Ala
                                   1
gtg aaa ccc atc tca atg aag act tgt tgc caa cat gga gat aga gga      283
Val Lys Pro Ile Ser Met Lys Thr Cys Cys Gln His Gly Asp Arg Gly
   5                               10                               15
tat tgg tct aca ggg tac tat tgg aga ggg ggt cct gat gac aac tta      331
Tyr Trp Ser Thr Gly Tyr Tyr Trp Arg Gly Gly Pro Asp Asp Asn Leu
  20                               25                               30                               35
att gaa ggt gga gga aca aaa ttt gtc tgc aaa cct gga gcc aga aac      379
Ile Glu Gly Gly Gly Thr Lys Phe Val Cys Lys Pro Gly Ala Arg Asn
   40                               45                               50
att acc gtc ata ttc cac cca tta cta aga ttt att cag gag att gak      427
Ile Thr Val Ile Phe His Pro Leu Leu Arg Phe Ile Gln Glu Ile Xaa
   55                               60                               65
cat gct ctg ggt ctt ggc cca gcc aaa cag tgt cct ctt cga gag ttt      475
His Ala Leu Gly Leu Gly Pro Ala Lys Gln Cys Pro Leu Arg Glu Phe
   70                               75                               80
ctc acc gtg tac atc aaa aac atc ttt ctc aat caa gtc ttg gct gag      523
Leu Thr Val Tyr Ile Lys Asn Ile Phe Leu Asn Gln Val Leu Ala Glu
   85                               90                               95
atc
Ile
100

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<210> 955  
<211> 552  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 263..550

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cgccactcca gcctaattcc aaccccaggg cgaasgtttt cttatttatt tccgttttct      180
cgccactaca gcctcctgac aaggtgatcc gggcgggccc cgcaggaatt ttatcccttc      240
accggcctca cactagtatc gc atg tcc act atc cag aac ctc caa tct ttc      292
                                   Met Ser Thr Ile Gln Asn Leu Gln Ser Phe
                                   1                               5                               10
gac ccc ttt gct gat gca act aag ggt gac gac tta ctc ccg gca ggg      340
Asp Pro Phe Ala Asp Ala Thr Lys Gly Asp Asp Leu Leu Pro Ala Gly
   15                               20                               25

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act gag gat tac att cat ata aga atc cag caa cgg aac ggc aga aag	388
Thr Glu Asp Tyr Ile His Ile Arg Ile Gln Gln Arg Asn Gly Arg Lys	
30 35 40	
aca ctg act act gtt cag ggc att gca gat gat tat gac aaa aag aaa	436
Thr Leu Thr Thr Val Gln Gly Ile Ala Asp Asp Tyr Asp Lys Lys Lys	
45 50 55	
ctt gtg aaa gct ttc aaa aag aaa ttt gcc tgt aat ggt act gtg att	484
Leu Val Lys Ala Phe Lys Lys Lys Phe Ala Cys Asn Gly Thr Val Ile	
60 65 70	
gaa cat cct gaa tac gga gag gtt att cag ctt caa ggt grc caa aga	532
Glu His Pro Glu Tyr Gly Glu Val Ile Gln Leu Gln Gly Xaa Gln Arg	
75 80 85 90	
aaa aca tct gcc agt ttc tc	552
Lys Thr Ser Ala Ser Phe	
95	

<210> 956  
 <211> 379  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 78..377

<400> 956	
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ttgaactttt ggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg	110
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met	
1 5 10	
aag aag ctg aag gcc cga atg gtg atg tcg agc ctg gca gag ctg gag	158
Lys Lys Leu Lys Ala Arg Met Val Met Ser Ser Leu Ala Glu Leu Glu	
15 20 25	
gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg gct tat tat gag	206
Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu	
30 35 40	
gag cag cac ccr gag ctc act cct cta ctt gaa aaa gaa aga gat gga	254
Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly	
45 50 55	
tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat gtt gag gat ccc	302
Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro	
60 65 70 75	
gca acc gag gag cct ggg gag agc ttt tgt gac aag gtc atg aga tgg	350
Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp	
80 85 90	
ttc cag gcc atg ctg cag cgg ctg cag ac	379
Phe Gln Ala Met Leu Gln Arg Leu Gln	
95 100	

<210> 957  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 117..422

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 ggggtgcgca sctcgagttt gagagctacc cggagctcca agacaggggc cggacc atg 119  
 Met  
 1  
 gga acc cca aag cca cgg atc ctg ccc tgg ctg gtg tgc cag ctg gac 167  
 Gly Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu Asp  
 5 10 15  
 ctg ggg caa ctg gag ggc gtg gcc tgg gtg aac aag agc cgc acg cgc 215  
 Leu Gly Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr Arg  
 20 25 30  
 ttc cgc atc cct tgg aag cac ggc cta cgg cag gat gca cag cag gag 263  
 Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln Glu  
 35 40 45  
 gat ttc gga atc ttc cag gcc tgg gcc gag gcc act ggt gca tat gtt 311  
 Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr Val  
 50 55 60 65  
 ccc ggg agg gat aag cca gac ctg cca acc tgg aag agg aat ttc cgc 359  
 Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe Arg  
 70 75 80  
 tct gcc ctt aac cgc aaa gaa ggg ttg cgt tta gca gag gac cgg agc 407  
 Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg Ser  
 85 90 95  
 aag gam cct cac gac 422  
 Lys Xaa Pro His Asp  
 100

<210> 958  
 <211> 389  
 <212> DNA  
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<220>  
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 <222> 62..388

<400> 958  
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 g atg aag ttc gtg tac aaa gaa gag cat ccg ttc gag aag cgc cgc tct 109  
 Met Lys Phe Val Tyr Lys Glu Glu His Pro Phe Glu Lys Arg Arg Ser  
 1 5 10 15  
 gag ggc gag aag atc cga aag aaa tac ccg gac cgg gtg ccg gtg ata 157  
 Glu Gly Glu Lys Ile Arg Lys Lys Tyr Pro Asp Arg Val Pro Val Ile  
 20 25 30  
 gta gaa aag gct ccc aaa gct cgg ata gga gac ctg gac aaa aag aaa 205  
 Val Glu Lys Ala Pro Lys Ala Arg Ile Gly Asp Leu Asp Lys Lys Lys  
 35 40 45

tac ctg gtg cct tct gat ctc aca gtt ggt cag ttc tac ttc ttg atc	253
Tyr Leu Val Pro Ser Asp Leu Thr Val Gly Gln Phe Tyr Phe Leu Ile	
50 55 60	
cgg aag cga att cat ctc cga gct gag gat gcc ttg ttt ttc ttt gtc	301
Arg Lys Arg Ile His Leu Arg Ala Glu Asp Ala Leu Phe Phe Phe Val	
65 70 75 80	
aac aat gtc att cca ccc acc agt gtt tcc ttg gtg ctc cca cag acc	349
Asn Asn Val Ile Pro Pro Thr Ser Val Ser Leu Val Leu Pro Gln Thr	
85 90 95	
ctg acc aat cat aac acc cat ctc act gaa tca cta tct a	389
Leu Thr Asn His Asn Thr His Leu Thr Glu Ser Leu Ser	
100 105	

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cgcaccacag gtctggactg ctaaccttga atcctgggtt cttaaattct gcctccgctt	120
ctgactgagg accactggat tttaggaaa ctttgggtctt aattcccgtg ctrattagtc	180
aacagtggaa aatctgaaga gatgcaagca ggaaaaagaa attaaaccag gcctgaggag	240
cgatgcgaca ggc atg atg gag gtc gag tcc tcc tac tcg gac ttc atc	289
Met Met Glu Val Glu Ser Ser Tyr Ser Asp Phe Ile	
1 5 10	
tcc tgt gac cgg aca ggc cgt cgg aat gcg gtc cct gac atc cag gga	337
Ser Cys Asp Arg Thr Gly Arg Arg Asn Ala Val Pro Asp Ile Gln Gly	
15 20 25	
gac tca gag gct gtg agc gtg agg aag ctg gct gga gac atg ggc gag	385
Asp Ser Glu Ala Val Ser Val Arg Lys Leu Ala Gly Asp Met Gly Glu	
30 35 40	
ctg gca ctc gag ggg gaa ccc tgg cac tgg ccc agc agc ctc ttc tct g	434
Leu Ala Leu Glu Gly Glu Pro Trp His Trp Pro Ser Ser Leu Phe Ser	
45 50 55 60	

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aggaaatccc agccctacaa cttcggaaca gtgaaatatt agtccargga tccagtgaga	120

gacacagaag tgctagaagc caststcrt gaactaagga gaaaaagaac agacaaggga 180  
 acascyrge c atg gya tca gag atc cac atg aca ggc cca atg tgc ctc 230  
                   Met Xaa Ser Glu Ile His Met Thr Gly Pro Met Cys Leu  
                   1                  5                  10  
 att gag aac act aat ggg cga ctg atg gcg aat cca gaa gct ctg aag 278  
 Ile Glu Asn Thr Asn Gly Arg Leu Met Ala Asn Pro Glu Ala Leu Lys  
                   15                  20                  25  
 atc ctt tct gcc att aca cag cct atg gtg gtg gtg gca att gtg ggc 326  
 Ile Leu Ser Ala Ile Thr Gln Pro Met Val Val Val Ala Ile Val Gly  
                   30                  35                  40                  45  
 ctc tac cgc aca ggc aaa tcc tac ctg atg aac aag ctg gct ggr aag 374  
 Leu Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys  
                   50                  55                  60  
 aaa aag ggc ttc tct ctg ggc tcc acr gtg cag tct cac act aaa gga 422  
 Lys Lys Gly Phe Ser Leu Gly Ser Thr Val Gln Ser His Thr Lys Gly  
                   65                  70                  75  
 atc tgg atg tgg tgt rtg ccc cay ccc aag aag cca ggc cac atc cta 470  
 Ile Trp Met Trp Cys Xaa Pro His Pro Lys Lys Pro Gly His Ile Leu  
                   80                  85                  90  
 gtt ctg ctg g 480  
 Val Leu Leu  
                   95  
  
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 <222> 132..503  
  
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 tccctaacag c atg gcc cct aaa cgc cag tct cca ctc ccg cct caa aag 170  
                   Met Ala Pro Lys Arg Gln Ser Pro Leu Pro Pro Gln Lys  
                   1                  5                  10  
 aag aaa cca aga cca cct cct gct ctg gga ccg gag gag aca tcg gcc 218  
 Lys Lys Pro Arg Pro Pro Pro Ala Leu Gly Pro Glu Glu Thr Ser Ala  
                   15                  20                  25  
 tct gca ggc ttg ccg aag aag gga gaa aaa gaa cag caa gaa gcg att 266  
 Ser Ala Gly Leu Pro Lys Lys Gly Glu Lys Glu Gln Gln Glu Ala Ile  
                   30                  35                  40                  45  
 gaa cac att gat gaa gta caa aat gaa ata gac aga ctt aat gaa caa 314  
 Glu His Ile Asp Glu Val Gln Asn Glu Ile Asp Arg Leu Asn Glu Gln  
                   50                  55                  60  
 gcc agt gag gag att ttg aaa gta gaa cag aaa tat aac aaa ctc cgc 362  
 Ala Ser Glu Glu Ile Leu Lys Val Glu Gln Lys Tyr Asn Lys Leu Arg  
                   65                  70                  75  
 caa cca ttt ttt cag aag agg tca gaa ttg atc gcc aaa atc cca aat 410  
 Gln Pro Phe Gln Lys Arg Ser Glu Leu Ile Ala Lys Ile Pro Asn  
                   80                  85                  90

ttt tgg gta aca aca ttt gtc aac cat cca caa gtg tct gca ctg ctt	458
Phe Trp Val Thr Thr Phe Val Asn His Pro Gln Val Ser Ala Leu Leu	
95 100 105	
ggg gag gaa gat gaa gag gca ctg cat tat ttg acc aga gtt gaa g	504
Gly Glu Glu Asp Glu Glu Ala Leu His Tyr Leu Thr Arg Val Glu	
110 115 120	

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<220>  
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 <222> 20..313

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Met Ala Ala Ser Ile Val Arg Arg Gly Met Leu	
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ctg gcg cgg caa gtg gtt ctt cct cag ctc tct cct gca ggt aaa aga	100
Leu Ala Arg Gln Val Val Leu Pro Gln Leu Ser Pro Ala Gly Lys Arg	
15 20 25	
tac ctg ctt tct tca gcc tat gta gac agc cac aaa tgg gaa gca aga	148
Tyr Leu Leu Ser Ser Ala Tyr Val Asp Ser His Lys Trp Glu Ala Arg	
30 35 40	
gaa aaa gaa cat tac tgt ctt gct gat ctt gca tct tta atg gat aaa	196
Glu Lys Glu His Tyr Cys Leu Ala Asp Leu Ala Ser Leu Met Asp Lys	
45 50 55	
aca ttt gag aga aag ttg cct gtt agt tct tta aca ata tca cgg ctt	244
Thr Phe Glu Arg Lys Leu Pro Val Ser Ser Leu Thr Ile Ser Arg Leu	
60 65 70 75	
ata gac aac att tcc tct cgg gaa gag ata gat cat gca gag tat tac	292
Ile Asp Asn Ile Ser Ser Arg Glu Glu Ile Asp His Ala Glu Tyr Tyr	
80 85 90	
ctt tac aag ttt cga cac agc cc	315
Leu Tyr Lys Phe Arg His Ser	
95	

<210> 963  
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 <212> DNA  
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 <222> 18..341

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ctg aag ctg aaa ggc gtc gca gag ctg gga gtg acc aag cgg aag aag	98
Leu Lys Leu Lys Gly Val Ala Glu Leu Gly Val Thr Lys Arg Lys Lys	
15 20 25	
aaa aag aag gac aaa gac aaa gcg aaa ctc ctg gaa gca atg gga acg	146
Lys Lys Lys Asp Lys Asp Lys Ala Lys Leu Leu Glu Ala Met Gly Thr	
30 35 40	
agc aaa aag aac gag gag gag aag cgg cgc ggc ctg gac aag cgg acc	194
Ser Lys Lys Asn Glu Glu Glu Lys Arg Arg Gly Leu Asp Lys Arg Thr	
45 50 55	
ccg gcc cag gcg gcc ttc gag aaa atg cag gag aag cgg caa atg gma	242
Pro Ala Gln Ala Ala Phe Glu Lys Met Gln Glu Lys Arg Gln Met Xaa	
60 65 70 75	
agg awc cta aag amg gca tcc aaa acc cac aag cag aag agt gga ggm	290
Arg Xaa Leu Lys Xaa Ala Ser Lys Thr His Lys Gln Lys Ser Gly Gly	
80 85 90	
ctt caa cag aca cct gga cas rct cac gga gca tta cga cat tcc caa	338
Leu Gln Gln Thr Pro Gly Xaa Xaa His Gly Ala Leu Arg His Ser Gln	
95 100 105	
agt	341
Ser	
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<222> 77..361	
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ccgcctcctt gcagcc atg tcc cgg ccc ctg tca gac caa gag aaa aga aag	112
Met Ser Arg Pro Leu Ser Asp Gln Glu Lys Arg Lys	
1 5 10	
caa atc agt gtg cgt ggc ctg gcc ggc gtg gag aac gtg act gag ctg	160
Gln Ile Ser Val Arg Gly Leu Ala Gly Val Glu Asn Val Thr Glu Leu	
15 20 25	
aaa aag aac ttc aac cgg cac ctg cat ttc aca ctc gta aag gac cgc	208
Lys Lys Asn Phe Asn Arg His Leu His Phe Thr Leu Val Lys Asp Arg	
30 35 40	
aat gtg gcc acc cca cga gac tac tac ttt gct ctg gcc cat acc gtg	256
Asn Val Ala Thr Pro Arg Asp Tyr Tyr Phe Ala Leu Ala His Thr Val	
45 50 55 60	
cgc gac cac ctc gtg ggg cgc tgg atc cgc acg cag cag cac tac tat	304
Arg Asp His Leu Val Gly Arg Trp Ile Arg Thr Gln Gln His Tyr Tyr	
65 70 75	
gag aag gac ccc aag gca gag gat cta cta cct gtc ttt aga gtt cta	352
Glu Lys Asp Pro Lys Ala Glu Asp Leu Leu Pro Val Phe Arg Val Leu	
80 85 90	
tat ggg acg ga	363
Tyr Gly Thr	
95	

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<220>  
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 <222> 145..474

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 atctaaaaga acttcatcat caag atg tct gat gat att gac tgg tta cgc 171  
 Met Ser Asp Asp Ile Asp Trp Leu Arg  
 1 5  
 agc cac agg ggt gtg tgc aag gta gat ctc tac aac cca gaa gga cag 219  
 Ser His Arg Gly Val Cys Lys Val Asp Leu Tyr Asn Pro Glu Gly Gln  
 10 15 20 25  
 caa gat cag gac cgg aaa gtg ata tgc ttt gtc gat gtg tcc acc ctg 267  
 Gln Asp Gln Asp Arg Lys Val Ile Cys Phe Val Asp Val Ser Thr Leu  
 30 35 40  
 aat gta gaa gat aaa gat tac aag gat gct gct agt tcc agc tca gaa 315  
 Asn Val Glu Asp Lys Asp Tyr Lys Asp Ala Ala Ser Ser Ser Ser Glu  
 45 50 55  
 ggc aac tta aac ctg gga agt ctg gaa gaa aaa gag att atc gtg atc 363  
 Gly Asn Leu Asn Leu Gly Ser Leu Glu Glu Lys Glu Ile Ile Val Ile  
 60 65 70  
 aag gac act gag aag aaa gac cag tct aag aca gag gga tct gta tgc 411  
 Lys Asp Thr Glu Lys Lys Asp Gln Ser Lys Thr Glu Gly Ser Val Cys  
 75 80 85  
 ctt ttc aaa caa gct ccc tct gat cct gta agt gtc ctc aac tgg ctt 459  
 Leu Phe Lys Gln Ala Pro Ser Asp Pro Val Ser Val Leu Asn Trp Leu  
 90 95 100 105  
 ctc agt gat ctc cag a 475  
 Leu Ser Asp Leu Gln  
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 <212> DNA  
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<220>  
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 <222> 63..281

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 cg atg gca aca agt atg gcg gct gct agt ggt aga ttt gaa agt gcg 107  
 Met Ala Thr Ser Met Ala Ala Ala Ser Gly Arg Phe Glu Ser Ala  
 1 5 10 15

aag agt atc gaa gag cgg aaa gaa cag acc cgg aat gcc agg gcc gag	155
Lys Ser Ile Glu Glu Arg Lys Glu Gln Thr Arg Asn Ala Arg Ala Glu	
20 25 30	
gtg ttg cgc cag gct aaa gcc aat ttt gaa aaa gaa gaa agg cgt aaa	203
Val Leu Arg Gln Ala Lys Ala Asn Phe Glu Lys Glu Glu Arg Arg Lys	
35 40 45	
gaa ctt aag cga ctt cgg ggt gag gat aca tgg atg cta cct gat gtg	251
Glu Leu Lys Arg Leu Arg Gly Glu Asp Thr Trp Met Leu Pro Asp Val	
50 55 60	
aat gag aga att gaa cag ttc tca cag gaa	281
Asn Glu Arg Ile Glu Gln Phe Ser Gln Glu	
65 70	

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 406..933

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tccagcccat cttgctgacc taattcagaa aagaagtgt acagctctgt gcctgtcatc	120
tttgcagtgt agcattttca ggtgatctag gaaacagtta tttttatgag caaataagag	180
aaacaggaat catgatgggg atatatattaa cagacccagt actggataaaa acttaaagcc	240
agttttctatt caacatagtg aaaagggtcac cttgcctggc tgagaaaagc agcaaaatat	300
cagctttgtt ggtttcagtt aacctcttag cccgggctaa tctcttttcc ttgatgttca	360
aaccaatttg ggatatctaa ctctaaagag agacacactg tactc atg gta gat gac	417
Met Val Asp Asp	
1	
aag gaa aag aac atg aaa tgt ctc acc ttc ttc ttg atg ctt cca gag	465
Lys Glu Lys Asn Met Lys Cys Leu Thr Phe Phe Leu Met Leu Pro Glu	
5 10 15 20	
acg gta aag aac agg tcc aag aaa agc tca aag aaa gca aat acc agc	513
Thr Val Lys Asn Arg Ser Lys Lys Ser Ser Lys Lys Ala Asn Thr Ser	
25 30 35	
agc agc agt agc aac agc agc aag ttg cca cca gtt tgt tat gaa ata	561
Ser Ser Ser Ser Asn Ser Ser Lys Leu Pro Pro Val Cys Tyr Glu Ile	
40 45 50	
att acc ttg aag act aaa aag aag aag atg gct gct gat ata ttc ccc	609
Ile Thr Leu Lys Thr Lys Lys Lys Lys Met Ala Ala Asp Ile Phe Pro	
55 60 65	
cgt aaa aag cca gcc aac tcc agc agc acc agc gtc cag cag tac cac	657
Arg Lys Lys Pro Ala Asn Ser Ser Ser Thr Ser Val Gln Gln Tyr His	
70 75 80	
cag cag aat ctc agt aac aac aac ctt atc ccg gcc cca aac tgg cag	705
Gln Gln Asn Leu Ser Asn Asn Asn Leu Ile Pro Ala Pro Asn Trp Gln	
85 90 95 100	
ggc ctt tat ccc acc att aga gag aga aat gcg atg atg ttc aat aat	753
Gly Leu Tyr Pro Thr Ile Arg Glu Arg Asn Ala Met Met Phe Asn Asn	
105 110 115	



gat ttg atg gca gat gta cat ttt gtg gtt ggg cca cca ggt ggg act	801
Asp Leu Met Ala Asp Val His Phe Val Val Gly Pro Pro Gly Gly Thr	
120 125 130	
caa cgg ttg cca gga cac aaa tat gtt tta gct gtt ggg agc tct gtg	849
Gln Arg Leu Pro Gly His Lys Tyr Val Leu Ala Val Gly Ser Ser Val	
135 140 145	
twc cat gcg atg ttt tac gga gaa ctt gca gag gac aaa gat gaa atc	897
Xaa His Ala Met Phe Tyr Gly Glu Leu Ala Glu Asp Lys Asp Glu Ile	
150 155 160	
cgt ata cca gat gtc gaa cct gct gct ttt ctc gct at	935
Arg Ile Pro Asp Val Glu Pro Ala Ala Phe Leu Ala	
165 170 175	

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 34..231

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Met Ala Cys Gly Phe Arg Arg	
1 5	
gct att gct tgc cag ctt tcc aga gtg ttg aat ctt cca cca gaa aac	102
Ala Ile Ala Cys Gln Leu Ser Arg Val Leu Asn Leu Pro Pro Glu Asn	
10 15 20	
ttg atc aca tca ata tct gca gtt cca att tcc caa aaa gaa gaa gta	150
Leu Ile Thr Ser Ile Ser Ala Val Pro Ile Ser Gln Lys Glu Glu Val	
25 30 35	
gct gat ttt cag ctt tct gtg gat tct tta ttg gaa aaa gac aat gac	198
Ala Asp Phe Gln Leu Ser Val Asp Ser Leu Glu Lys Asp Asn Asp	
40 45 50 55	
cat tca aga cca gat att caa gtt caa gcc aag ag	233
His Ser Arg Pro Asp Ile Gln Val Gln Ala Lys	
60 65	

<210> 969  
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 <212> DNA  
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<220>  
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 <222> 80..589

<400> 969	
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ggggcgctga gctgttggg atg agc ttt gat cca aac ctt ctc cac aac aat	112
Met Ser Phe Asp Pro Asn Leu Leu His Asn Asn	

	1	5	10	
gga cat aat ggg tac cct aat ggt act tca gca gca ctg cgt gaa act				160
Gly His Asn Gly Tyr Pro Asn Gly Thr Ser Ala Ala Leu Arg Glu Thr				
	15	20	25	
ggg gtt att gaa aaa ctg tta acc tct tac gga ttt att cag tgt tca				208
Gly Val Ile Glu Lys Leu Leu Thr Ser Tyr Gly Phe Ile Gln Cys Ser				
	30	35	40	
gaa cgt caa gct aga ctt ttc ttc cac tgt tca cag tat aat ggc aac				256
Glu Arg Gln Ala Arg Leu Phe Phe His Cys Ser Gln Tyr Asn Gly Asn				
	45	50	55	
ctg caa gac tta aaa gta gga gat gat gtt gaa ttt gaa gta tca tcg				304
Leu Gln Asp Leu Lys Val Gly Asp Asp Val Glu Phe Glu Val Ser Ser				
	60	65	70	75
gac cga cgg act ggg aaa ccc att gct gtt aaa ctg gtg aag ata aaa				352
Asp Arg Arg Thr Gly Lys Pro Ile Ala Val Lys Leu Val Lys Ile Lys				
	80	85	90	
caa gaa atc ctc cct gaa gaa cga atg aat gga caa gaa gtg ttt tat				400
Gln Glu Ile Leu Pro Glu Glu Arg Met Asn Gly Gln Glu Val Phe Tyr				
	95	100	105	
ctg act tac acc cct gaa gat gtc gaa ggg aac gtt cak ytg gaa act				448
Leu Thr Tyr Thr Pro Glu Asp Val Glu Gly Asn Val Xaa Leu Glu Thr				
	110	115	120	
gga gat aaa ata aac ttt gta att gat aac aat aaa cat act ggt gct				496
Gly Asp Lys Ile Asn Phe Val Ile Asp Asn Asn Lys His Thr Gly Ala				
	125	130	135	
gta agt gct cgc aac att atg ctg ttg aaa aag aaa caa gcc cgc tgt				544
Val Ser Ala Arg Asn Ile Met Leu Leu Lys Lys Lys Gln Ala Arg Cys				
	140	145	150	155
cag gga gta gtt tgt gcc atg aag gag gca ttt ggc ttt att gaa				589
Gln Gly Val Val Cys Ala Met Lys Glu Ala Phe Gly Phe Ile Glu				
	160	165	170	

&lt;210&gt; 970

&lt;211&gt; 976

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 467..976

&lt;400&gt; 970

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ggggcgctga gctgttggt atgaagtgt acagaacaga ctttaccacc tgaaactgct	120
gcttcaagtt cagatcaggc aaggaacaaa cctcgtaaca actaacaaga ccaaagaaga	180
gtacacttaa gttgaagaca caacacttga tctgaaacaa gaagtttggtg cctactcaac	240
agctttgaaa gagcacttcc caacgctgct agtagtcttt gttttcttca gtgctgtact	300
gtgagattgc ccggtacagc agcagttgta ttctttatta gcttggtaga tcattttctc	360
tcgctctttt ttttaatact agcaactttc atcctttgaa acgtgtgctg aaaaagaaga	420
atcagcaaat actactgaaa gtgcaatatt tgagtatcac tgcgag atg agc ttt	475
	Met Ser Phe
	1

gat cca aac ctt ctc cac aac aat gga cat aat ggg tac cct aat ggt	523
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Asp	Pro	Asn	Leu	Leu	His	Asn	Asn	Gly	His	Asn	Gly	Tyr	Pro	Asn	Gly		
5						10				15							
act	tca	gca	gca	ctg	cgt	gaa	act	ggg	gtt	att	gaa	aaa	ctg	tta	acc		571
Thr	Ser	Ala	Ala	Leu	Arg	Glu	Thr	Gly	Val	Ile	Glu	Lys	Leu	Leu	Thr		
20					25					30					35		
tct	tac	gga	ttt	att	cag	tgt	tca	gaa	cgt	caa	gct	aga	ctt	ttc	ttc		619
Ser	Tyr	Gly	Phe	Ile	Gln	Cys	Ser	Glu	Arg	Gln	Ala	Arg	Leu	Phe	Phe		
				40					45					50			
cac	tgt	tca	cag	tat	aat	ggc	aac	ctg	caa	gac	tta	aaa	gta	gga	gat		667
His	Cys	Ser	Gln	Tyr	Asn	Gly	Asn	Leu	Gln	Asp	Leu	Lys	Val	Gly	Asp		
			55					60					65				
gat	gtt	gaa	ttt	gaa	gta	tca	tcg	gac	cga	cgg	act	ggg	aaa	ccc	att		715
Asp	Val	Glu	Phe	Glu	Val	Ser	Ser	Asp	Arg	Arg	Thr	Gly	Lys	Pro	Ile		
		70					75					80					
gct	gtt	aaa	ctg	gtg	aag	ata	aaa	caa	gaa	atc	ctc	cct	gaa	gaa	cga		763
Ala	Val	Lys	Leu	Val	Lys	Ile	Lys	Gln	Glu	Ile	Leu	Pro	Glu	Glu	Arg		
		85				90					95						
atg	aat	gga	caa	gaa	gtg	ttt	tat	ctg	act	tac	acc	cct	gaa	gat	gtc		811
Met	Asn	Gly	Gln	Glu	Val	Phe	Tyr	Leu	Thr	Tyr	Thr	Pro	Glu	Asp	Val		
100					105					110					115		
gaa	ggg	aac	gtt	cak	ytg	gaa	act	gga	gat	aaa	ata	aac	ttt	gta	att		859
Glu	Gly	Asn	Val	Xaa	Leu	Glu	Thr	Gly	Asp	Lys	Ile	Asn	Phe	Val	Ile		
				120					125					130			
gat	aac	aat	aaa	cat	act	ggt	gct	gta	agt	gct	cgc	aac	att	atg	ctg		907
Asp	Asn	Asn	Lys	His	Thr	Gly	Ala	Val	Ser	Ala	Arg	Asn	Ile	Met	Leu		
			135					140					145				
ttg	aaa	aag	aaa	caa	gcc	cgc	tgt	cag	gga	gta	gtt	tgt	gcc	atg	aag		955
Leu	Lys	Lys	Lys	Gln	Ala	Arg	Cys	Gln	Gly	Val	Val	Cys	Ala	Met	Lys		
		150				155						160					
gag	gca	ttt	ggc	ttt	att	gaa											976
Glu	Ala	Phe	Gly	Phe	Ile	Glu											
		165				170											

<210> 971  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 180..332

<400>	971																
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aggcaaggaa	gctggtgcat	gcagtgtctc	tgggcaaggt	tatgcaaacc	aaaaagaaga											120	
atgtacttca	tctggttggg	ctggattccc	tctgataagc	cttcccagtt	gactgaaag											179	
atg agg cta	ggc tct agc	aag ttg aag	tca aac	cag ctc	ctt caa	gaa										227	
Met Arg Leu	Gly Ser Ser	Lys Leu Lys	Ser Asn	Gln Leu	Leu Gln	Glu											
1		5		10		15											
gct ttg agc	aga atg aag	tgg gga gga	ccc agc	ttc cag	ccc agg	aag										275	
Ala Leu Ser	Arg Met Lys	Trp Gly Gly	Pro Ser	Phe Gln	Pro Arg	Lys											
		20		25		30											
ccc act gta	cct gga gcc	atc tgg gat	aag act	ttg acc	cat gac	tcc										323	

Pro Thr Val Pro Gly Ala Ile Trp Asp Lys Thr Leu Thr His Asp Ser  
 35 40 45  
 cat atc cac  
 His Ile His  
 50

332

<210> 972  
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 <212> DNA  
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<220>  
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 <222> 30..515

<400> 972

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 Met Phe Leu Leu Pro Leu Pro Ala  
 1 5  
 gcg ggg cga gta gtc gtc cga cgt ctg gcc gtg aga cgt ttc ggg agc 101  
 Ala Gly Arg Val Val Val Arg Arg Leu Ala Val Arg Arg Phe Gly Ser  
 10 15 20  
 cgg agt ctc tcc acc gca gac atg acg aag ggc ctt gtt tta gga atc 149  
 Arg Ser Leu Ser Thr Ala Asp Met Thr Lys Gly Leu Val Leu Gly Ile  
 25 30 35 40  
 tat tcc aaa gaa aaa gaa gat gat gtg cca cag ttc aca agt gca gga 197  
 Tyr Ser Lys Glu Lys Glu Asp Asp Val Pro Gln Phe Thr Ser Ala Gly  
 45 50 55  
 gag aat ttt gat aaa ttg tta gct gga aag ctg aga gag act ttg aac 245  
 Glu Asn Phe Asp Lys Leu Leu Ala Gly Lys Leu Arg Glu Thr Leu Asn  
 60 65 70  
 ata tct gga cca cct ctg aag gca ggg aag act cga acc ttt tat ggt 293  
 Ile Ser Gly Pro Pro Leu Lys Ala Gly Lys Thr Arg Thr Phe Tyr Gly  
 75 80 85  
 ctg cat cag gac ttc ccc agc gtg gtg cta gtt ggc ctc ggc aaa aag 341  
 Leu His Gln Asp Phe Pro Ser Val Val Leu Val Gly Leu Gly Lys Lys  
 90 95 100  
 gca gct gga atc gac gaa cag gaa aac tgg cat gaa ggc aaa gaa aac 389  
 Ala Ala Gly Ile Asp Glu Gln Glu Asn Trp His Glu Gly Lys Glu Asn  
 105 110 115 120  
 atc aga gct gct gtt gca gcg rgg tgc agg cag att caa gac ctg gag 437  
 Ile Arg Ala Ala Val Ala Ala Xaa Cys Arg Gln Ile Gln Asp Leu Glu  
 125 130 135  
 ctc tcg tct gtg gag gtg gat ccc tgt gga gac gct cag gct gct gcg 485  
 Leu Ser Ser Val Glu Val Asp Pro Cys Gly Asp Ala Gln Ala Ala Ala  
 140 145 150  
 gag gga gcg gtg ctt ggt ctc tat gaa tac 515  
 Glu Gly Ala Val Leu Gly Leu Tyr Glu Tyr  
 155 160

<210> 973  
 <211> 461  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 66..461

<400> 973

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ccaaa atg gct ggg cga aaa ctt gct cta aaa acc att gac tgg gta gct 110  
Met Ala Gly Arg Lys Leu Ala Leu Lys Thr Ile Asp Trp Val Ala  
1 5 10 15  
ttt gca gag atc ata ccc cag aac caa aag gcc att gct agt tcc ctg 158  
Phe Ala Glu Ile Ile Pro Gln Asn Gln Lys Ala Ile Ala Ser Ser Leu  
20 25 30  
aaa tcc tgg aat gag acc ctc acc tcc agg ttg gct gct tta cct gag 206  
Lys Ser Trp Asn Glu Thr Leu Thr Ser Arg Leu Ala Ala Leu Pro Glu  
35 40 45  
aat cca cca gct atc gac tgg gct tac tac aag gcc aat gtg gcc aag 254  
Asn Pro Pro Ala Ile Asp Trp Ala Tyr Tyr Lys Ala Asn Val Ala Lys  
50 55 60  
gct ggc ttg gtg gat gac ttt gag aag aag ttt aat gcg ctg aag gtt 302  
Ala Gly Leu Val Asp Asp Phe Glu Lys Lys Phe Asn Ala Leu Lys Val  
65 70 75  
ccc gtg cca gag gat aaa tat act gcc cag gtg gat gcc gaa gaa aaa 350  
Pro Val Pro Glu Asp Lys Tyr Thr Ala Gln Val Asp Ala Glu Glu Lys  
80 85 90 95  
gaa gat gtg aaa tct tgt gct gag tgg gtg tct ctc tca aag gcc agg 398  
Glu Asp Val Lys Ser Cys Ala Glu Trp Val Ser Leu Ser Lys Ala Arg  
100 105 110  
att gta gaa tat gag aaa gag atg gag aag atg aag aac tta att cca 446  
Ile Val Glu Tyr Glu Lys Glu Met Glu Lys Met Lys Asn Leu Ile Pro  
115 120 125  
ttt gat cag atg acc 461  
Phe Asp Gln Met Thr  
130

<210> 974

<211> 557

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 181..555

<400> 974

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tggagcaggg gccttggtggg taccgggttg ggcagggaga ggtgcggctc tgcgacggaa 120  
acaatcgcca gagatgccgg ggctagcctt cccaccagt agctgctgct ggtggtgaca 180  
atg tca aat aac ggc cta gac att caa gac aaa ccc cca gcc cct ccg 228  
Met Ser Asn Asn Gly Leu Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro  
1 5 10 15

atg aga aat acc agc act atg att gga gcc ggc agc aaa gat gct gga	276
Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Ala Gly	
20 25 30	
acc cta aac cat ggt tct aaa cct ctg cct cca aac cca gag gag ang	324
Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Xaa	
35 40 45	
aaa aag aag gac cga ttt tac cga tcc att tta cct gga gat aar aca	372
Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr	
50 55 60	
aat aaa aag aaa gag aaa gag cgg cca gag att tct ctc cct tca gat	420
Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp	
65 70 75 80	
ttt gaa cac aca att cat gtc ggt ttt gat gct gtc aca ggg gag ttt	468
Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe	
85 90 95	
acg gga atg cca gag cag tgg gcc cgc ttg ctt cag aca tca aat atc	516
Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile	
100 105 110	
act aag tcg gag cag aag aaa aac ccg cag ctg ttc tgg at	557
Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Leu Phe Trp	
115 120 125	

<210> 975  
 <211> 492  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 204..491

<400> 975	
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atctgttcta aaagaagggc tgaactgatg gaaggaatgc tgtagcctg agactcagga	120
agacaacttc tgcagggtca ctccctggct tctggaggaa agagaaggag ggcagtgtc	180
cagtgtgtaca gaagtgtgac ata atg gaa tca ggc ttc acc tcc aag gac acc	233
Met Glu Ser Gly Phe Thr Ser Lys Asp Thr	
1 5 10	
tat cta agc cat ttt aac cct cgg gat tac cta gaa aaa tat tac aag	281
Tyr Leu Ser His Phe Asn Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys	
15 20 25	
ttt ggt tct agg cac tct gca gaa agc cag att ctt aag cac ctt ctg	329
Phe Gly Ser Arg His Ser Ala Glu Ser Gln Ile Leu Lys His Leu Leu	
30 35 40	
aaa aat ctt ttc aag ata ttc tgc cta gac ggt gtg aag gga gac ctg	377
Lys Asn Leu Phe Lys Ile Phe Cys Leu Asp Gly Val Lys Gly Asp Leu	
45 50 55	
ctg att gac atc ggc tct ggc ccc act atc tat cag ctc ctc tct gct	425
Leu Ile Asp Ile Gly Ser Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala	
60 65 70	
tgt gaa tcc ttt aag gag atc gtc gtc act gac tac tca gnc cag aac	473
Cys Glu Ser Phe Lys Glu Ile Val Val Thr Asp Tyr Ser Xaa Gln Asn	
75 80 85 90	

ctg cag gag ctg gag aaa g  
 Leu Gln Glu Leu Glu Lys  
 95

492

<210> 976  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 208..537

<400> 976  
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 tataaagtga tgcaaacaga aattccacca gcctccatgt atcatcatgt gtcataactc 120  
 agtcaagctc agtgagcatt ctcagcacat tgcctcaaca gcttcaaggt gagccagctc 180  
 aagactttgc tctccaccag gcagaag atg aca gac tgt gaa ttt gga tat att 234  
 Met Thr Asp Cys Glu Phe Gly Tyr Ile

	1	5	
tac agg ctg gct cag gac tat ctg cag tgc gtc cta cag ata cca caa			282
Tyr Arg Leu Ala Gln Asp Tyr Leu Gln Cys Val Leu Gln Ile Pro Gln			
10 15 20 25			
cct gga tca ggt cca agc aaa acg tcc aga gtg cta caa aat gtt gcg			330
Pro Gly Ser Gly Pro Ser Lys Thr Ser Arg Val Leu Gln Asn Val Ala			
30 35 40			
ttc tca gtc caa aaa gaa gtg gaa aag aat ctg aag tca tgc ttg gac			378
Phe Ser Val Gln Lys Glu Val Glu Lys Asn Leu Lys Ser Cys Leu Asp			
45 50 55			
aat gtt aat gtt gtg tcc gta gac act gcc aga aca cta ttc aac caa			426
Asn Val Asn Val Val Ser Val Asp Thr Ala Arg Thr Leu Phe Asn Gln			
60 65 70			
gtg atg gaa aag gag ttt gaa gac ggc atc att aac tgg gga aga att			474
Val Met Glu Lys Glu Phe Glu Asp Gly Ile Ile Asn Trp Gly Arg Ile			
75 80 85			
gta acc ata ttt gca ttt gaa ggt att ctc atc aag aaa ctt cta cga			522
Val Thr Ile Phe Ala Phe Glu Gly Ile Leu Ile Lys Lys Leu Leu Arg			
90 95 100 105			
cag caa att gcc ccg			537
Gln Gln Ile Ala Pro			
110			

<210> 977  
 <211> 334  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 79..333

<400> 977

ataattaagg ataaagctaa aggaaaaaag agtaaagctg ctgctaaagc tggatcttct	60
aaataccagt ggggcatt atg aaa tcc ctt ggc ctg tct gat gaa gag ata	111
Met Lys Ser Leu Gly Leu Ser Asp Glu Glu Ile	
1 5 10	
gta aaa ttt tct gaa gca gaa cat tgg ctt gat tat ttc ccg cca ctg	159
Val Lys Phe Ser Glu Ala Glu His Trp Leu Asp Tyr Phe Pro Pro Leu	
15 20 25	
gct att cag gat tta aaa aga atg ggt ttg aag gta gac tgg cgt cgt	207
Ala Ile Gln Asp Leu Lys Arg Met Gly Leu Lys Val Asp Trp Arg Arg	
30 35 40	
tcc ttc atc acc act gat gtt aat cct tac tat gat tca ttt gtc aga	255
Ser Phe Ile Thr Thr Asp Val Asn Pro Tyr Tyr Asp Ser Phe Val Arg	
45 50 55	
tgg caa ttt tta aca tta aga gaa aga aac aaa att aaa ttt ggg aag	303
Trp Gln Phe Leu Thr Leu Arg Glu Arg Asn Lys Ile Lys Phe Gly Lys	
60 65 70 75	
cgg tat aca att tac tct ccg aaa gat aga c	334
Arg Tyr Thr Ile Tyr Ser Pro Lys Asp Arg	
80 85	

<210> 978  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 122..535

<400> 978	
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cgaaaattga gacggttttc gcactccags ggctgctcct ggcggctctg cggccgtcac	120
c atg cca cag aat gaa tat att gaa tta cac cgt aaa cgc tat gga tac	169
Met Pro Gln Asn Glu Tyr Ile Glu Leu His Arg Lys Arg Tyr Gly Tyr	
1 5 10 15	
cgt ttg gat tac cat gag aaa aag aga aag aag gaa agt cga gag gct	217
Arg Leu Asp Tyr His Glu Lys Lys Arg Lys Lys Glu Ser Arg Glu Ala	
20 25 30	
cat gaa cgt tca aag aag gca aag aaa atg att ggt ctg aag gct aag	265
His Glu Arg Ser Lys Lys Ala Lys Lys Met Ile Gly Leu Lys Ala Lys	
35 40 45	
ctt tac cat aaa cag cgt cat gct gag aaa ata caa atg aaa aag act	313
Leu Tyr His Lys Gln Arg His Ala Glu Lys Ile Gln Met Lys Lys Thr	
50 55 60	
atc aag atg cat gaa aag aga aac acc aaa caa aag aat gat gaa aag	361
Ile Lys Met His Glu Lys Arg Asn Thr Lys Gln Lys Asn Asp Glu Lys	
65 70 75 80	
aca cca cag gga gca gta cct gcc tat ctg ctg gac aga gag gga caa	409
Thr Pro Gln Gly Ala Val Pro Ala Tyr Leu Leu Asp Arg Glu Gly Gln	
85 90 95	
tct cga gct aaa gta ctt tcc aat atg att aaa cag aaa aga aaa gag	457
Ser Arg Ala Lys Val Leu Ser Asn Met Ile Lys Gln Lys Arg Lys Glu	
100 105 110	



aag gcg gga aaa tgg gaa gtc cct ctg cct aaa gta cgt gcc cag gga 505  
 Lys Ala Gly Lys Trp Glu Val Pro Leu Pro Lys Val Arg Ala Gln Gly  
           115                          120                          125

gaa aca gaa gta tta aaa gtt att cga aca 535  
 Glu Thr Glu Val Leu Lys Val Ile Arg Thr  
           130                          135

<210> 979  
 <211> 648  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 377..646

<400> 979  
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 ttgcttgagt tcttcggaaa gtctcatcca cccccacatc gcctcttttag gaagtcactt 120  
 aatgttgggc ttcattattc ccacatccct ttccttacta cttgcctgca cttcttgaga 180  
 aaaagactgc agaaaggaga ggtgggggctt tcagtagaaa caagcaaacc gcagtcacctg 240  
 tgggggggact ctccaggaag aagggttaatt tcctgcctcc ttaaattggc tgctactgtc 300  
 agtkattttg ctcccaaccc cagagcttca cttgctcctt cacttcccag ttccgcaaga 360  
 accgtgggag acagtt atg gag aag cgt ctg cag gag gct cag ctg tac aag 412  
                           Met Glu Lys Arg Leu Gln Glu Ala Gln Leu Tyr Lys  
                                   1                          5                          10  
 gag gaa ggg aac cag cgc tac cgg gaa ggg aag tac cga gat gct gtg 460  
 Glu Glu Gly Asn Gln Arg Tyr Arg Glu Gly Lys Tyr Arg Asp Ala Val  
           15                          20                          25  
 agt agg tac cat cga gct ctg ctt cag ctg cgg ggt ctg gat ccg agt 508  
 Ser Arg Tyr His Arg Ala Leu Leu Gln Leu Arg Gly Leu Asp Pro Ser  
           30                          35                          40  
 ctg ccc tct ccg tta cct aat ctc gga cct cag ggc ccg gcc ctc acg 556  
 Leu Pro Ser Pro Leu Pro Asn Leu Gly Pro Gln Gly Pro Ala Leu Thr  
           45                          50                          55                          60  
 cct gaa caa gaa aac ata ttg cat acc acc cag aca gac tgc tat aac 604  
 Pro Glu Gln Glu Asn Ile Leu His Thr Thr Gln Thr Asp Cys Tyr Asn  
           65                          70                          75  
 aat cta gct gct tgt ctc ctt cag atg gag ccc gtg aac tac ga 648  
 Asn Leu Ala Ala Cys Leu Leu Gln Met Glu Pro Val Asn Tyr  
           80                          85                          90

<210> 980  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 106..372

<400> 980

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 ttaccccggc tctccgcccc tcctttctcgc ggcgctcgag ggacc atg gcc gat cct 117  
 Met Ala Asp Pro

1  
 cgc gtg aga cag atc aag atc aag acc ggc gtg gtg aag cgg ttg gtc 165  
 Arg Val Arg Gln Ile Lys Ile Lys Thr Gly Val Val Lys Arg Leu Val  
 5 10 15 20  
 aaa gaa aaa gtg atg tat gaa aaa gag gca aaa caa caa gaa gaa aag 213  
 Lys Glu Lys Val Met Tyr Glu Lys Glu Ala Lys Gln Gln Glu Glu Lys  
 25 30 35  
 att gaa aaa atg aga gct gaa gac ggt gaa aat tat gac att ama aag 261  
 Ile Glu Lys Met Arg Ala Glu Asp Gly Glu Asn Tyr Asp Ile Xaa Lys  
 40 45 50  
 cag gca gag agg tca cta cct tca gcc cac acc tcc aca ccc gca tct 309  
 Gln Ala Glu Arg Ser Leu Pro Ser Ala His Thr Ser Thr Pro Ala Ser  
 55 60 65  
 gcc tcc cca atg gct gtc agt tcg gta aag tca mcc tct cct tct act 357  
 Ala Ser Pro Met Ala Val Ser Ser Val Lys Ser Xaa Ser Pro Ser Thr  
 70 75 80  
 ctg gta tta cca cga 372  
 Leu Val Leu Pro Arg  
 85

<210> 981  
 <211> 405  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 110..403

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 ttcggagcgg gagtgttcgt tgtgccagcg actaaaaaga gaattaaat atg ggt gat 118  
 Met Gly Asp

1  
 gtt gag aaa ggc aag aag att ttt att atg aag tgt tcc cag tgc cac 166  
 Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser Gln Cys His  
 5 10 15  
 acc gtt gaa aag gga ggc aag cac aag act ggg cca aat ctc cat ggt 214  
 Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn Leu His Gly  
 20 25 30 35  
 ctc ttt ggg cgg aag aca ggt cag gcc cct gga tac tct tac aca gcc 262  
 Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser Tyr Thr Ala  
 40 45 50  
 gcc aat aag aac aaa ggc atc atc tgg gga gag gat aca ctg atg gag 310  
 Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr Leu Met Glu  
 55 60 65  
 tat ttg gag aat ccc aag aag tac atc cct gga aca aaa atg atc ttt 358  
 Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys Met Ile Phe  
 70 75 80  
 gtc ggc att aag aag aag gaa gaa agg gca gac tta ata gct tat ct 405

Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile Ala Tyr  
 85 90 95

<210> 982  
 <211> 466  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 36..464

<400> 982  
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 aat gca tta tat aag tgg gaa ttt gaa gaa tct gaa gaa gat cca gtg 101  
 Asn Ala Leu Tyr Lys Trp Glu Phe Glu Glu Ser Glu Glu Asp Pro Val  
 10 15 20  
 aca agt att cca tac caa ctt caa agg ctt ttt gtt ttg tta caa acc 149  
 Thr Ser Ile Pro Tyr Gln Leu Gln Arg Leu Phe Val Leu Leu Gln Thr  
 25 30 35  
 agc aaa aag aga gca att gaa acc aca gat gtt aca agg agc ttt gga 197  
 Ser Lys Lys Arg Ala Ile Glu Thr Thr Asp Val Thr Arg Ser Phe Gly  
 40 45 50  
 tgg gat agt agt gag gct tgg cag cag cat gat gta caa gaa cta tgc 245  
 Trp Asp Ser Ser Glu Ala Trp Gln Gln His Asp Val Gln Glu Leu Cys  
 55 60 65 70  
 aga gtc atg ttt gat gct ttg gaa cag aaa tgg aag caa aca gaa cag 293  
 Arg Val Met Phe Asp Ala Leu Glu Gln Lys Trp Lys Gln Thr Glu Gln  
 75 80 85  
 gct gat ctt ata aat gag cta tat caa ggc aag ctg aag gac tac gtg 341  
 Ala Asp Leu Ile Asn Glu Leu Tyr Gln Gly Lys Leu Lys Asp Tyr Val  
 90 95 100  
 aga tgt ctg gaa tgt ggt tat gag ggc tgg cga atc gac aca tat ctt 389  
 Arg Cys Leu Glu Cys Gly Tyr Glu Gly Trp Arg Ile Asp Thr Tyr Leu  
 105 110 115  
 gat att cca ttg gtc atc cga cct tat ggg tcc agc caa gca ttt gct 437  
 Asp Ile Pro Leu Val Ile Arg Pro Tyr Gly Ser Ser Gln Ala Phe Ala  
 120 125 130  
 agt gtg gaa gaa gca ttg cat gca ttt at 466  
 Ser Val Glu Glu Ala Leu His Ala Phe  
 135 140

<210> 983  
 <211> 532  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 300..530

&lt;400&gt; 983

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aattgtgaca tatgatcttc tgtcagtcac ttgccatcat ggaactgcaa gtagtggaca      120
ctatataagc ctactgccga aacaatctaa ataatctctg gtatgaattt gatkatcaga      180
gtgtcactga agtttcagaa tctactgtac aaaatgcaga agcttacggt cttttctata      240
ggaagagcag cgaagaggca caaaaagaga ggagaaggat atcaaattta ttgaacata      299
atg gaa cca agc ctc ctt cag ttt tat att tct cga cag tgg ctt aat      347
Met Glu Pro Ser Leu Leu Gln Phe Tyr Ile Ser Arg Gln Trp Leu Asn
1          5          10          15
aaa ttt aag acc ttt gcc gaa cct ggc cct att tca aay aat gac ttt      395
Lys Phe Lys Thr Phe Ala Glu Pro Gly Pro Ile Ser Asn Asn Asp Phe
20          25          30
ctt tgt att cat gga ggt gtt cct cca aga aaa gct ggt tat att gaa      443
Leu Cys Ile His Gly Gly Val Pro Pro Arg Lys Ala Gly Tyr Ile Glu
35          40          45
gac ctg gtt ttg atg ctg cct cag aac att tgg gat aac cta tat agc      491
Asp Leu Val Leu Met Leu Pro Gln Asn Ile Trp Asp Asn Leu Tyr Ser
50          55          60
agg tat ggt gga gga cca gct gtc acc atc tgt aca ttt gt      532
Arg Tyr Gly Gly Gly Pro Ala Val Thr Ile Cys Thr Phe
65          70          75

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&lt;210&gt; 984

&lt;211&gt; 270

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 66..269

&lt;400&gt; 984

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tgtgatctgg agccaccttc tgtttctaac catcagtttc cttccctgaa aatggggaag      60
tggggg atg ata att ctt att ctg cct cac tgc agg gta gtc aaa aag agc      110
Met Ile Ile Leu Ile Leu Pro His Cys Arg Val Val Lys Lys Ser
1          5          10          15
gta att agt gag ccc cag ggc ctt ttg tat atg gat tgg ggg aga agg      158
Val Ile Ser Glu Pro Gln Gly Leu Leu Tyr Met Asp Trp Gly Arg Arg
20          25          30
gct acc atc ttt tcc att gcc agg gag ctg ccc tgt ctg tct cca agg      206
Ala Thr Ile Phe Ser Ile Ala Arg Glu Leu Pro Cys Leu Ser Pro Arg
35          40          45
aat cca gcc acg aga cag agt acc cac agg cca ggc cct ggg ctg aaa      254
Asn Pro Ala Thr Arg Gln Ser Thr His Arg Pro Gly Pro Gly Leu Lys
50          55          60
ttt cca cca cac cca g
Phe Pro Pro His Pro
65

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&lt;210&gt; 985

&lt;211&gt; 489

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 82..489

<400> 985

agccccggcc ccgccccgcg agcgccggga cttgttgccc gcggagactg cgaccctctt 60  
ctctcagtct gccttactac c atg ccg ctc tac gag ggc ctg ggg agc ggc 111  
Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly  
1 5 10  
ggg gag aag acg gcg gtc gtg atc gac ctg gga gag gcc ttt acc aag 159  
Gly Glu Lys Thr Ala Val Val Ile Asp Leu Gly Glu Ala Phe Thr Lys  
15 20 25  
tgt gga ttt gct gga gaa act ggt cca aga tgt ata att cct agt gtg 207  
Cys Gly Phe Ala Gly Glu Thr Gly Pro Arg Cys Ile Ile Pro Ser Val  
30 35 40  
ata aaa aga gct ggg atg cct aag cct gtc aga gtt gtt cag tat aat 255  
Ile Lys Arg Ala Gly Met Pro Lys Pro Val Arg Val Val Gln Tyr Asn  
45 50 55  
atc aat aca gaa gaa ttn kat tcc tac cta aag gaa ttc atc cac ata 303  
Ile Asn Thr Glu Glu Xaa Xaa Ser Tyr Leu Lys Glu Phe Ile His Ile  
60 65 70  
cta tat ttc agg cat cta ttg gtg aat ccc aga gac cgc cga gtt gtg 351  
Leu Tyr Phe Arg His Leu Leu Val Asn Pro Arg Asp Arg Arg Val Val  
75 80 85 90  
att atc gaa tcg gta tta tgt cct tct cac ttc aga gag aca ctc act 399  
Ile Ile Glu Ser Val Leu Cys Pro Ser His Phe Arg Glu Thr Leu Thr  
95 100 105  
cgt gtt ctt ttc aaa tat ttt gag gtt cca tct gtc ttg ctt gct cca 447  
Arg Val Leu Phe Lys Tyr Phe Glu Val Pro Ser Val Leu Leu Ala Pro  
110 115 120  
agt cat cta atg gct ctt ctg acg ctt gga att aat tct gcc 489  
Ser His Leu Met Ala Leu Leu Thr Leu Gly Ile Asn Ser Ala  
125 130 135

<210> 986

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 238..414

<400> 986

tcccctcagg aagtaaagtc cactagcagg agggcctaaa tcgtctgagc cctccttggc 60  
tcttacaatg ctcaactgtt ttcacaatgc agcaaatga aatgccttag aaaaagagta 120  
acattccaga aaacggtgta atttatTTTT cttocttaat tgccccatct gtggaggatt 180  
tctttgctga acmncnacat caaagggatc ttctgcattt aaaatagaag aggcac 237  
atg ctg aag agg gag ggg aag gtc caa cct tac act aaa acc ctg gat 285  
Met Leu Lys Arg Glu Gly Lys Val Gln Pro Tyr Thr Lys Thr Leu Asp

1	5	10	15	
gga gga tgg gga tgg atg att gtg att cat ttt ttc ctg gtc ccc tgg				333
Gly Gly Trp Gly Trp Met Ile Val Ile His Phe Phe Leu Val Pro Trp				
	20	25	30	
ttg cta tta ttt gtg aca tac ttg gag aga aaa cta cct cat tct tgg				381
Leu Leu Leu Phe Val Thr Tyr Leu Glu Arg Lys Leu Pro His Ser Trp				
	35	40	45	
ggc ttt tgt kgt wac tgg tgg ata tct gat cag				414
Gly Phe Cys Xaa Xaa Trp Trp Ile Ser Asp Gln				
	50	55		

<210> 987  
 <211> 366  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 119..364

<400> 987	
aaaaaagata aaatttgaaa tctgggttagg ctggtgtggc aggcctcccc agaggactgg	60
ggagctggtg agggcctgag cagtccacac tggccagagc tgggtgggtt gcaggtgg	118
atg gac ccc ggg cag cac agt cct ggg cac cat gcc ctg ttt gtg agg	166
Met Asp Pro Gly Gln His Ser Pro Gly His His Ala Leu Phe Val Arg	
1	5
act gtt aga gcc cca gat ggg cgt tcc cca ggt ggt ggg tgc agc ggg	214
Thr Val Arg Ala Pro Asp Gly Arg Ser Pro Gly Gly Gly Cys Ser Gly	
	20
ccc aga gcc cag ttt tac agg gat agt agt aat tgg gtt ggg cac ctt	262
Pro Arg Ala Gln Phe Tyr Arg Asp Ser Ser Asn Trp Val Gly His Leu	
	35
gaa cct ctc tcc cga gtg ggc cct ttt ctg gac ttt aac cct ctc tgc	310
Glu Pro Leu Ser Arg Val Gly Pro Phe Leu Asp Phe Asn Pro Leu Cys	
	50
agt gcc gca tgg aga cag cag agc ctg ggg gtg gat ggg aga ggg gct	358
Ser Ala Ala Trp Arg Gln Gln Ser Leu Gly Val Asp Gly Arg Gly Ala	
	65
gct gag ga	70
Ala Glu	75
	80
	366

<210> 988  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 181..393

<400> 988	
agttctaggt gaatccacag tgtgtggatc tgggttagac ctgtgctccc catgctgcgc	60

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tgtgtctggg actggtctgc atcgggaggc tctggtggcw mgccttgagt agtggaaactc 120
tctagggtat aaggtgctgg gaaatcccaa agagctctat taccagggtt taaattcgcc 180
atg atc gtg tct tct gca ctc atg ata tgg aaa ggc ttg atc gtg ctc 228
Met Ile Val Ser Ser Ala Leu Met Ile Trp Lys Gly Leu Ile Val Leu
1 5 10 15
aca ggc agt gag agc ccc atc gtg gtg gtg ctg agt ggc agt atg gag 276
Thr Gly Ser Glu Ser Pro Ile Val Val Val Leu Ser Gly Ser Met Glu
20 25 30
ccg gcc ttt cac aga gga gac ctc ctg ttc ctc aca aat ttc cgg gaa 324
Pro Ala Phe His Arg Gly Asp Leu Leu Phe Leu Thr Asn Phe Arg Glu
35 40 45
gac cca atc aga gct ggt gaa ata gtt gtt ttt aag ttg aag acg aga 372
Asp Pro Ile Arg Ala Gly Glu Ile Val Val Phe Lys Leu Lys Thr Arg
50 55 60
cat tcc aat agt tca cag agt 393
His Ser Asn Ser Ser Gln Ser
65 70

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<210> 989  
 <211> 257  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 36..257

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<400> 989
aaaaagatat gtccaaatcc taaccctggg aacct atg aaa atc cta acc ctg 53
Met Lys Ile Leu Thr Leu
1 5
gga acc tat gaa ggt att tcc tta ttt ggt gtg ttt tgt ttt ggt ttg 101
Gly Thr Tyr Glu Gly Ile Ser Leu Phe Gly Val Phe Cys Phe Gly Leu
10 15 20
gtt tgg ttt ggt ttg ttt gat aca gag tct tgc tct gtc gcc cag gct 149
Val Trp Phe Gly Leu Phe Asp Thr Glu Ser Cys Ser Val Ala Gln Ala
25 30 35
gga gtg cag tgg tgt gat ctc ggc tca ctg caa cct ctg cct ccg ggt 197
Gly Val Gln Trp Cys Asp Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly
40 45 50
tca agc gat tgt cct gcc tca gcc tcc cag gta gct ggg att acg ggc 245
Ser Ser Asp Cys Pro Ala Ser Ala Ser Gln Val Ala Gly Ile Thr Gly
55 60 65 70
acg cgc cac cac 257
Thr Arg His His

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<210> 990  
 <211> 479  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 185..478

<400> 990

agcgcttagr gagctcggtg gaagctgcta aaggcggagg cggggctctg gcgagttctc 60  
cttcacacct cccccacct tctctgcaa ccgctgtttc agccccctagc tggattccag 120  
ccattgctgc agctgctcca cagccctttt caggacccaa acaaccgcag ccgctgttcc 180  
cagg atg gtg atc cgt gta tat att gca tct tcc tct ggc tct aca gcg 229  
Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala  
1 5 10 15  
att aag aag aaa caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa 277  
Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys  
20 25 30  
ata gga ttt gaa gaa aaa gat att gca gcc aat gaa gag aat cgg aag 325  
Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys  
35 40 45  
tgg atg aga gaa aat gta cct gaa aat agt cga cca gcc aca ggt tac 373  
Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Tyr  
50 55 60  
ccc ctg cca cct cag att ttc aat gaa agc cag tat cgc ggg gac tat 421  
Pro Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr  
65 70 75  
gat gcc ttc ttt gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta 469  
Asp Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu  
80 85 90 95  
ggc ttg acg g 479  
Gly Leu Thr

<210> 991

<211> 286

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 118..285

<400> 991

gacagtgacc cggaagtaga agtggccctt gcaggcaaga gtgctggagg gcggcagcgg 60  
cgaccggagc ggtaggagca gcaatttatc cgtgtgcagc cccaaactgg aaagaag 117  
atg cta att aaa gtg aag acg ctg acc gga aag gag att gag att gac 165  
Met Leu Ile Lys Val Lys Thr Leu Thr Gly Lys Glu Ile Glu Ile Asp  
1 5 10 15  
att gaa cct aca gac aag gtg gag cga atc aag gag cgt gtg gag gag 213  
Ile Glu Pro Thr Asp Lys Val Glu Arg Ile Lys Glu Arg Val Glu Glu  
20 25 30  
aaa gag gga atc ccc cca caa cag cag agg ctc atc tac agt ggc aag 261  
Lys Glu Gly Ile Pro Pro Gln Gln Gln Arg Leu Ile Tyr Ser Gly Lys  
35 40 45  
cag atg aat gat gag aag aca gca g 286  
Gln Met Asn Asp Glu Lys Thr Ala  
50 55



<210> 992  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 55..471

<400> 992  
 ttcctctcgg tcccatattg aactcgagtt ggaagaggcg agtccgggtct caaa atg 57  
 Met  
 1  
 gag ggc cat gat cca aag gaa cca gag cag ttg aga aaa ctg ttt att 105  
 Glu Gly His Asp Pro Lys Glu Pro Glu Gln Leu Arg Lys Leu Phe Ile  
 5 10 15  
 ggt ggt ctg agc ttt gaa act aca gat gat agt tta cga gaa cat ttt 153  
 Gly Gly Leu Ser Phe Glu Thr Thr Asp Asp Ser Leu Arg Glu His Phe  
 20 25 30  
 gag aaa tgg ggc aca ctc aca gat tgt gtg gta atg aga gac ccc caa 201  
 Glu Lys Trp Gly Thr Leu Thr Asp Cys Val Val Met Arg Asp Pro Gln  
 35 40 45  
 aca aaa cgt tcc agg ggc ttt ggt ttt gtg act tat tct tgt gtt gaa 249  
 Thr Lys Arg Ser Arg Gly Phe Gly Phe Val Thr Tyr Ser Cys Val Glu  
 50 55 60 65  
 gag gtg gat gca gca atg tgt gct cga cca cac aag gtt gat ggg cgt 297  
 Glu Val Asp Ala Ala Met Cys Ala Arg Pro His Lys Val Asp Gly Arg  
 70 75 80  
 gta gtg gaa cca aag aga gct gtt tct aga gag gat tct gta aag cct 345  
 Val Val Glu Pro Lys Arg Ala Val Ser Arg Glu Asp Ser Val Lys Pro  
 85 90 95  
 ggt gcc cat mta aca gtg aag aaa att ttt gtt ggt ggt att aaa gaa 393  
 Gly Ala His Xaa Thr Val Lys Lys Ile Phe Val Gly Gly Ile Lys Glu  
 100 105 110  
 gat aca gaa gaa tat aat ttg aga gac tac ttt gaa aag tat ggc aag 441  
 Asp Thr Glu Glu Tyr Asn Leu Arg Asp Tyr Phe Glu Lys Tyr Gly Lys  
 115 120 125  
 att gaw acc ata gaa gtt atg gaa gac agg 471  
 Ile Xaa Thr Ile Glu Val Met Glu Asp Arg  
 130 135

<210> 993  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 55..537

<400> 993  
 ttcctctcgg tcccatattg aactcgagtt ggaagaggcg agtccgggtct caaa atg 57

Met  
1

gag gta aaa ccg ccg ccc ggt cgc ccc cag ccc gac tcc ggc cgt cgc	105
Glu Val Lys Pro Pro Pro Gly Arg Pro Gln Pro Asp Ser Gly Arg Arg	
5 10 15	
cgt cgc cgc cgg ggg gag gag ggc cat gat cca aag gaa cca gag cag	153
Arg Arg Arg Arg Gly Glu Glu Gly His Asp Pro Lys Glu Pro Glu Gln	
20 25 30	
ttg aga aaa ctg ttt att ggt ggt ctg agc ttt gaa act aca gat gat	201
Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu Thr Thr Asp Asp	
35 40 45	
agt tta cga gaa cat ttt gag aaa tgg ggc aca ctc aca gat tgt gtg	249
Ser Leu Arg Glu His Phe Glu Lys Trp Gly Thr Leu Thr Asp Cys Val	
50 55 60 65	
gta atg aga gac ccc caa aca aaa cgt tcc agg ggc ttt ggt ttt gtg	297
Val Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly Phe Gly Phe Val	
70 75 80	
act tat tct tgt gtt gaa gag gtg gat gca gca atg tgt gct cga cca	345
Thr Tyr Ser Cys Val Glu Glu Val Asp Ala Ala Met Cys Ala Arg Pro	
85 90 95	
cac aag gtt gat ggg cgt gta gtg gna cca aag aga gct gnt tct nga	393
His Lys Val Asp Gly Arg Val Val Xaa Pro Lys Arg Ala Xaa Ser Xaa	
100 105 110	
gag grt tct gta aag cct gnt gcc cat cta aca gtg aag aaa att ttt	441
Glu Xaa Ser Val Lys Pro Xaa Ala His Leu Thr Val Lys Lys Ile Phe	
115 120 125	
gtt ggt ggt att aaa gaa gat aca gaa gaa tat aat ttg aga gac tac	489
Val Gly Gly Ile Lys Glu Asp Thr Glu Glu Tyr Asn Leu Arg Asp Tyr	
130 135 140 145	
ttt gaa aag tat ggc aag att gaw acc ata gaa gtt atg gaa gac agg	537
Phe Glu Lys Tyr Gly Lys Ile Xaa Thr Ile Glu Val Met Glu Asp Arg	
150 155 160	

<210> 994  
<211> 358  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 68..358

<400> 994	
acagaaccgg aagcagcgtg tagttctctt cccttttgcg gccatcacccg aagcgggagc	60
gnccaaa atg aag ttt aat ccc ttt gtg act tcc gac cga agc aag aat	109
Met Lys Phe Asn Pro Phe Val Thr Ser Asp Arg Ser Lys Asn	
1 5 10	
cgc aaa agg cat ttc aat gca cct tcc cac att cga agg aag att atg	157
Arg Lys Arg His Phe Asn Ala Pro Ser His Ile Arg Arg Lys Ile Met	
15 20 25 30	
tct tcc cct ctt tcc aaa gag ctg aga cag aag tac aac gtg cga tcc	205
Ser Ser Pro Leu Ser Lys Glu Leu Arg Gln Lys Tyr Asn Val Arg Ser	
35 40 45	

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atg ccc atc cga aag gat gat gaa gtt cag gtt gta cgt gga cac tat      253
Met Pro Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly His Tyr
      50                      55                      60
aaa ggt cag caa att ggc aaa gta gtc cag gtt tac agg aag aaa tat      301
Lys Gly Gln Gln Ile Gly Lys Val Val Gln Val Tyr Arg Lys Lys Tyr
      65                      70                      75
gtt atc tac att gaa mgg gyg cag mgg gma rmg ggc ttg ggc agc atg      349
Val Ile Tyr Ile Glu Arg Xaa Gln Arg Xaa Xaa Gly Leu Gly Ser Met
      80                      85                      90
agg ccc gga
Arg Pro Gly
95

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<210> 995  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 9..308

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<400> 995
accatggg atg tac tct gag cgc aga gga gag agc cgc cct cga gcg gas      50
      Met Tyr Ser Glu Arg Arg Gly Glu Ser Arg Pro Arg Ala Xaa
      1                      5                      10
aag gcg att gag aaa aac ctc aaa gag gat ggc ats agc gcc gcc aaa      98
Lys Ala Ile Glu Lys Asn Leu Lys Glu Asp Gly Xaa Ser Ala Ala Lys
15                      20                      25                      30
gac gtg aaa tta ctc ctg ctc ggg gct gga gaa tca gga aaa agc acc      146
Asp Val Lys Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr
      35                      40                      45
att gtg aag cag atg aag atc atc cat gaa gat ggc ttc tcc gga gaa      194
Ile Val Lys Gln Met Lys Ile Ile His Glu Asp Gly Phe Ser Gly Glu
      50                      55                      60
gac gtg aaa cag tac aag cct gtt gtc tac agc aac act atc cag tcc      242
Asp Val Lys Gln Tyr Lys Pro Val Val Tyr Ser Asn Thr Ile Gln Ser
      65                      70                      75
ctg gca gcc atc gtc cgg gcc atg gac act ttg ggc atc gaa tat ggt      290
Leu Ala Ala Ile Val Arg Ala Met Asp Thr Leu Gly Ile Glu Tyr Gly
      80                      85                      90
gat aag gag aga aag gct g
Asp Lys Glu Arg Lys Ala
95                      100

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<210> 996  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 186..452

&lt;400&gt; 996

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atccggttct tctgggcgct aagggarctg acggagaggg ccaccgcca gcaatagacg      60
gtgcctcagc ctgcygagcc gcagtttccg tgggtgtgagt gagtccgggc ccgtgtcccc      120
tctcccgccg ccgcatggg ctgcacgttg agcgccgaag acaaggcggc agtggagcga      180
acaag atg atc gac cgc aac tta cgg gag gac ggg gaa aaa gcg gcc aaa      230
      Met Ile Asp Arg Asn Leu Arg Glu Asp Gly Glu Lys Ala Ala Lys
        1             5             10             15
gaa gtg aag ctg ctg cta ctc ggt gct gga gaa tct ggt aaa agc acc      278
Glu Val Lys Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr
              20             25             30
att gtg aaa cag atg aaa atc att cat gag gat ggc tat tca gag gat      326
Ile Val Lys Gln Met Lys Ile Ile His Glu Asp Gly Tyr Ser Glu Asp
              35             40             45
gaa tgt aaa caa tat aaa gta gtt gtc tac agc aat act ata cag tcc      374
Glu Cys Lys Gln Tyr Lys Val Val Val Tyr Ser Asn Thr Ile Gln Ser
              50             55             60
atc att gca atc ata aga gcc atg gga cgg cta aag att gac ttt ggg      422
Ile Ile Ala Ile Ile Arg Ala Met Gly Arg Leu Lys Ile Asp Phe Gly
              65             70             75
gaa gct gcc agg gca gat gat gcc ggc aat ta      454
Glu Ala Ala Arg Ala Asp Asp Ala Gly Asn
80             85

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&lt;210&gt; 997

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 204..572

&lt;400&gt; 997

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acaccactgg gtcaggccak ggaagataga agcaagaagg actgaagagc attccatggc      60
tttgctctga gcacctgggt agatggggat gccgtctact gaggatcatc catgaagatg      120
gcttctccgg agaagacgtg aaacagtaca agmctgttgt ctacagcaac actatccagt      180
ccctggcagc catcgtccgg gcc atg gac act ttg ggc atc gaa tat ggt gat      230
      Met Asp Thr Leu Gly Ile Glu Tyr Gly Asp
        1             5             10
aag gag aga aag gct gac gcc aag awg gtg tgt gat gtg gtg agt cgg      281
Lys Glu Arg Lys Ala Asp Ala Lys Xaa Val Cys Asp Val Val Ser Arg
              15             20             25
atg gaa gac acc gag ccc ttc tct gca gag ctg ctt tct gcc atg atg      329
Met Glu Asp Thr Glu Pro Phe Ser Ala Glu Leu Leu Ser Ala Met Met
              30             35             40
cgg ctc tgg ggc gac tca gga atc caa gag tgc ttc aac cgg tcc cgg      377
Arg Leu Trp Gly Asp Ser Gly Ile Gln Glu Cys Phe Asn Arg Ser Arg
              45             50             55
gag tat cag ctc aac gac tct gcc aaa tac tac ctg gac agc ctg gat      425
Glu Tyr Gln Leu Asn Asp Ser Ala Lys Tyr Tyr Leu Asp Ser Leu Asp
              60             65             70

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cgg att ggg gcc gcn nac tac cag ccc acc gag cag gac atc ctc cga 473  
 Arg Ile Gly Ala Ala Xaa Tyr Gln Pro Thr Glu Gln Asp Ile Leu Arg  
 75 80 85 90  
 acc agg gtc aaa acc act ggc atc gta gaa acc cac ttc aca ttc aag 521  
 Thr Arg Val Lys Thr Thr Gly Ile Val Glu Thr His Phe Thr Phe Lys  
 95 100 105  
 aac ctc cac ttc agg ctg ttt gac gtc gga ggc cag cga tct gaa cgc 569  
 Asn Leu His Phe Arg Leu Phe Asp Val Gly Gly Gln Arg Ser Glu Arg  
 110 115 120  
 aag aa 574  
 Lys

<210> 998  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 190..420

<400> 998  
 aatgttcaaa tgcgcastct tagtcgctggg ccgactgggtg tttatccgtc actcgccgag 60  
 gttccttggg tcatgggtgcc agcctgactg agaagaggac gctcccggga gacgaatgag 120  
 gaaccacctc ctctactgt tcaagtacag gggcctgggtc cgcaaaggga agaaaagcaa 180  
 aagacgaaa atg gct aaa ttc gtg atc cgc cca gcc act gcc gcc gac tgc 231  
 Met Ala Lys Phe Val Ile Arg Pro Ala Thr Ala Ala Asp Cys  
 1 5 10  
 agt gac ata ctg cgg ctg atc aag gag ctg gct aaa tat gaa tac atg 279  
 Ser Asp Ile Leu Arg Leu Ile Lys Glu Leu Ala Lys Tyr Glu Tyr Met  
 15 20 25 30  
 gaa gaa caa gta atc tta act gaa aaa gat ctg cta gaa gat ggt ttt 327  
 Glu Glu Gln Val Ile Leu Thr Glu Lys Asp Leu Leu Glu Asp Gly Phe  
 35 40 45  
 gga gag cac ccc ttt tac cac tgc ctg gtt gca gaa gtg ccg aaa gag 375  
 Gly Glu His Pro Phe Tyr His Cys Leu Val Ala Glu Val Pro Lys Glu  
 50 55 60  
 cac tgg act ccg gaa gga cac agc att gtt ggt ttt gcc atg tac ta 422  
 His Trp Thr Pro Glu Gly His Ser Ile Val Gly Phe Ala Met Tyr  
 65 70 75

<210> 999  
 <211> 456  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 28..456

<400> 999  
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Met Ala Glu Gly Glu Asp Val Pro Xaa																
							1								5	
ctg	cca	acg	tcg	agc	ggc	gac	ggc	tgg	gaa	aaa	gat	ctt	gaa	gaa	gct	102
Leu	Pro	Thr	Ser	Ser	Gly	Asp	Gly	Trp	Glu	Lys	Asp	Leu	Glu	Glu	Ala	
10					15					20					25	
ctg	gaa	gca	gga	ggg	tgt	gat	ctt	gaa	acg	ttg	aga	aat	ata	att	caa	150
Leu	Glu	Ala	Gly	Gly	Cys	Asp	Leu	Glu	Thr	Leu	Arg	Asn	Ile	Ile	Gln	
				30					35					40		
gga	aga	ccg	ctg	cct	gct	gat	ctg	agg	gcc	aaa	gtt	tgg	aag	att	gct	198
Gly	Arg	Pro	Leu	Pro	Ala	Asp	Leu	Arg	Ala	Lys	Val	Trp	Lys	Ile	Ala	
			45				50					55				
ctg	aat	gtt	gca	gga	aaa	ggg	gat	agt	ttg	gca	tca	tgg	gat	ggg	att	246
Leu	Asn	Val	Ala	Gly	Lys	Gly	Asp	Ser	Leu	Ala	Ser	Trp	Asp	Gly	Ile	
	60					65						70				
tta	gac	ttg	cca	gaa	cag	aac	act	att	cac	aaa	gat	tgc	ctg	cag	ttt	294
Leu	Asp	Leu	Pro	Glu	Gln	Asn	Thr	Ile	His	Lys	Asp	Cys	Leu	Gln	Phe	
	75					80					85					
att	gac	cag	ctt	tca	gtg	cca	gag	gag	aag	gca	gca	gaa	tta	ctt	ttg	342
Ile	Asp	Gln	Leu	Ser	Val	Pro	Glu	Glu	Lys	Ala	Ala	Glu	Leu	Leu	Leu	
	90				95					100					105	
gat	att	gaa	tct	gta	att	acc	ttt	tat	tgt	aaa	tca	cgt	aac	att	aaa	390
Asp	Ile	Glu	Ser	Val	Ile	Thr	Phe	Tyr	Cys	Lys	Ser	Arg	Asn	Ile	Lys	
				110					115					120		
tat	agc	aca	tcc	ctt	agc	tgg	ata	cat	cta	ctg	aaa	cca	ttg	gtg	cat	438
Tyr	Ser	Thr	Ser	Leu	Ser	Trp	Ile	His	Leu	Leu	Lys	Pro	Leu	Val	His	
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ctt	caa	ctg	cca	cgc	agc											456
Leu	Gln	Leu	Pro	Arg	Ser											
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atgg	ccgggg	agct	ccagg	gaccc	aggcg	ccgt	cgcttc	gg	cgagctg	ggct	gaccag					180
ccag	gacagc	gggg	taaacc	cga	acaattc	tg	cgaggt	aggg	aggcc	atg	gcg	tcc				238
															Met Ala Ser	
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ggc	agt	aac	tgg	ctc	tcc	ggg	gtg	aat	gtc	gtg	ctg	gtg	atg	gcc	tac	286
Gly	Ser	Asn	Trp	Leu	Ser	Gly	Val	Asn	Val	Val	Leu	Val	Met	Ala	Tyr	
	5				10						15					
ggg	agc	ctg	gtg	ttt	gta	ctg	cta	kyt	att	ttt	gtg	nag	agg	caa	atc	334
Gly	Ser	Leu	Val	Phe	Val	Leu	Leu	Xaa	Ile	Phe	Val	Xaa	Arg	Gln	Ile	
	20				25				30					35		
atg	cgc	ttt	gca	atg	rnn	tct	cga	agg	gga	cct	cat	gtc	cct	gtg	gga	382

Met	Arg	Phe	Ala	Met	Xaa	Ser	Arg	Arg	Gly	Pro	His	Val	Pro	Val	Gly		
				40					45					50			
cac	aat	gcc	ccc	aag	gac	ttg	aaa	gag	gag	att	gat	att	cga	ctc	tcc		430
His	Asn	Ala	Pro	Lys	Asp	Leu	Lys	Glu	Glu	Ile	Asp	Ile	Arg	Leu	Ser		
				55					60					65			
agg	gtt	cag	gat	atc	aag	tat	gag	ccc	cag	ctc	ctt	gca	gat	gat	gat		478
Arg	Val	Gln	Asp	Ile	Lys	Tyr	Glu	Pro	Gln	Leu	Leu	Ala	Asp	Asp	Asp		
				70					75					80			
gct	aga	cta	cta	caa	ctg	gaa	acc	cag	gga	aat	caa	agt	tgc	tac	aac		526
Ala	Arg	Leu	Leu	Gln	Leu	Glu	Thr	Gln	Gly	Asn	Gln	Ser	Cys	Tyr	Asn		
				85					90					95			
tat	ctg	tat	agg	atg	aaa	gct	ctg	gat	gcc	att	cgt	acc	tct	gag	atc		574
Tyr	Leu	Tyr	Arg	Met	Lys	Ala	Leu	Asp	Ala	Ile	Arg	Thr	Ser	Glu	Ile		
					105					110					115		
cca	ttt	cat	tct	gaa	ggc	cgg	cat	ccc	cgt	tcc	tta	atg	ggc	aag	aat		622
Pro	Phe	His	Ser	Glu	Gly	Arg	His	Pro	Arg	Ser	Leu	Met	Gly	Lys	Asn		
					120					125					130		
ttc	cgc	tcc	tac	ctg	ctg	gat	ctg	cga	aac	act	agt	acg	cct	ttc	aag		670
Phe	Arg	Ser	Tyr	Leu	Leu	Asp	Leu	Arg	Asn	Thr	Ser	Thr	Pro	Phe	Lys		
					135				140					145			
ggt	gta	cgc	aaa	gca	ctc	att	gat	acc	ctt	ttg	gat	ggc	tat	gaa	aca		718
Gly	Val	Arg	Lys	Ala	Leu	Ile	Asp	Thr	Leu	Leu	Asp	Gly	Tyr	Glu	Thr		
					150				155					160			
gcc	cgc	tat	ggg	aca	ggg	gtc	ttt	ggc	cag	aat	gag	tac	cta	cgc	tat		766
Ala	Arg	Tyr	Gly	Thr	Gly	Val	Phe	Gly	Gln	Asn	Glu	Tyr	Leu	Arg	Tyr		
					165				170					175			
cag	gag	gcc	ctg	agt	gag	ctg	gcc	act	gcg	gtt	aaa	gca	cga	att	ggg		814
Gln	Glu	Ala	Leu	Ser	Glu	Leu	Ala	Thr	Ala	Val	Lys	Ala	Arg	Ile	Gly		
					180				185					190			
agc	tct	cag	cga	cat	cac	cag	tca	gca	gcc	aaa	gac	cta	act	crg	tcc		862
Ser	Ser	Gln	Arg	His	His	Gln	Ser	Ala	Ala	Lys	Asp	Leu	Thr	Xaa	Ser		
					200				205					210			
cct	gag	gtc	tcc	cca	aca	acc	atc	cag	ttg	aca	tac	ccc					901
Pro	Glu	Val	Ser	Pro	Thr	Thr	Ile	Gln	Leu	Thr	Tyr	Pro					
				215					220								

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<220>  
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 <222> 238..399

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ccattctcgg	cgggtgtacc	tgtccccgt	ggccctgagg	acgtgtgggc	caggggcggc												120
cccgaata	ggaagcggag	ggggagcagt	ctgcaggtct	gcggggctaa	gtgtcgcggc												180
ggcgacctc	gcgtcaagaa	tccggaggag	gagactgcaa	ggataggccc	aggagta												237
atg gag tcc	aaa gag gaa	cta gcg gca	aac aat	ctc aac ggg	gaa aat												285
Met Glu Ser	Lys Glu Glu	Leu Ala Ala	Asn Asn	Leu Asn	Gly Glu Asn												
1	5		10		15												

gcc caa caa gaa aac gaa gga ggg gag cag gcc ccc acg cag aat gaa 333  
 Ala Gln Gln Glu Asn Glu Gly Gly Glu Gln Ala Pro Thr Gln Asn Glu  
           20                                  25                                  30  
 gaa gaa tcc cgc cat ttg gga ggg ggt gaa ggc cag aag cct gga gga 381  
 Glu Glu Ser Arg His Leu Gly Gly Gly Glu Gly Gln Lys Pro Gly Gly  
           35                                  40                                  45  
 aat atc agg cgg ggg cga gt 401  
 Asn Ile Arg Arg Gly Arg  
           50

<210> 1002  
 <211> 485  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 202..483

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 gctgccctga gctcggcggg ctggcattcg gcccggggaa aagcggasag gtctgcgagg 120  
 ctaagtgtct ccgcggcgca cctcgcggcg agaatccgga ggagaaggag actgcaagga 180  
 taggcccagg aaaacgaaga g atg gag cag cct atg cag aat gga gag gaa 231  
                                   Met Glu Gln Pro Met Gln Asn Gly Glu Glu  
                                   1                                  5                                  10  
 gac cgc cct ttg gga gga ggt gaa ggc cac cag cct gca gga aat cga 279  
 Asp Arg Pro Leu Gly Gly Gly Glu Gly His Gln Pro Ala Gly Asn Arg  
                                   15                                  20                                  25  
 cgg gga cag gct cgc cga ctt gcc cct aat ttt cga tgg gcc ata ccc 327  
 Arg Gly Gln Ala Arg Arg Leu Ala Pro Asn Phe Arg Trp Ala Ile Pro  
                                   30                                  35                                  40  
 aat agg cag atc aat gat ggg atg ggt gra gat gga gat gat atg gaa 375  
 Asn Arg Gln Ile Asn Asp Gly Met Gly Xaa Asp Gly Asp Asp Met Glu  
                                   45                                  50                                  55  
 ata ttc atg gag gag atg aga gaa atc aga aga aaa ctt agg gag ctg 423  
 Ile Phe Met Glu Glu Met Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu  
                                   60                                  65                                  70  
 cak ttg agg aat tgt ctg cgt atc ctt atg ggg gak ctc tct aat cac 471  
 Xaa Leu Arg Asn Cys Leu Arg Ile Leu Met Gly Xaa Leu Ser Asn His  
                                   75                                  80                                  85                                  90  
 cat gac cat cat ga 485  
 His Asp His His

<210> 1003  
 <211> 532  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 219..530

0014220" 666E1560



<400> 1003

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gctgccctga gctcggcggg ctggcattcg gcccggggaa aagcggasag gtctgcgagg      120
ctaagtgtct ccgcggcgca cctcgcggcg agaatccgga ggagaaggag actgcaagga      180
taggcccaga aaaacaacca gaaaaaaaaa atctcatc atg gca aat att cac cag      236
                                Met Ala Asn Ile His Gln
                                1           5
gaa aac gaa gag atg gag cag cct atg cag aat gga gag gaa gac cgc      284
Glu Asn Glu Glu Met Glu Gln Pro Met Gln Asn Gly Glu Glu Asp Arg
                                10           15           20
cct ttg gga gga ggt gaa ggc cac cag cct gca gga aat cga cgg gga      332
Pro Leu Gly Gly Glu Gly His Gln Pro Ala Gly Asn Arg Arg Gly
                                25           30           35
mag gct cgc cga ytt gcc cct aat ttt cga tgg gcc ata ccc aat agg      380
Xaa Ala Arg Arg Xaa Ala Pro Asn Phe Arg Trp Ala Ile Pro Asn Arg
                                40           45           50
cag atc aat gat ggg atg ggt gra gat gga gat gat atg gaa ata ttc      428
Gln Ile Asn Asp Gly Met Gly Xaa Asp Gly Asp Asp Met Glu Ile Phe
55                                60           65           70
atg gag gag atg aga gaa atc aga aga aaa ctt agg gag ctg cak ttg      476
Met Glu Glu Met Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Xaa Leu
                                75           80           85
agg aat tgt ctg cgt atc ctt atg ggg gak ctc tct aat cac cat gac      524
Arg Asn Cys Leu Arg Ile Leu Met Gly Xaa Leu Ser Asn His His Asp
                                90           95           100
cat cat ga
His His

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<210> 1004

<211> 381

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..380

<400> 1004

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                                1           5           10
agg gcg aga gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg      98
Arg Ala Arg Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr
                                15           20           25
gct cca gaa gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga      146
Ala Pro Glu Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg
                                30           35           40
cag gag tcg aaa aag atg cct gtg gct gga gga aaa gct aat aag gac      194
Gln Glu Ser Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp
45                                50           55           60
agg aca gaa gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag      242
Arg Thr Glu Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys

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	65		70		75	
ggc aaa gct cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct						290
Gly Lys Ala Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala						
	80		85		90	
cat gtg tat tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag						338
His Val Tyr Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln						
	95		100		105	
acc aat ctc cag ttc aac aac aac aag tac tat ctg att cag c						381
Thr Asn Leu Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln						
	110		115		120	

<210> 1005  
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<220>  
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 <222> 100..483

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gggtgatggc aggagagctg gctgacaaaa aggaccgtg atg cat cac ctt cca	114
	Met His His Leu Pro
	1 5
agg agg aaa gga agc gat cac gga ctc ctg aca gag agc ggg ata gag	162
Arg Arg Lys Gly Ser Asp His Gly Leu Leu Thr Glu Ser Gly Ile Glu	
	10 15 20
acc ggg acc gga agt ctt ccc cat cta aag ata gaa agc ggc atc gtt	210
Thr Gly Thr Gly Ser Leu Pro His Leu Lys Ile Glu Ser Gly Ile Val	
	25 30 35
caa ggg ata gac gtc gag gag gca gcc gtt ctc gct ctc gtt ccc gtt	258
Gln Gly Ile Asp Val Glu Glu Ala Val Leu Ala Leu Val Pro Val	
	40 45 50
cca aat ctg cag aaa gag aac gac ggc aca aag aac gag aac gag ata	306
Pro Asn Leu Gln Lys Glu Asn Asp Gly Thr Lys Asn Glu Asn Glu Ile	
	55 60 65
agg agc ggg atc gga ata aga agg acc gag atc gag aca agg atg ggc	354
Arg Ser Gly Ile Gly Ile Arg Arg Thr Glu Ile Glu Thr Arg Met Gly	
	70 75 80 85
aca gac ggg aca agg acc gta aac gat cca gct tat ctc ctg gtc gag	402
Thr Asp Gly Thr Arg Thr Val Asn Asp Pro Ala Tyr Leu Leu Val Glu	
	90 95 100
gaa aag act tta aat ctc gga agg aca gag act cta aga agg atg aag	450
Glu Lys Thr Leu Asn Leu Gly Arg Thr Glu Thr Leu Arg Arg Met Lys	
	105 110 115
agg atg aac atg gtg ata aga agc cta rgc cca	483
Arg Met Asn Met Val Ile Arg Ser Leu Xaa Pro	
	120 125

<210> 1006  
 <211> 461  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 127..459

<400> 1006

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ggcckwaaag atggcggtct tggcacctct aattgctctc gtgtattcgg tgccgcgact 120  
ttcacg atg gct cgc cca acc tta cta cct tct gtc ggc cct gag tat 168  
Met Ala Arg Pro Thr Leu Leu Pro Ser Val Gly Pro Glu Tyr  
1 5 10  
atc aag tac ttc aat gat aaa acc att gat gag gaa cta gaa cgg gac 216  
Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp  
15 20 25 30  
aag agg gtc act tgg att gtg gag ttc ttt gcc aan tgg tct aat gac 264  
Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Xaa Trp Ser Asn Asp  
35 40 45  
tgc caa tca ttt gcc cct atc tat gct gac ctc tcc ctt aaa tac aac 312  
Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn  
50 55 60  
tgt aca ggg cta aat ttt ggg aag gtg gat gtt gga cgc tat act gat 360  
Cys Thr Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg Tyr Thr Asp  
65 70 75  
gtt agt acg cgg tac aaa gtg agc aca tca ccc ctc acc aag caa ctc 408  
Val Ser Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr Lys Gln Leu  
80 85 90  
cct acc ctg atc ctg ttc caa ggt ggc aag gag gca atg cgg cgg cca 456  
Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met Arg Arg Pro  
95 100 105 110  
cag at 461  
Gln

<210> 1007

<211> 446

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 135..446

<400> 1007

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tataatgggc ccagttgtct gcgggctgcg gggagctaag tccccagatt ggaggaggct 120  
ggctctggtc ttcg atg cac agg agt ggc cgt tat gga acg cag cag cag 170  
Met His Arg Ser Gly Arg Tyr Gly Thr Gln Gln Gln  
1 5 10  
cgt gca ggg tca aag aca gcc ggc ccc cca tgt cag tgg tct agg atg 218  
Arg Ala Gly Ser Lys Thr Ala Gly Pro Pro Cys Gln Trp Ser Arg Met  
15 20 25  
gcc agt gaa ggc acc aac atc cca agt cct gtg gtg cgc cag att gac 266

Ala	Ser	Glu	Gly	Thr	Asn	Ile	Pro	Ser	Pro	Val	Val	Arg	Gln	Ile	Asp	
30						35				40						
aag	cag	ttt	ctg	att	tgc	agt	ata	tgc	ctg	gaa	cgg	tac	aag	aat	ccc	314
Lys	Gln	Phe	Leu	Ile	Cys	Ser	Ile	Cys	Leu	Glu	Arg	Tyr	Lys	Asn	Pro	
45					50				55					60		
aag	gtt	ctc	ccc	tgt	ctg	cac	act	ttc	tgc	gag	agg	tgc	ctg	cag	aac	362
Lys	Val	Leu	Pro	Cys	Leu	His	Thr	Phe	Cys	Glu	Arg	Cys	Leu	Gln	Asn	
				65				70					75			
tac	att	cct	gcc	cac	agt	tta	acc	ctc	tcc	tgc	cca	gtg	tgc	cgc	cag	410
Tyr	Ile	Pro	Ala	His	Ser	Leu	Thr	Leu	Ser	Cys	Pro	Val	Cys	Arg	Gln	
			80					85					90			
acc	tcc	atc	ctg	ccc	gag	aaa	ggg	gtg	gcc	gcg	ctc					446
Thr	Ser	Ile	Leu	Pro	Glu	Lys	Gly	Val	Ala	Ala	Leu					
	95						100									

<210> 1008  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 113..409

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					Met Ala											
					1											
ttg aag cag att tcc agc aac aag tgc ttt ggg gga ttg cag aaa gtt							166									
Leu Lys Gln Ile Ser Ser Asn Lys Cys Phe Gly Gly Leu Gln Lys Val																
	5					10						15				
ttt gaa cat gac agt gtt gaa cta aac tgc aaa atg aaa ttt gct gtc							214									
Phe Glu His Asp Ser Val Glu Leu Asn Cys Lys Met Lys Phe Ala Val																
	20					25						30				
tac tta cca cca aag gca gaa aca gga aag tgc cct gca ctg tat tgg							262									
Tyr Leu Pro Pro Lys Ala Glu Thr Gly Lys Cys Pro Ala Leu Tyr Trp																
	35				40							45			50	
ctc tma ggt tta act tgc aca gag caa aat ttt ata tca aaa tct ggt							310									
Leu Xaa Gly Leu Thr Cys Thr Glu Gln Asn Phe Ile Ser Lys Ser Gly																
			55			60								65		
tat cat cag tct gct tca gaa cat ggt ctt gtt gtc att gct cca gat							358									
Tyr His Gln Ser Ala Ser Glu His Gly Leu Val Val Ile Ala Pro Asp																
			70			75								80		
acc agc cct cgt ggc tgc aat att aaa ggt gaa gat gag agc tgg gac							406									
Thr Ser Pro Arg Gly Cys Asn Ile Lys Gly Glu Asp Glu Ser Trp Asp																
	85					90								95		
ttt																409
Phe																

<210> 1009  
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<213> Homo sapiens

<220>

<221> CDS

<222> 113..277

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                                     Met Ala
                                     1
ttg aag cag att tcc agc aac aag tgc ttt ggg gga ttg cag aaa gtt      166
Leu Lys Gln Ile Ser Ser Asn Lys Cys Phe Gly Gly Leu Gln Lys Val
      5              10              15
ttt gaa cat gac agt cat caa caa gaa aag ttg ctt aga ata atg tgg      214
Phe Glu His Asp Ser His Gln Gln Glu Lys Leu Leu Arg Ile Met Trp
      20              25              30
aaa aag aaa atc acc aat atg cag aga atg gaa agg agc ata cag aaa      262
Lys Lys Lys Ile Thr Asn Met Gln Arg Met Glu Arg Ser Ile Gln Lys
      35              40              45              50
act tcc cat gat ggg      277
Thr Ser His Asp Gly
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<212> DNA

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<220>

<221> CDS

<222> 99..437

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                                     Met Gln Leu Lys Pro Met
                                     1              5
gag atc aac ccc gag atg ctg aac aaa gtg ctg tcc cgg ctg ggg gtc      164
Glu Ile Asn Pro Glu Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val
      10              15              20
gcc ggc cag tgg cgc ttc gtg gac gtg ctg ggg ctg gaa gag gag tct      212
Ala Gly Gln Trp Arg Phe Val Asp Val Leu Gly Leu Glu Glu Glu Ser
      25              30              35
ctg ggc tcg gtg cca gcg cct gcc tgc gcg ctg ctg ctg ctg ttt ccc      260
Leu Gly Ser Val Pro Ala Pro Ala Cys Ala Leu Leu Leu Leu Phe Pro
      40              45              50
ctc acg gcc cag cat gag aac ttc agg aaa aag cag att gaa gag ctg      308
Leu Thr Ala Gln His Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu
      55              60              65              70
aag gga caa gaa gtt agt cct aaa gtg tac ttc atg aag cag acc att      356
Lys Gly Gln Glu Val Ser Pro Lys Val Tyr Phe Met Lys Lys Thr Ile
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	75		80		85	
ggg aat tcc tgt ggc aca atc gga ctt att cac gca gtg ncc aat aat						404
Gly Asn Ser Cys Gly Thr Ile Gly Leu Ile His Ala Val Xaa Asn Asn						
	90		95		100	
caa gac aaa ctg gga ttt gag gat gga tca gtt ct						439
Gln Asp Lys Leu Gly Phe Glu Asp Gly Ser Val						
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 <212> DNA  
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<220>  
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 <222> 389..547

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 gcacgctacg agagtacaag gtagtgggtc gctgcctgcc ccccccaaa tgccacacgc 120  
 cgccccctcta ccgcatgcga atctttgctc ctaatcatgt cgctgcctgc ccacccccaa 180  
 atgccacacg ccgccccctc accgcatgat catgtcgtcg ccaagtcccg cttctggtct 240  
 actgtgggca ggtgtttgag aagtcccccc tgcgggtgaa gaacttcggg atctggctgc 300  
 gctatgactc ccggagcggc acccacaaca tgtaccggga ataccgggac ctgaccaccg 360  
 cagcgtctgc acccagtgtc accgagac atg ggt gcc cgg cac cgc gcc cga 412  
 Met Gly Ala Arg His Arg Ala Arg  
 1 5  
 gcc cac tcc att cag atc atg aag gtg gag gag atc gcg gcc agc aag 460  
 Ala His Ser Ile Gln Ile Met Lys Val Glu Glu Ile Ala Ala Ser Lys  
 10 15 20  
 tgc cgc cgg ccg gct gtc aag yag ttc cac gac tcc aag atc aag ttc 508  
 Cys Arg Arg Pro Ala Val Lys Xaa Phe His Asp Ser Lys Ile Lys Phe  
 25 30 35 40  
 ccg ctg ccc cac cgg gtc ctg cgc cgt cag cac aag cca 547  
 Pro Leu Pro His Arg Val Leu Arg Arg Gln His Lys Pro  
 45 50

<210> 1012  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 48..332

<400> 1012  
 agaggncact tcctttttgcg ggtggcggcg aacgcggaga gcacgcc atg aag gcc 56  
 Met Lys Ala  
 1  
 tcg ggc acg cta cga gag tac aag gta gtg ggt cgc tgc ctg ccc acc 104  
 Ser Gly Thr Leu Arg Glu Tyr Lys Val Val Gly Arg Cys Leu Pro Thr

5	10	15	
ccc aaa tgc cac acg ccg ccc ctc tac cgc atg cga atc ttt gcg cct			152
Pro Lys Cys His Thr Pro Pro Leu Tyr Arg Met Arg Ile Phe Ala Pro			
20	25	30	35
aat cat gtc gtc gcc aag tcc cgc ttc tgg tac ttt gta tct cag tta			200
Asn His Val Val Ala Lys Ser Arg Phe Trp Tyr Phe Val Ser Gln Leu			
	40	45	50
aag aag atg aag aag tct tca ggg gag att gtc tac tgt ggg cag gtg			248
Lys Lys Met Lys Lys Ser Ser Gly Glu Ile Val Tyr Cys Gly Gln Val			
	55	60	65
ttt gag aag tcc ccc ctg cgg gtg aag aac ttc ggg atc tgg ctg cgc			296
Phe Glu Lys Ser Pro Leu Arg Val Lys Asn Phe Gly Ile Trp Leu Arg			
	70	75	80
tat gac tcc cgg agc ggc acc gcg ccc gag ccc act			332
Tyr Asp Ser Arg Ser Gly Thr Ala Pro Glu Pro Thr			
85	90	95	

<210> 1013  
 <211> 629  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 99..629

<400> 1013

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gtcttcccta ggctatttct gccgggcgct ccgcgaag atg cag ctc aag ccg atg	116
	Met Gln Leu Lys Pro Met
	1 5
gag atc aac ccc gag atg ctg aac aaa gtg ctg tcc cgg ctg ggg gtc	164
Glu Ile Asn Pro Glu Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val	
	10 15 20
gcc ggc cag tgg cgc ttc gtg gac gtg ctg ggg ctg gaa gag gag tct	212
Ala Gly Gln Trp Arg Phe Val Asp Val Leu Gly Leu Glu Glu Ser	
	25 30 35
ctg ggc tcg gtg cca gcg cct gcc tgc gcg ctg ctg ctg ttt ccc	260
Leu Gly Ser Val Pro Ala Pro Ala Cys Ala Leu Leu Leu Phe Pro	
	40 45 50
ctc acg gcc cag cat gag aac ttc agg aaa aag cag att gaa gag ctg	308
Leu Thr Ala Gln His Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu	
	55 60 65 70
aag ttc tca tgc tgg gcc gtg agg kga aac agc agc gca gtt cgg cgg	356
Lys Phe Ser Cys Trp Ala Val Arg Xaa Asn Ser Ser Ala Val Arg Arg	
	75 80 85
tcc cgc ggg tct gtc tct tgc ttc aac agt gtt tgg acg gaa cag atc	404
Ser Arg Gly Ser Val Ser Cys Phe Asn Ser Val Trp Thr Glu Gln Ile	
	90 95 100
cgg gga ctc tct tcc agc ctc cga ccg ccc tcc gat ttc ctc tcc gct	452
Arg Gly Leu Ser Ser Ser Leu Arg Pro Pro Ser Asp Phe Leu Ser Ala	
	105 110 115
tgc aac ctc cgg gac cat ctt ctc ggc cat ctc ctg ctt ctg gga cct	500





<210> 1015  
 <211> 508  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 99..506

<400> 1015  
 acagtgcgtc tggccggcgc tttatagctg cagcctgggc ggctccgcta gctgtttttc 60  
 gtcttccta ggctatttct gccgggcgct ccgcgaag atg cag ctc aag ccg atg 116  
 Met Gln Leu Lys Pro Met  
 1 5  
 gag atc aac ccc gag atg ctg aac aaa gtg ctg tcc cgg ctg ggg gtc 164  
 Glu Ile Asn Pro Glu Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val  
 10 15 20  
 gcc ggc cag tgg cgc ttc gtg gac gtg ctg ggg ctg gaa gag gag tct 212  
 Ala Gly Gln Trp Arg Phe Val Asp Val Leu Gly Leu Glu Glu Glu Ser  
 25 30 35  
 ctg ggc tcg gtg cca gcg cct gcc tgc gcg ctg ctg ctg ctg ttt ccc 260  
 Leu Gly Ser Val Pro Ala Pro Ala Cys Ala Leu Leu Leu Leu Phe Pro  
 40 45 50  
 ctc acg gcc cag cat gag aac ttc agg aaa aag cag att gaa gag ctg 308  
 Leu Thr Ala Gln His Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu  
 55 60 65 70  
 aag ttc tca tgc tgg gcc gtg agg kga aac agc agc ngc agt tcg gcg 356  
 Lys Phe Ser Cys Trp Ala Val Arg Xaa Asn Ser Ser Xaa Ser Ser Ala  
 75 80 85  
 gtc ccg cgg gtc tgt ctc ttg ctt caa cag tgt ttg gac gga aca gat 404  
 Val Pro Arg Val Cys Leu Leu Leu Gln Gln Cys Leu Asp Gly Thr Asp  
 90 95 100  
 ccg ggg act ctc ttc cag cct ccg acc gcc ctc cga ttt cct ctc cca 452  
 Pro Gly Thr Leu Phe Gln Pro Pro Thr Ala Leu Arg Phe Pro Leu Pro  
 105 110 115  
 gaa gca gga gat ggc cga gaa gat ggt ccc gga ggt tgc aag cgg aga 500  
 Glu Ala Gly Asp Gly Arg Glu Asp Gly Pro Gly Gly Cys Lys Arg Arg  
 120 125 130  
 gga aat cg 508  
 Gly Asn  
 135

<210> 1016  
 <211> 317  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 48..317

004220"666E1560

&lt;400&gt; 1016

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agaggncaact tccttttgcg ggtggcggcg aacgcggaga gcacgcc atg aag gcc      56
                                   Met Lys Ala
                                   1
tcg ggc acg cta cga gag tac aag gta gtg ggt cgc tgc ctg ccc acc      104
Ser Gly Thr Leu Arg Glu Tyr Lys Val Val Gly Arg Cys Leu Pro Thr
   5              10              15
ccc aaa tgc cac acg ccg ccc ctc tac cgc atg cga atc ttt gcg cct      152
Pro Lys Cys His Thr Pro Pro Leu Tyr Arg Met Arg Ile Phe Ala Pro
  20              25              30              35
aat cat gtc gtc gcc aag tcc cgc ttc tgg tac ttt gta tct cag tta      200
Asn His Val Val Ala Lys Ser Arg Phe Trp Tyr Phe Val Ser Gln Leu
              40              45              50
aag aag rtg rag gag atc gcg gcc agc aag tgc cgc cgg ccg gct gtc      248
Lys Lys Xaa Xaa Glu Ile Ala Ala Ser Lys Cys Arg Arg Pro Ala Val
              55              60              65
aag cag ttc cac gac tcc aag atc aag ttc ccg ctg ccc cac cgg gtc      296
Lys Gln Phe His Asp Ser Lys Ile Lys Phe Pro Leu Pro His Arg Val
              70              75              80
ctg cgc cgt cag cac aag cca      317
Leu Arg Arg Gln His Lys Pro
   85              90

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&lt;210&gt; 1017

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 318..476

&lt;400&gt; 1017

```

agaggncaact tccttttgcg ggtggcggcg aacgcggaga gcacgccatg aaggcctcgg      60
gcacgctacg agagtacaag gtagtgggtc gctgcctgcc ccccccaaa tgccacacgc      120
cgccccctcta ccgcatgac atgtcgtcgc caagtccgc ttctggtcta ctgtgggcag      180
gtgtttgaga agtccccct gcgggtgaag aacttcggga tctggctgcg ctatgactcc      240
cggagcggca cccacaacat gtaccgggaa taccgggacc tgaccaccgc agcgtgtca      300
cccagtgcta ccgagac atg ggt gcc cgg cac cgc gcc cga gcc cac tcc      350
                                   Met Gly Ala Arg His Arg Ala Arg Ala His Ser
                                   1              5              10
att cag atc atg aag gtg gag gag atc gcg gcc agc aag tgc cgc cgg      398
Ile Gln Ile Met Lys Val Glu Glu Ile Ala Ala Ser Lys Cys Arg Arg
              15              20              25
ccg gct gtc aag yag ttc cac gac tcc aag atc aag ttc ccg ctg ccc      446
Pro Ala Val Lys Xaa Phe His Asp Ser Lys Ile Lys Phe Pro Leu Pro
              30              35              40
cac cgg gtc ctg cgc cgt cag cac aag cca      476
His Arg Val Leu Arg Arg Gln His Lys Pro
   45              50

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&lt;210&gt; 1018

&lt;211&gt; 388

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 206..388

<400> 1018  
agaggncact tccttttgcg ggtggcggcg aacgcggaga gcacgccatg aaggcctcgg 60  
gcacgctacg agagtacaag gtagtgggtc gctgcctgcc ccccccaaa tgccacacgc 120  
cgccccctcta ccgcatgcga atctttgcgc ctaatcatgt cgctgcctgc ccacccccaa 180  
atgccacacg ccgccccctct accgc atg cga atc ttt gcg cct aat cat gtc 232  
Met Arg Ile Phe Ala Pro Asn His Val  
1 5  
gtc gcc aag tcc cgc ttc tgg tac ttt gta tct cag tta aag aag rtg 280  
Val Ala Lys Ser Arg Phe Trp Tyr Phe Val Ser Gln Leu Lys Lys Xaa  
10 15 20 25  
rag gag atc gcg gcc agc aag tgc cgc cgg ccg gct gtc aag cag ttc 328  
Xaa Glu Ile Ala Ala Ser Lys Cys Arg Arg Pro Ala Val Lys Gln Phe  
30 35 40  
cac gac tcc aag atc aag ttc ccg ctg ccc cac cgg gtc ctg cgc cgt 376  
His Asp Ser Lys Ile Lys Phe Pro Leu Pro His Arg Val Leu Arg Arg  
45 50 55  
cag cac aag cca 388  
Gln His Lys Pro  
60

<210> 1019  
<211> 403  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 206..403

<400> 1019  
agaggncact tccttttgcg ggtggcggcg aacgcggaga gcacgccatg aaggcctcgg 60  
gcacgctacg agagtacaag gtagtgggtc gctgcctgcc ccccccaaa tgccacacgc 120  
cgccccctcta ccgcatgcga atctttgcgc ctaatcatgt cgctgcctgc ccacccccaa 180  
atgccacacg ccgccccctct accgc atg cga atc ttt gcg cct aat cat gtc 232  
Met Arg Ile Phe Ala Pro Asn His Val  
1 5  
gtc gcc aag tcc cgc ttc tgg tac ttt gta tct cag tta aag aag atg 280  
Val Ala Lys Ser Arg Phe Trp Tyr Phe Val Ser Gln Leu Lys Lys Met  
10 15 20 25  
aag aag tct tca ggg gag att gtc tac tgt ggg cag gtg ttt gag aag 328  
Lys Lys Ser Ser Gly Glu Ile Val Tyr Cys Gly Gln Val Phe Glu Lys  
30 35 40  
tcc ccc ctg cgg gtg aag aac ttc ggg atc tgg ctg cgc tat gac tcc 376  
Ser Pro Leu Arg Val Lys Asn Phe Gly Ile Trp Leu Arg Tyr Asp Ser  
45 50 55

cgg agc ggc acc gcg ccc gag ccc act  
 Arg Ser Gly Thr Ala Pro Glu Pro Thr  
 60 65

403

<210> 1020  
 <211> 426  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 176..424

<400> 1020  
 ctttccagtg gacctgggct gttgttgagg ttgttttctt tctctccgtg caacgctggc 60  
 aagtctcaaa gtcgccacag aaacatgccc ctgattcagt gcctctgctt agctgtaaca 120  
 tgtaaatcag aactacctgg catcttctctg aacaagactt tcaatagggg ccagt atg 178  
 Met  
 1  
 ctt cgc ttc atc cag aag ttt tct caa gca tct tca aag ata ctg aag 226  
 Leu Arg Phe Ile Gln Lys Phe Ser Gln Ala Ser Ser Lys Ile Leu Lys  
 5 10 15  
 tac tct ttc cca gtg gga cta aga acc agc aga aca gat ata ctt tct 274  
 Tyr Ser Phe Pro Val Gly Leu Arg Thr Ser Arg Thr Asp Ile Leu Ser  
 20 25 30  
 ctc aag atg tct ctc cag caa aac ttt tcc cca tgt cca agg cct tgg 322  
 Leu Lys Met Ser Leu Gln Gln Asn Phe Ser Pro Cys Pro Arg Pro Trp  
 35 40 45  
 ctt tcc tca tca ttt cca gcg tat atg agc aag aca cag tgc tat cat 370  
 Leu Ser Ser Ser Phe Pro Ala Tyr Met Ser Lys Thr Gln Cys Tyr His  
 50 55 60 65  
 aca tcc ccc tgc akc ttt aaa aag cag cag agc gaa gca ctt cta gcc 418  
 Thr Ser Pro Cys Xaa Phe Lys Lys Gln Gln Ser Glu Ala Leu Leu Ala  
 70 75 80  
 aga ccc tc 426  
 Arg Pro

<210> 1021  
 <211> 383  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 128..382

<400> 1021  
 ttgagctgtc tgcagcagag ctgagaggac cagccatttt acttatggaa aacagtgtgg 60  
 catattctgc tgagcttcgc cctggaagaa gcctctttta tacatctctt caggggaagag 120  
 agaagca atg ggc atg tta gaa ctg agg tgg gct agt ggg ggt gag atg 169  
 Met Gly Met Leu Glu Leu Arg Trp Ala Ser Gly Gly Glu Met  
 1 5 10

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gtg acg ctg gac gtg ggg ccg gag gat gag ctg ccc gac tgg gcc gcc      217
Val Thr Leu Asp Val Gly Pro Glu Asp Glu Leu Pro Asp Trp Ala Ala
15                20                25                30
gcc aaa gag ttt tac cag aag tac gac cct aag gac gtc atc ggc aga      265
Ala Lys Glu Phe Tyr Gln Lys Tyr Asp Pro Lys Asp Val Ile Gly Arg
35                40                45
gga gtg agc tct gtg gtc cgc cgt tgt gtt cat cga gct act ggc cac      313
Gly Val Ser Ser Val Val Arg Arg Cys Val His Arg Ala Thr Gly His
50                55                60
gag ttt gcg gtg aag att atg gaa gtg aca gct gag cgg ctg agt cct      361
Glu Phe Ala Val Lys Ile Met Glu Val Thr Ala Glu Arg Leu Ser Pro
65                70                75
gag cag ctg gag gag gtg cgg g
Glu Gln Leu Glu Glu Val Arg
80                85

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<210> 1022  
 <211> 431  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 174..431

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<400> 1022
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ggccgtgttg ctgatcgctt ggggtgttgt tggcgtgtcc ctgcagcgaa ggatcctgrc      120
agtgaaaaag cagtctggct cccgaggtcc accccttata cccaaggctc cag atg      176
Met
1
gcg gcc aac gtg ggt gat caa cgt agc aca gat tgg tct tct cag tac      224
Ala Ala Asn Val Gly Asp Gln Arg Ser Thr Asp Trp Ser Ser Gln Tyr
5                10                15
agc atg gtg gct ggg gca ggc cga gag aat ggc atg gag acg ccg atg      272
Ser Met Val Ala Gly Ala Gly Arg Glu Asn Gly Met Glu Thr Pro Met
20                25                30
cac gag aac ccg gag tgg gag aag gcc cgt cag gcc ctg gcc agc atc      320
His Glu Asn Pro Glu Trp Glu Lys Ala Arg Gln Ala Leu Ala Ser Ile
35                40                45
agc aag tca gga gct gcc ggc ggc tct gcc aag tcc agc agc rnn ggg      368
Ser Lys Ser Gly Ala Ala Gly Gly Ser Ala Lys Ser Ser Ser Xaa Gly
50                55                60                65
cct gtg gcm agt gca cag tac gtg tcc cag gca gaa gcc tca agc ttt      416
Pro Val Ala Ser Ala Gln Tyr Val Ser Gln Ala Glu Ala Ser Ser Phe
70                75                80
gca gca gca gca gta
Ala Ala Ala Ala Val
85

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<210> 1023  
 <211> 386  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 87..386

<400> 1023

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catcggacct cggccagtca taaaag atg aca aca gca gcc agg cca acc ttt 113  
Met Thr Thr Ala Ala Arg Pro Thr Phe  
1 5  
gaa cct gcc aga ggt gga agg gga aaa gga gaa ggt gat ttg agc caa 161  
Glu Pro Ala Arg Gly Gly Arg Gly Lys Gly Glu Gly Asp Leu Ser Gln  
10 15 20 25  
ctt tca aag cag tat tca agc aga gac cta ccc tct cat aca aag ata 209  
Leu Ser Lys Gln Tyr Ser Ser Arg Asp Leu Pro Ser His Thr Lys Ile  
30 35 40  
aaa tac aga cag act act cag gat gcc cct gaa gag gtt cgt aac cgt 257  
Lys Tyr Arg Gln Thr Thr Gln Asp Ala Pro Glu Glu Val Arg Asn Arg  
45 50 55  
gac ttc agg aga gag ttg gaa gaa aga gag aga gct gct gca aga gag 305  
Asp Phe Arg Arg Glu Leu Glu Glu Arg Glu Arg Ala Ala Ala Arg Glu  
60 65 70  
aaa aat agg gat cgt cca acc cga gaa cat aca acc tcc tct tca gtg 353  
Lys Asn Arg Asp Arg Pro Thr Arg Glu His Thr Thr Ser Ser Ser Val  
75 80 85  
tca aaa aag cca cgg tta gac cag att ccy gcc 386  
Ser Lys Lys Pro Arg Leu Asp Gln Ile Pro Ala  
90 95 100

<210> 1024

<211> 297

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 71..295

<400> 1024

gaagattacc ggaagctacc gagtctgacc caaagcatca ctctctgcc aaagatccca 60  
acaagacaac atg gct ccc aag aag cct gag cct aag aag gag gca gcc 109  
Met Ala Pro Lys Lys Pro Glu Pro Lys Lys Glu Ala Ala  
1 5 10  
aag cca gct cca gct cca gct cca gcc cct gca cca gcc cct gcc cca 157  
Lys Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro  
15 20 25  
gct cct gag gct ccc aag gaa cct gcc ttt gac ccc aag agt gta aag 205  
Ala Pro Glu Ala Pro Lys Glu Pro Ala Phe Asp Pro Lys Ser Val Lys  
30 35 40 45  
ata gac ttc act gcc gac cag att gaa gag ttc aaa gag gcc ttt tca 253  
Ile Asp Phe Thr Ala Asp Gln Ile Glu Glu Phe Lys Glu Ala Phe Ser

	50		55		60										
ttg	ttt	gac	cgg	acc	ccg	act	gga	gag	atg	aag	atc	acc	tac	gg	297
Leu	Phe	Asp	Arg	Thr	Pro	Thr	Gly	Glu	Met	Lys	Ile	Thr	Tyr		
			65						70				75		

<210> 1025  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 73..522

<400> 1025	
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cgcaggggaga ag atg gcg gtc gcc gtg aga act ttg cag gaa cag ctg gaa	111
Met Ala Val Ala Val Arg Thr Leu Gln Glu Gln Leu Glu	
aag gcc aaa gag agt ctt aag aac gtg gat gag aac att cgc aag ctc	159
Lys Ala Lys Glu Ser Leu Lys Asn Val Asp Glu Asn Ile Arg Lys Leu	
15 20 25	
acc ggg cgg gat ccg aat gac gtg agg ccc atc caa gcc aga ttg ctg	207
Thr Gly Arg Asp Pro Asn Asp Val Arg Pro Ile Gln Ala Arg Leu Leu	
30 35 40 45	
gcc ctt tct ggt cct ggt gga ggt aga gga cgt ggt agt tta tta ctg	255
Ala Leu Ser Gly Pro Gly Gly Gly Arg Gly Arg Gly Ser Leu Leu Leu	
50 55 60	
agg cgt gga ttc tca gat agt gga gga gga ccc cca gcc aaa cag aga	303
Arg Arg Gly Phe Ser Asp Ser Gly Gly Gly Pro Pro Ala Lys Gln Arg	
65 70 75	
gac ctt gaa ggg gca gtc agt agg ctg ggc ggg gag cgt cgg acc aga	351
Asp Leu Glu Gly Ala Val Ser Arg Leu Gly Gly Glu Arg Arg Thr Arg	
80 85 90	
aga gaa tca cgc cag gaa agc gac ccg gag gat gat gat gtt aaa aag	399
Arg Glu Ser Arg Gln Glu Ser Asp Pro Glu Asp Asp Asp Val Lys Lys	
95 100 105	
cca gca ttg cag tct tca gtt gta gct acc tcc aaa gag cgc aca cgt	447
Pro Ala Leu Gln Ser Ser Val Val Ala Thr Ser Lys Glu Arg Thr Arg	
110 115 120 125	
aga gac ctt atc cag gat caa aat atg gat gaa aag gga aag caa agg	495
Arg Asp Leu Ile Gln Asp Gln Asn Met Asp Glu Lys Gly Lys Gln Arg	
130 135 140	
aac cgg nna ata ttt ggc ttg ttr nnn gg	524
Asn Arg Xaa Ile Phe Gly Leu Leu Xaa	
145 150	

<210> 1026  
 <211> 367  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 160..366

<400> 1026

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agaagggtcag caaaggaaag tggaagttgg attctgaaag atcgaggtgc ccayaggaat      60
tttatgggtcg tcggattttg aagacttgaa ctagactggg ggttctcctt gcatttcttg      120
cctgttgccct atctttgtcc tctctcttcc ggcttcgag atg aat gtg cag ccc      174
                               Met Asn Val Gln Pro
                               1               5
tgt tct agg tgt ggg tat ggg gtt tat cct gcc gag aag atc agc tgt      222
Cys Ser Arg Cys Gly Tyr Gly Val Tyr Pro Ala Glu Lys Ile Ser Cys
                10               15               20
ata gat cag ata tgg cat aaa gcc tgt ttt cac tgt gaa gtt tgc aag      270
Ile Asp Gln Ile Trp His Lys Ala Cys Phe His Cys Glu Val Cys Lys
                25               30               35
atg atg ctg tct gtt aat aac ttt gtg agt cac cag aaa aag ccg tac      318
Met Met Leu Ser Val Asn Asn Phe Val Ser His Gln Lys Lys Pro Tyr
                40               45               50
tgt cac gcc cat aac cct aag aac aac act ttc acc agt gtc tat cac a      367
Cys His Ala His Asn Pro Lys Asn Asn Thr Phe Thr Ser Val Tyr His
                55               60               65

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<210> 1027  
<211> 568  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 331..567

<400> 1027

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gcctgcgcgc ccttcgcggc cgagttctgg agactcaaca tgaagctacc ggccagggtt      60
ttctttactc tgggggtccc gctgccctgt ggcctcgctc ctcgagggtt tttcagttat      120
gggacaaaaa tattatatca aaacactgaa gctttgcaat ctaaaattctt ttcacctctt      180
caaaaagcga tgctaccacc taatagtttt caaggaaaag tggcattcat tactggggga      240
ggtactggcc ttggtaaagg aatgacaact cttctgtcca gcctagggtgc tcagtgcgtg      300
atagccagcc gaaatgcttt tctttaagct atg gat tct ctg tat tct tca att      354
                               Met Asp Ser Leu Tyr Ser Ser Ile
                               1               5
tat gaa att gaa aaa tat aat atg aag tca tac aag gtg ttt att tct      402
Tyr Glu Ile Glu Lys Tyr Asn Met Lys Ser Tyr Lys Val Phe Ile Ser
                10               15               20
agg aag atg gat gtt ttg aaa gct acc gca gaa caa att tct tct caa      450
Arg Lys Met Asp Val Leu Lys Ala Thr Ala Glu Gln Ile Ser Ser Gln
                25               30               35               40
act gga aat aag gtt cat gca att cag tgt gat gtg agg gay cct gat      498
Thr Gly Asn Lys Val His Ala Ile Gln Cys Asp Val Arg Asp Pro Asp
                45               50               55
atg gtt caa aac act gtg tca gaa ctg atc aaa gtt gca gga cat cct      546
Met Val Gln Asn Thr Val Ser Glu Leu Ile Lys Val Ala Gly His Pro
                60               65               70

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aat att gtg ata aac aat gca g  
 Asn Ile Val Ile Asn Asn Ala  
 75

568

<210> 1028  
 <211> 475  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 40..474

<400> 1028  
 gcctgcgcgcg ccttcgcggcc cgagttctgg agactcaac atg aag cta ccg gcc 54  
 Met Lys Leu Pro Ala  
 1 5  
 agg gtt ttc ttt act ctg ggg tcc cgg ctg ccc tgt ggc ctc gct cct 102  
 Arg Val Phe Phe Thr Leu Gly Ser Arg Leu Pro Cys Gly Leu Ala Pro  
 10 15 20  
 cgg agg ttt ttc agt tat ggg aca aaa ata tta tat caa aac act gaa 150  
 Arg Arg Phe Phe Ser Tyr Gly Thr Lys Ile Leu Tyr Gln Asn Thr Glu  
 25 30 35  
 gct ttg caa tct aaa ttc ttt tca cct ctt caa aaa gcg atg cta cca 198  
 Ala Leu Gln Ser Lys Phe Phe Ser Pro Leu Gln Lys Ala Met Leu Pro  
 40 45 50  
 cct aat agt ttt caa gga aaa gtg gca ttc att act ggg gga ggt act 246  
 Pro Asn Ser Phe Gln Gly Lys Val Ala Phe Ile Thr Gly Gly Gly Thr  
 55 60 65  
 ggc ctt ggt aaa gga atg aca act ctt ctg tcc agc cta ggt gct cag 294  
 Gly Leu Gly Lys Gly Met Thr Thr Leu Leu Ser Ser Leu Gly Ala Gln  
 70 75 80 85  
 tgc gtg ata gcc agc cgg aag atg gat gtt ttg aaa gct acc gca gaa 342  
 Cys Val Ile Ala Ser Arg Lys Met Asp Val Leu Lys Ala Thr Ala Glu  
 90 95 100  
 caa att tct tct caa act gga aat aag gtt cat gca att cag tgt gat 390  
 Gln Ile Ser Ser Gln Thr Gly Asn Lys Val His Ala Ile Gln Cys Asp  
 105 110 115  
 gtg agg gat cct gat atg gtt caa aac act gtg tca gaa ctg atc aaa 438  
 Val Arg Asp Pro Asp Met Val Gln Asn Thr Val Ser Glu Leu Ile Lys  
 120 125 130  
 gtt gca gga cat cct aat att gtg ata aac aat gca g 475  
 Val Ala Gly His Pro Asn Ile Val Ile Asn Asn Ala  
 135 140 145

<210> 1029  
 <211> 272  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 113..271

<400> 1029

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gcctgcgccg ccttccggcc cgagttctgg agactcaaca tgaagctacc ggccagggtt      60
ttctttactc tgggggtccc gctgcctgtg ggckcgctc ctcggaggga ag atg gat      118
                                     Met Asp
                                     1
gtt ttg aaa gct acc gca gaa caa att tct tct caa act gga aat aag      166
Val Leu Lys Ala Thr Ala Glu Gln Ile Ser Ser Gln Thr Gly Asn Lys
      5      10      15
gtt cat gca att cag tgt gat gtg agg gat cct gat atg gtt caa aac      214
Val His Ala Ile Gln Cys Asp Val Arg Asp Pro Asp Met Val Gln Asn
      20      25      30
act gtg tca gaa ctg atc aaa gtt gca gga cat cct aat att gtg ata      262
Thr Val Ser Glu Leu Ile Lys Val Ala Gly His Pro Asn Ile Val Ile
      35      40      45      50
aac aat gca g
Asn Asn Ala
                                     272

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<210> 1030

<211> 556

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 160..555

<400> 1030

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tggggagggt tcttccggaa gggtcgggag gcttctggaa aaagcgccgc gcgctggggc      60
ggcccgtcgc tatataaggc aggcgcgggg gtggcgctc agttgcttca gcgtcccggg      120
gtggctgtgc cgttggtcct gtgcggtcac ttagccaag atg cct gag gaa acc      174
                                     Met Pro Glu Glu Thr
                                     1      5
cag acc caa gac caa ccg atg gag gag gag gag gtt gag acg ttc gcc      222
Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu Val Glu Thr Phe Ala
      10      15      20
ttt cag gca gaa att gcc cag ttg atg tca ttg atc atc aat act ttc      270
Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe
      25      30      35
tac tcg aac aaa gag atc ttt ctg aga gag ctc att tca aat tca tca      318
Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser
      40      45      50
gat gca ttg gac aaa atc cgg tat gaa agc ttg aca gat ccc agt aaa      366
Asp Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys
      55      60      65
tta gac tct ggg aaa gag ctg cat att aac ctt ata ccg aac aaa caa      414
Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu Ile Pro Asn Lys Gln
      70      75      80      85
gat cga act ctc act att gtg gat act gga att gga atg acc aag gct      462
Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile Gly Met Thr Lys Ala
      90      95      100
gac ttg atc aat aac ctt ggt act atc gcc aag tct ggg acc aaa gcg      510

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&lt;400&gt; 1032

acaaaaagcg ccggcaattg gggtcgcagc tggag atg ctg cgg ccg gca ggg 53  
 Met Leu Arg Pro Ala Gly  
 1 5  
 ctc tgg cgc tta tgt cgg cga cct tgg gcg gcg agg gtc cca gcg gag 101  
 Leu Trp Arg Leu Cys Arg Arg Pro Trp Ala Ala Arg Val Pro Ala Glu  
 10 15 20  
 aat ctt ggc cgt agg gaa gtc acc tct ggt gtc tct ccc cgc ggt agc 149  
 Asn Leu Gly Arg Arg Glu Val Thr Ser Gly Val Ser Pro Arg Gly Ser  
 25 30 35  
 acc tcg ccc aga acc ctg aat att ttc gac cgg gat ttg aaa agg aaa 197  
 Thr Ser Pro Arg Thr Leu Asn Ile Phe Asp Arg Asp Leu Lys Arg Lys  
 40 45 50  
 cag aag aac tgg gca gcc cgg cag ccc gag ccg acc aaa ttt gac tac 245  
 Gln Lys Asn Trp Ala Ala Arg Gln Pro Glu Pro Thr Lys Phe Asp Tyr  
 55 60 65 70  
 ctg aag gag gag gtt gga agt cgg atc gca gac cgt gta tat grc ata 293  
 Leu Lys Glu Glu Val Gly Ser Arg Ile Ala Asp Arg Val Tyr Xaa Ile  
 75 80 85  
 ccc aga aat ttc ccc ctt gct ttg gat ctt gnn gtt gka aga ggt tac 341  
 Pro Arg Asn Phe Pro Leu Ala Leu Asp Leu Xaa Val Xaa Arg Gly Tyr  
 90 95 100  
 att gca caa tat ttg aat aag gaa act att gga aag 377  
 Ile Ala Gln Tyr Leu Asn Lys Glu Thr Ile Gly Lys  
 105 110

&lt;210&gt; 1033

&lt;211&gt; 325

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 137..325

&lt;400&gt; 1033

agtgctaaag gagcccgcg gaggcagcgg tgggtttggg actgaggcgc tggatctgtg 60  
 gtcgcggctg gggacgtgcg cccgcgccac catcttcggc tgaagaggca attgcttttg 120  
 gatcgttcca ttaca atg gcg cag aga act gga ctc gag gat cca gag agg 172  
 Met Ala Gln Arg Thr Gly Leu Glu Asp Pro Glu Arg  
 1 5 10  
 tat ctc ttt gtg gac agg gct gtc atc tac aac cct gcc act caa gct 220  
 Tyr Leu Phe Val Asp Arg Ala Val Ile Tyr Asn Pro Ala Thr Gln Ala  
 15 20 25  
 gat tgg aca gct aaa aag cta gtg tgg att cca tca gaa cgc cat ggt 268  
 Asp Trp Thr Ala Lys Lys Leu Val Trp Ile Pro Ser Glu Arg His Gly  
 30 35 40  
 ttt gag gca gct agt atc aaa gaa gaa cgg gga gat gaa gtt atg gtg 316  
 Phe Glu Ala Ala Ser Ile Lys Glu Glu Arg Gly Asp Glu Val Met Val  
 45 50 55 60  
 gag ttg gca 325

Glu Leu Ala

<210> 1034

<211> 503

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 120..503

<400> 1034

gcaacaaact gctgagacgc acagtctccg tgccggtgga ggggcggccc cacggcgagc 60  
atgaatacca cttgggtcgc tcgaggagga agagtgtccc aggggggaag cagtacagc 119  
atg gag ggt gcc ctg sct gcg ccc ttc cgg ccc tcg caa ggc ttc ctg 167  
Met Glu Gly Ala Leu Xaa Ala Pro Phe Arg Pro Ser Gln Gly Phe Leu  
1 5 10 15  
agc cga cgg cta aaa agc tcc atc aaa cga acg aag tca caa ccc aaa 215  
Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr Lys Ser Gln Pro Lys  
20 25 30  
ctt gac cgg acc agc agc ttt cgc cag atc ctg cct cgc ttc cga agt 263  
Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu Pro Arg Phe Arg Ser  
35 40 45  
gct gac cat gac cgg gcc cgg ctg atg caa agc ttt aag gag tca cac 311  
Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser Phe Lys Glu Ser His  
50 55 60  
tct cat gag tcc ttg ctg agt cct agc agt gca gct gag gca ttg gag 359  
Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala Ala Glu Ala Leu Glu  
65 70 75 80  
ctc aac ttg gat gaa gat tcc att atc aag cca gtg cac agc tcc atc 407  
Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro Val His Ser Ser Ile  
85 90 95  
ctg ggc cag gag ttc tgt ttt gag gta aca act tca tca gga aca aaa 455  
Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr Ser Ser Gly Thr Lys  
100 105 110  
tgc ttt gcc tgt cgg tct gcg gcc gaa aga gac aaa tgg att gag aat 503  
Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp Lys Trp Ile Glu Asn  
115 120 125

<210> 1035

<211> 302

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 96..302

<400> 1035

agggtgacccg gtcgcctggc cgcagattgt cagtggcttc gccccgagga gagctgactg 60  
ccctgggctg ctgcctccgg cagagctgag ccaaa atg tcc ccg gaa tct aaa 113  
Met Ser Pro Glu Ser Lys

aag ctt ttc aac atc att att tta gga gtt gcc ttt atg ttt atg ttc	1	5	161
Lys Leu Phe Asn Ile Ile Ile Leu Gly Val Ala Phe Met Phe Met Phe			
10 15 20			
act gcc ttt caa act tgt gga aat gtg gcg caa act gtc atc agg agc			209
Thr Ala Phe Gln Thr Cys Gly Asn Val Ala Gln Thr Val Ile Arg Ser			
25 30 35			
tta aat agg aca gat ttt cac ggc agt gga tat acc agc atg gct att			257
Leu Asn Arg Thr Asp Phe His Gly Ser Gly Tyr Thr Ser Met Ala Ile			
40 45 50			
atc tat gga gtg ttc tct gct tca aat ttg att aca ccg tca gtg			302
Ile Tyr Gly Val Phe Ser Ala Ser Asn Leu Ile Thr Pro Ser Val			
55 60 65			

<210> 1036  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 206..412

<400> 1036	
ggcsggcggg ccaaaaagcg cggastcacg gctggaggga gggggascgg aattagcggg	60
cagttggaaa gcccgcgaaa cgctttttcc gcctgggagg ccggacgacg gcgattgggc	120
aggaggaaga ggaggattgt cagtggcttc gccccgagga gagctgactg ccctgggctg	180
ctgcctcccg cagagctgag ccaaa atg tcc ccg gaa tct aaa aag ctt ttc	232
Met Ser Pro Glu Ser Lys Lys Leu Phe	
1 5	
aac atc att att tta gga gtt gcc ttt atg ttt atg ttc act gcc ttt	280
Asn Ile Ile Ile Leu Gly Val Ala Phe Met Phe Met Phe Thr Ala Phe	
10 15 20 25	
caa act tgt gga aat gtg gcg caa act gtc atc agg agc tta aat agg	328
Gln Thr Cys Gly Asn Val Ala Gln Thr Val Ile Arg Ser Leu Asn Arg	
30 35 40	
aca gat ttt cac ggc agt gga tat acc agc atg gct att atc tat gga	376
Thr Asp Phe His Gly Ser Gly Tyr Thr Ser Met Ala Ile Ile Tyr Gly	
45 50 55	
gtg ttc tct gct tca aat ttg att aca ccg tca gtg	412
Val Phe Ser Ala Ser Asn Leu Ile Thr Pro Ser Val	
60 65	

<210> 1037  
 <211> 486  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 66..485

<400> 1037

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ctctccaagc cggagggggtc ctgaggtgac agcgcttgca actgaaattt cagcagcggg    60
agaag atg gac aag aga aag ctc ggg cga cgg cca tct tca tcc gaa atc    110
      Met Asp Lys Arg Lys Leu Gly Arg Arg Pro Ser Ser Ser Glu Ile
        1           5           10           15
atc aca gar gga aaa agg aaa aag tca tct tct gat tta tcg gag ata    158
Ile Thr Glu Gly Lys Arg Lys Lys Ser Ser Ser Asp Leu Ser Glu Ile
           20           25           30
aga aag atg tta aat gca aaa cca gag gat gtc cat gtt caa tca cca    206
Arg Lys Met Leu Asn Ala Lys Pro Glu Asp Val His Val Gln Ser Pro
           35           40           45
ctg tcc aaa ttc aga agc tca gaa cgc tgg act ctc cct ttg cag tgg    254
Leu Ser Lys Phe Arg Ser Ser Glu Arg Trp Thr Leu Pro Leu Gln Trp
           50           55           60
gaa aga agc cta agg aat aaa gtc atc tct cta gac cat aaa aat aaa    302
Glu Arg Ser Leu Arg Asn Lys Val Ile Ser Leu Asp His Lys Asn Lys
           65           70           75
aaa cat atc cga ggg tgt cct gtt act tcc aag tca tca cca gaa agg    350
Lys His Ile Arg Gly Cys Pro Val Thr Ser Lys Ser Ser Pro Glu Arg
           80           85           90           95
caa ctc aaa gtt atg ttg acg aat gtc cta tgg acg gat tta gga cga    398
Gln Leu Lys Val Met Leu Thr Asn Val Leu Trp Thr Asp Leu Gly Arg
           100           105           110
aaa ttc aga aag acc cta cct aga aac gat gct aat tta tgt gat gcc    446
Lys Phe Arg Lys Thr Leu Pro Arg Asn Asp Ala Asn Leu Cys Asp Ala
           115           120           125
aac aag gtg caa tca gac tca ttg cct tcg aca tct gtt g    486
Asn Lys Val Gln Ser Asp Ser Leu Pro Ser Thr Ser Val
           130           135           140

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<210> 1038

<211> 447

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 153..446

<400> 1038

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aatggaaacc agatgaagaa gatgagattt cggaggaatt gaaagaaaag gccaagattg    60
aagatgagaa aaaagatgaa gaaaaagaag ascccaaagg aattcctgaa ttttggttaa    120
ctgttttttaa gaatgttgac ttgctcagtg at atg gtt cag gaa cac gat gaa    173
      Met Val Gln Glu His Asp Glu
        1           5
cct att ctg aag cac ttg aaa gat att aaa gtg aag ttc tca gat gct    221
Pro Ile Leu Lys His Leu Lys Asp Ile Lys Val Lys Phe Ser Asp Ala
           10           15           20
ggc cag cct atg agt ttt gtc tta gaa ttt cac ttt gaa ccc aat gaa    269
Gly Gln Pro Met Ser Phe Val Leu Glu Phe His Phe Glu Pro Asn Glu
           25           30           35
tat ttt aca aat gaa gtg ctg aca aag aca tac agg atg agg tca gaa    317
Tyr Phe Thr Asn Glu Val Leu Thr Lys Thr Tyr Arg Met Arg Ser Glu

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40		45		50		55	
cca gat gat tct	gat ccc ttt tct ttt	gat gga cca gaa att atg ggt	365				
Pro Asp Asp Ser	Asp Pro Phe Ser Phe Asp Gly Pro Glu Ile Met Gly						
	60	65	70				
tgt aca ggg tgc	cag ata gat tgg aaa aaa gga aag aat gtc act ttg	413					
Cys Thr Gly Cys	Gln Ile Asp Trp Lys Lys Gly Lys Asn Val Thr Leu						
	75	80	85				
aaa act att aag aag aag cag	aaa cac aag gga c	447					
Lys Thr Ile Lys Lys Lys Gln	Lys His Lys Gly						
	90	95					

<210> 1039  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 142..537

<400> 1039	
gggaggcggg gcggggcggg gcgggcctcg cctgcctag ggaggatgtg gcgggtataa	60
aagccccacc caggccagcc ggctctgctc agcatttggg gacgctctca gctctcggcg	120
cacggccccag cttccttcaa a atg tct act gtt cac gaa atc ctg tgc aag	171
	Met Ser Thr Val His Glu Ile Leu Cys Lys
	1 5 10
ctc agc ttg gag ggt gat cac tct aca ccc cca agt gca tat ggg tct	219
Leu Ser Leu Glu Gly Asp His Ser Thr Pro Pro Ser Ala Tyr Gly Ser	
	15 20 25
gtc aaa gcc tat act aac ttt gat gct gag cgg gat gct ttg aac att	267
Val Lys Ala Tyr Thr Asn Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile	
	30 35 40
gaa aca gcc atc aag acc aaa ggt gtg gat gag gtc acc att gtc aac	315
Glu Thr Ala Ile Lys Thr Lys Gly Val Asp Glu Val Thr Ile Val Asn	
	45 50 55
att ttg acc aac cgc agc aat gca cag aga cag gat att gcc ttc gcc	363
Ile Leu Thr Asn Arg Ser Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala	
	60 65 70
tac cag aga agg acc aaa aag gaa ctt gca tca gca ctg aag tca gcc	411
Tyr Gln Arg Arg Thr Lys Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala	
	75 80 85 90
tta tct ggc cac ctg gag acg gtg att ttg ggc cta ttg aag aca cct	459
Leu Ser Gly His Leu Glu Thr Val Ile Leu Gly Leu Leu Lys Thr Pro	
	95 100 105
gct cag tat gac gct tct gag cta aaa gct tcc atg aag ggg ctg gga	507
Ala Gln Tyr Asp Ala Ser Glu Leu Lys Ala Ser Met Lys Gly Leu Gly	
	110 115 120
acc gac gag gac tct ctc att gag atc atc	537
Thr Asp Glu Asp Ser Leu Ile Glu Ile Ile	
	125 130

<210> 1040  
 <211> 456



<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 234..455

<400> 1040

attacttccc gttttctcga tctgctgctc gtctcaggct cgtagttcgc cttcaacatg 60  
ccggaaccag cgaagtccgc tcccgcgccc aagaagggct cgaagaaagc cgtgactaag 120  
gcgcagaaga aggacggcaa gaagcgcaas gcagccgcaa ggagagctac tccgtatacg 180  
tgtacaaggt gctgaarcag gtccaccccc acaccggcat ctctctctaaa gcc atg 236  
Met  
1  
ggg atc atg aat tcc ttt gtc aac gac atc ttc gag cgc atc gcc ggc 284  
Gly Ile Met Asn Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly  
5 10 15  
gag gct tcc cgc ctg gcg cat tac aac aaa gcg ctc gac cat cac ctc 332  
Glu Ala Ser Arg Leu Ala His Tyr Asn Lys Ala Leu Asp His His Leu  
20 25 30  
cag gga gat cca gac ggc cgt gcg cct gct gct tcc cgg gga gct ggc 380  
Gln Gly Asp Pro Asp Gly Arg Ala Pro Ala Ala Ser Arg Gly Ala Gly  
35 40 45  
caa gca cgc tgt gtc aga ggg cac caa ggc cgt tac caa gta cac cag 428  
Gln Ala Arg Cys Val Arg Gly His Gln Gly Arg Tyr Gln Val His Gln  
50 55 60 65  
ctc caa gta aac ttg tcc ctg caa ctg c 456  
Leu Gln Val Asn Leu Ser Leu Gln Leu  
70

<210> 1041

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 222..443

<400> 1041

aaaacttctt ttcttggtta agccgcggtt gtactgtgtc ttaccatgcc tgaaccggca 60  
aaatccgctc cggcccctaa aaagggtctc aagaaagccg tcaccaaagc ccagaagaaa 120  
gacggcaaga agcgcaagsc agccgcaaag agagctactc catctacgtg tacaaggtgc 180  
tgaagcaggt ccaccccgac accggcatct cstcyaargc c atg ggs atc atg aay 236  
Met Gly Ile Met Asn  
1 5  
tcc tty gtc aac gac atc ttc gag cgc atc gcs ggm gag gct tcc cgc 284  
Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg  
10 15 20  
ctg gcg cay tac aac aaa gcg ctc sac cat cac mtc cmg sga gat cca 332  
Leu Ala His Tyr Asn Lys Ala Leu Xaa His His Xaa Xaa Xaa Asp Pro  
25 30 35

gac ggc cgt gcg cct gct gct kcc cgg sga gct ggc caa gca cgc ygt 380  
 Asp Gly Arg Ala Pro Ala Ala Xaa Arg Xaa Ala Gly Gln Ala Arg Xaa  
 40 45 50  
 gtc mga ggg cac caa ggc cgt yac caa gta cac cag ctc caa gta aac 428  
 Val Arg Gly His Gln Gly Arg Xaa Gln Val His Gln Leu Gln Val Asn  
 55 60 65  
 ttg tcc ctg caa ctg c 444  
 Leu Ser Leu Gln Leu  
 70

<210> 1042  
 <211> 437  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 215..436

<400> 1042  
 attcttggtta ttgagtgct ctttcactct cctccgccat gcccgaccgg gctaaatctg 60  
 ctctgcccc caaaaagggc tccaagaaag ccgtaaccaa ggcccagaaa aaggacggca 120  
 agaagcgcaa cgcagccgca aagagagtta ctctatctac gtgtacaagg tgctgaarca 180  
 rgtccacccc gacaccggca tctcctctaa agcc atg ggg atc atg aat tcc ttt 235  
 Met Gly Ile Met Asn Ser Phe  
 1 5  
 gtc aac gac atc ttc gag cgc atc gcc ggc gag gct tcc cgc ctg gcg 283  
 Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg Leu Ala  
 10 15 20  
 cat tac aac aaa gcg ctc gac cat cac ctc cag gga gat cca gac ggc 331  
 His Tyr Asn Lys Ala Leu Asp His His Leu Gln Gly Asp Pro Asp Gly  
 25 30 35  
 cgt gcg cct gct gct tcc cgg gga gct ggc caa gca cgc tgt gtc aga 379  
 Arg Ala Pro Ala Ala Ser Arg Gly Ala Gly Gln Ala Arg Cys Val Arg  
 40 45 50 55  
 ggg cac caa ggc cgt tac caa gta cac cag ctc caa gta aac ttg tcc 427  
 Gly His Gln Gly Arg Tyr Gln Val His Gln Leu Gln Val Asn Leu Ser  
 60 65 70  
 ctg caa ctg c 437  
 Leu Gln Leu

<210> 1043  
 <211> 449  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 227..448

<400> 1043  
 gttgagcctt cactttgggg tgtattctta ctcttttacc ttgttgcaat gcctgatcca 60

gctaagtccg ctcccccccc gaagaagggc tccaagaagg nsggtgacca aggcgcagaa 120  
 gaaggatggc aagaagcgta aacgcagccg caaggagagc tactccgtat acgtttacaa 180  
 ggtgctgaag caagtccacc ccgacaccgg catctctctcy aaagcc atg ggg atc 235  
 Met Gly Ile

1

atg aat tcc ttt gtc aac gay atc ttc gag cgc atc gcc ggc gag gct 283  
 Met Asn Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala  
 5 10 15

tcc cgc ctg gck cat tac aac aaa gcg ytc gac cat cac ctc cag gga 331  
 Ser Arg Leu Ala His Tyr Asn Lys Ala Xaa Asp His His Leu Gln Gly  
 20 25 30 35

gat cca gac rgc cgt gcg cct gct gct kcc ygg gga rct ggc caa gca 379  
 Asp Pro Asp Xaa Arg Ala Pro Ala Ala Xaa Xaa Gly Xaa Gly Gln Ala  
 40 45 50

cgc ygt gtc mga ggg cac yaa ggc cgt tac caa gta cac cag ctc caa 427  
 Arg Xaa Val Arg Gly His Xaa Gly Arg Tyr Gln Val His Gln Leu Gln  
 55 60 65

gta aac ttg tcc ctg caa ctg c 449  
 Val Asn Leu Ser Leu Gln Leu  
 70

&lt;210&gt; 1044

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 277..498

&lt;400&gt; 1044

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 cttgcgttct cgggggctcg tgctcggtctt gggctctggcc atgcctgagc ctgcaaagtt 120  
 cgcgcgggct cccaagaagg gctccaagaa agccgtcacc aaagcccaga agaaagacgg 180  
 caagaagcgc aacgcagccg caaggagagc tactccatct acgtgtacaa ggtgctgaar 240  
 crggtccacc ccgacaccgg catctsstsy aargcc atg ggs atc atg aay tcc 294  
 Met Gly Ile Met Asn Ser

1

5

tty stc aac gac atc ttc gag cgc atc gcc ggc gag gct tcc cgc ctg 342  
 Phe Xaa Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg Leu  
 10 15 20

gcg cat tac aac aaa gcg ctc gac cat cac ctc cag gga gat cca gac 390  
 Ala His Tyr Asn Lys Ala Leu Asp His His Leu Gln Gly Asp Pro Asp  
 25 30 35

ggc cgt gcg cct gct gct tcc cgg gga gct ggc caa gca cgc tgt gtc 438  
 Gly Arg Ala Pro Ala Ala Ser Arg Gly Ala Gly Gln Ala Arg Cys Val  
 40 45 50

aga ggg cac caa ggc cgt tac caa gta cac cag ctc caa gta aac ttg 486  
 Arg Gly His Gln Gly Arg Tyr Gln Val His Gln Leu Gln Val Asn Leu  
 55 60 65 70

tcc ctg caa ctg c 499  
 Ser Leu Gln Leu

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<220>  
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 <222> 76..351

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 taaatttggt tcccg atg gcg ttc cag tac gta tgg ctt tcg ctc gag cag 111  
                   1                  5                  10  
 tta cct tat tta acc tct tct agg ctg tac cca gct ctg cct tgc ttt 159  
 Leu Pro Tyr Leu Thr Ser Ser Arg Leu Tyr Pro Ala Leu Pro Cys Phe  
                   15                  20                  25  
 gct tcc ccc tca ccc cct gat tcc atc tct gca gcc cac ggg aca tcg 207  
 Ala Ser Pro Ser Pro Pro Asp Ser Ile Ser Ala Ala His Gly Thr Ser  
                   30                  35                  40  
 gga aga tgc cag acc acc agg cag gat agt ctg caa ggg gag gga ctt 255  
 Gly Arg Cys Gln Thr Thr Arg Gln Asp Ser Leu Gln Gly Glu Gly Leu  
                   45                  50                  55                  60  
 tct ctg gaa ttt cct gat atg acc aag aaa gct tct tat caa aag aag 303  
 Ser Leu Glu Phe Pro Asp Met Thr Lys Lys Ala Ser Tyr Gln Lys Lys  
                   65                  70                  75  
 cac aat tgc ctt cgg tta cct can kat cta ctg cag aaa aga aga cga 351  
 His Asn Cys Leu Arg Leu Pro Xaa Xaa Leu Leu Gln Lys Arg Arg Arg  
                   80                  85                  90  
 ga 353

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<220>  
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 <222> 315..593

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 gtgagtactg ggtatgtgtc acattgccaa atcccggatc acaagtctcc atgaactgct 180  
 ggtgagctag gataataaaa ccctgacat caccattcca gaagcttcac aagactgcat 240  
 atataagggg ctggctgtag ctgcagctga aggagctgac cagccagctg acccctcaca 300  
 ctcacctagc cacc atg gac atc gcc atc cac cac ccc tgg atc cgc cgc 350  
                   Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg  
                   1                  5                  10  
 ccc ttc ttt cct ttc cac tcc ccc agc cgc ctc ttt gac cag ttc ttc 398  
 Pro Phe Phe Pro Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe  
                   15                  20                  25

gga gag cac ctg ttg gag tct gat ctt ttc ccg acg tct act tcc ctg	446
Gly Glu His Leu Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu	
30 35 40	
agt ccc ttc tac ctt cgg cca ccc tcc ttc ctg cgg gca ccc agc tgg	494
Ser Pro Phe Tyr Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp	
45 50 55 60	
ttt gac act gga ctc tca gag gtg agt ctc ccc aca gct agg acg gga	542
Phe Asp Thr Gly Leu Ser Glu Val Ser Leu Pro Thr Ala Arg Thr Gly	
65 70 75	
gag tcc tta ctg gaa cct cct gga aac ttc tcc atc cat ttt cct ttc	590
Glu Ser Leu Leu Glu Pro Pro Gly Asn Phe Ser Ile His Phe Pro Phe	
80 85 90	
cta cc	595
Leu	

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tcccgatca caagtctcca tgaactgctg gtgagctagg ataataaaac ccctgacatc	180
accattccag aagcttcaca agactgcata tataaggggc tggctgtagc tgcagctgaa	240
ggagctgacc agccagctga cccctcacac tcacctagcc acc atg gac atc gcc	295
Met Asp Ile Ala	
1	
atc cac cac ccc tgg atc cgc cgc ccc ttc ttt cct ttc cac tcc ccc	343
Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro Phe His Ser Pro	
5 10 15 20	
agc cgc ctc ttt gac cag ttc ttc gga gag cac ctg ttg gag tct gat	391
Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu Leu Glu Ser Asp	
25 30 35	
ctt ttc ccg acg tct act tcc ctg agt ccc ttc tac ctt cgg cca ccc	439
Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr Leu Arg Pro Pro	
40 45 50	
tcc ttc ctg cgg gca ccc agc tgg ttt gac act gga ctc tca gag gtg	487
Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly Leu Ser Glu Val	
55 60 65	
agt ctc ccc aca gct agg acg gga gag tcc tta ctg gaa cct cct gga	535
Ser Leu Pro Thr Ala Arg Thr Gly Glu Ser Leu Leu Glu Pro Pro Gly	
70 75 80	
aac ttc tcc atc cat ttt cct ttc cta cc	564
Asn Phe Ser Ile His Phe Pro Phe Leu	
85 90	

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<212> DNA  
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<222> 4..507

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Met Thr Ser Ala Phe Lys Leu Asp Phe Leu Pro Asp Met Met Val  
1 5 10 15  
gas ggc cgc ctg ctc gtt cct gac aga att aac ggc aca gcc aac aag 96  
Xaa Gly Arg Leu Leu Val Pro Asp Arg Ile Asn Gly Thr Ala Asn Lys  
20 25 30  
atg aac gga gct ttg gat cas kca gac caa cca gac cca gat gcc att 144  
Met Asn Gly Ala Leu Asp Xaa Xaa Asp Gln Pro Asp Pro Asp Ala Ile  
35 40 45  
aag atg ttt gtc ggr sag atc ccc cgg tca tgg tcg grr aag gag ctg 192  
Lys Met Phe Val Gly Xaa Ile Pro Arg Ser Trp Ser Xaa Lys Glu Leu  
50 55 60  
acc agc cag ctg acc cct cac act cac cta gcc acc atg gac atc gcc 240  
Thr Ser Gln Leu Thr Pro His Thr His Leu Ala Thr Met Asp Ile Ala  
65 70 75  
atc cac cac ccc tgg atc cgc cgc ccc ttc ttt cct ttc cac tcc ccc 288  
Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro Phe His Ser Pro  
80 85 90 95  
agc cgc ctc ttt gac cag ttc ttc gga gag cac ctg ttg gag tct gat 336  
Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu Leu Glu Ser Asp  
100 105 110  
ctt ttc ccg acg tct act tcc ctg agt ccc ttc tac ctt cgg cca ccc 384  
Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr Leu Arg Pro Pro  
115 120 125  
tcc ttc ctg cgg gca ccc agc tgg ttt gac act gga ctc tca gag gtg 432  
Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly Leu Ser Glu Val  
130 135 140  
agt ctc ccc aca gct agg acg gga gag tcc tta ctg gaa cct cct gga 480  
Ser Leu Pro Thr Ala Arg Thr Gly Glu Ser Leu Leu Glu Pro Pro Gly  
145 150 155  
aac ttc tcc atc cat ttt cct ttc cta cc 509  
Asn Phe Ser Ile His Phe Pro Phe Leu  
160 165

<210> 1049  
<211> 580  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 300..578

<400> 1049

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gtgtcacatt gccaaatccc ggatcacaaag tctccatgaa ctgctggtga gctaggataa      180
taaaacccct gacatcacca ttccagaagc ttcacaagac tgcataatata aggggctggc      240
tgtagctgca gctgaaggag ctgaccagcc agctgacccc tcacactcac ctagccacc      299
atg gac atc gcc atc cac cac ccc tgg atc cgc cgc ccc ttc ttt cct      347
Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
1          5          10          15
ttc cac tcc ccc agc cgc ctc ttt gac cag ttc ttc gga gag cac ctg      395
Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
20          25          30
ttg gag tct gat ctt ttc ccg acg tct act tcc ctg agt ccc ttc tac      443
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
35          40          45
ctt cgg cca ccc tcc ttc ctg cgg gca ccc agc tgg ttt gac act gga      491
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
50          55          60
ctc tca gag gtg agt ctc ccc aca gct agg acg gga gag tcc tta ctg      539
Leu Ser Glu Val Ser Leu Pro Thr Ala Arg Thr Gly Glu Ser Leu Leu
65          70          75          80
gaa cct cct gga aac ttc tcc atc cat ttt cct ttc cta cc      580
Glu Pro Pro Gly Asn Phe Ser Ile His Phe Pro Phe Leu
85          90

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<222> 180..404

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accgaaaaag gagctgagga gactccatat tagacttgcg ttccaaatas cgctctaadc      120
ctkgacttag cctacctaata tagtctctct gtgttaccag taacggcaca gccaaacaag      179
atg aac gga gct ttg gat cac tca kac caa cca gac cca gat gcc att      227
Met Asn Gly Ala Leu Asp His Ser Xaa Gln Pro Asp Pro Asp Ala Ile
1          5          10          15
aag atg ttt gtc gga cag atc ccc cgg tca tgg tgg gaa aag gag ctg      275
Lys Met Phe Val Gly Gln Ile Pro Arg Ser Trp Ser Glu Lys Glu Leu
20          25          30
aaa gaa ctt ttt gag cct tac gga gcc gtc tac cag atc aac gtc ctc      323
Lys Glu Leu Phe Glu Pro Tyr Gly Ala Val Tyr Gln Ile Asn Val Leu
35          40          45
cgg gac cgg agt cag aac cct ccg cag agt aaa ggt tgt tgt ttc gta      371
Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys Cys Phe Val
50          55          60
aca ttt tat aca aga aaa gct gca ctt gag gcc      404
Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala
65          70          75

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 <211> 546  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 266..544

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agagcagctc	agtgagtact	gggtatgtgt	cacattgcc	aatcccggat	cacaagtctc	120	
catgaactgc	tgggtgagcta	ggataataaa	acccctgaca	tcaccattcc	agaagcttca	180	
caagactgca	tatataaggg	gctggctgta	gctgcagctg	aaggagctga	ccagccagct	240	
gacccctcac	actcacctag	ccacc atg	gac atc	gcc atc	cac cac	ccc tgg 292	
		Met Asp	Ile Ala	Ile His	His Pro	Trp	
		1		5			
atc cgc	cgc ccc	ttc ttt	cct ttc	cac tcc	ccc agc	cgc ctc	ttt gac 340
Ile Arg	Arg Pro	Phe Phe	Pro Phe	His Ser	Pro Ser	Arg Leu	Phe Asp
10		15		20		25	
cag ttc	ttc gga	gag cac	ctg ttg	gag tct	gat ctt	ttc ccg	acg tct 388
Gln Phe	Phe Gly	Glu His	Leu Leu	Glu Ser	Asp Leu	Phe Pro	Thr Ser
		30		35		40	
act tcc	ctg agt	ccc ttc	tac ctt	cgg cca	ccc tcc	ttc ctg	cgg gca 436
Thr Ser	Leu Ser	Pro Phe	Tyr Leu	Arg Pro	Pro Ser	Phe Leu	Arg Ala
		45		50		55	
ccc agc	tgg ttt	gac act	gga ctc	tca gag	gtg agt	ctc ccc	aca gct 484
Pro Ser	Trp Phe	Asp Thr	Gly Leu	Ser Glu	Val Ser	Leu Pro	Thr Ala
		60		65		70	
agg acg	gga gag	tcc tta	ctg gaa	cct cct	gga aac	ttc tcc	atc cat 532
Arg Thr	Gly Glu	Ser Leu	Leu Glu	Pro Pro	Gly Asn	Phe Ser	Ile His
		75		80		85	
ttt cct	ttc cta	cc					546
Phe Pro	Phe Leu						
90							

<210> 1052  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 301..564

<400> 1052

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gtgtcacatt	gccaaatccc	ggatcacaag	tctccatgaa	ctgctggtga	gctaggataa	180
taaaacccct	gacatcacca	ttnnccagaag	cttcacaaga	ctgcatatat	aaggggctgg	240
ctgtagctgc	agctgaagga	gctgaccagc	cagctgaccc	ctcacactca	cctagccacc	300
atg gac	atc gcc	atc cac	cac ccc	ttc ttc	ctt ccc	agg 348



004220-666T560

Met	Asp	Ile	Ala	Ile	His	His	Pro	Phe	Xaa	Pro	Phe	His	Ser	Pro	Ser		
1				5					10					15			
cgc	ctc	ttt	gac	cag	ttc	ttc	ggr	gag	cac	ctg	ttg	gag	tck	gat	stt		396
Arg	Leu	Phe	Asp	Gln	Phe	Phe	Gly	Glu	His	Leu	Leu	Glu	Ser	Asp	Xaa		
			20					25					30				
ttc	ccg	acg	tct	act	tcc	ctg	agt	ccc	ttc	tac	ctt	cgg	cca	ccc	tcc		444
Phe	Pro	Thr	Ser	Thr	Ser	Leu	Ser	Pro	Phe	Tyr	Leu	Arg	Pro	Pro	Ser		
		35					40					45					
ttc	ctg	cgg	gca	ccc	agc	tgg	ttt	gac	act	gga	ctc	tca	gag	gtg	agt		492
Phe	Leu	Arg	Ala	Pro	Ser	Trp	Phe	Asp	Thr	Gly	Leu	Ser	Glu	Val	Ser		
	50					55					60						
ctc	ccc	aca	gct	agg	acg	gga	gag	tcc	tta	ctg	gaa	cct	cct	gga	aac		540
Leu	Pro	Thr	Ala	Arg	Thr	Gly	Glu	Ser	Leu	Leu	Glu	Pro	Pro	Gly	Asn		
65					70					75				80			
ttc	tcc	atc	cat	ttt	cct	ttc	cta	cc									566
Phe	Ser	Ile	His	Phe	Pro	Phe	Leu										
				85													

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 <222> 42..404

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						Met	Ala	Ala	Thr	Thr							
						1				5							
ggc	tcg	gga	gta	aaa	gtc	cct	cg	aat	ttc	cga	ctg	ttg	gaa	gaa	ctc		104
Gly	Ser	Gly	Val	Lys	Val	Pro	Arg	Asn	Phe	Arg	Leu	Leu	Glu	Glu	Leu		
				10					15					20			
gaa	gaa	ggc	cag	aaa	gga	gta	gga	gat	ggc	aca	gtt	agc	tgg	ggt	cta		152
Glu	Glu	Gly	Gln	Lys	Gly	Val	Gly	Asp	Gly	Thr	Val	Ser	Trp	Gly	Leu		
			25					30					35				
gaa	gat	gac	gaa	gac	atg	aca	ctt	aca	aga	tgg	aca	ggg	atg	ata	att		200
Glu	Asp	Asp	Glu	Asp	Met	Thr	Leu	Thr	Arg	Trp	Thr	Gly	Met	Ile	Ile		
	40					45					50						
ggg	cct	cca	aga	aca	att	tat	gaa	aac	cga	ata	tac	agc	ctt	aaa	ata		248
Gly	Pro	Pro	Arg	Thr	Ile	Tyr	Glu	Asn	Arg	Ile	Tyr	Ser	Leu	Lys	Ile		
	55				60					65							
gaa	tgt	gga	cct	aaa	tac	cca	gaa	gca	ccc	ccc	ttt	gta	aga	ttt	gta		296
Glu	Cys	Gly	Pro	Lys	Tyr	Pro	Glu	Ala	Pro	Pro	Phe	Val	Arg	Phe	Val		
	70				75				80					85			
aca	aaa	att	aat	atg	aat	gga	gta	aat	agt	tct	aat	gga	gtg	gtg	gac		344
Thr	Lys	Ile	Asn	Met	Asn	Gly	Val	Asn	Ser	Ser	Asn	Gly	Val	Val	Asp		
			90					95					100				
cca	aga	gcc	ata	tca	gtg	cta	gca	aaa	tgg	cag	nat	tca	tat	agc	atc		392
Pro	Arg	Ala	Ile	Ser	Val	Leu	Ala	Lys	Trp	Gln	Xaa	Ser	Tyr	Ser	Ile		
			105					110					115				
aaa	ggt	gtc	ctg														404

Lys Val Val Leu  
120

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<212> DNA  
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<400> 1054

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Thr Gly Val Lys Val Pro Arg Asn Phe Arg Leu Leu Glu Glu Leu Glu  
5 10 15 20  
gaa gga caa aaa gga gta ggc gac ggt aca gtt agc tgg ggc ctt gaa 150  
Glu Gly Gln Lys Gly Val Gly Asp Gly Thr Val Ser Trp Gly Leu Glu  
25 30 35  
gat gat gaa gat atg aca ctt aca agg tgg aca ggc atg att att ggg 198  
Asp Asp Glu Asp Met Thr Leu Thr Arg Trp Thr Gly Met Ile Ile Gly  
40 45 50  
cca cca agg aca aat tat gaa aac aga ata tat agc ctg aaa gta gaa 246  
Pro Pro Arg Thr Asn Tyr Glu Asn Arg Ile Tyr Ser Leu Lys Val Glu  
55 60 65  
tgt gga cct aaa tac cca gaa gct cct ccg tca gtt aga ttt gta aca 294  
Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro Ser Val Arg Phe Val Thr  
70 75 80  
aaa att aat atg aac gga ata aat aat tcc agt ggg atg gtg gat gcc 342  
Lys Ile Asn Met Asn Gly Ile Asn Asn Ser Ser Gly Met Val Asp Ala  
85 90 95 100  
cgg agc ata cca gtg tta gca aaa tgg caa aat tca tat agc att aaa 390  
Arg Ser Ile Pro Val Leu Ala Lys Trp Gln Asn Ser Tyr Ser Ile Lys  
105 110 115  
gtt gta ctt caa gag cta aga cgt cta at 419  
Val Val Leu Gln Glu Leu Arg Arg Leu  
120 125

<210> 1055  
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<212> DNA  
<213> Homo sapiens

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<222> 72..467

<400> 1055

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cggcgggcga c atg gac aac gcg ggg aag gag cgt gag gca gta cag ctg 110  
                   Met Asp Asn Ala Gly Lys Glu Arg Glu Ala Val Gln Leu  
                   1                  5                  10  
 atg gcg gag gcc gag aag cga gtc aag gcc tcc cac tcc ttc ctc cga 158  
 Met Ala Glu Ala Glu Lys Arg Val Lys Ala Ser His Ser Phe Leu Arg  
                   15                  20                  25  
 ggg ctg ttt gga gga aac aca aga ata gaa gag gct tgt gaa atg tat 206  
 Gly Leu Phe Gly Gly Asn Thr Arg Ile Glu Glu Ala Cys Glu Met Tyr  
                   30                  35                  40                  45  
 acc aga gct gca aat atg ttc aag atg gct aaa aat tgg agt gct gca 254  
 Thr Arg Ala Ala Asn Met Phe Lys Met Ala Lys Asn Trp Ser Ala Ala  
                   50                  55                  60  
 gga aac gca ttt tgt cag gca gcc aag ctc cac atg cag ctt cag agc 302  
 Gly Asn Ala Phe Cys Gln Ala Ala Lys Leu His Met Gln Leu Gln Ser  
                   65                  70                  75  
 aaa cat gac tct gct acc agc ttt gtg gat gct gga aat gct tac aaa 350  
 Lys His Asp Ser Ala Thr Ser Phe Val Asp Ala Gly Asn Ala Tyr Lys  
                   80                  85                  90  
 aag gca gat ccc caa gag gct atc aac tgc tta aat gca gcc atc gac 398  
 Lys Ala Asp Pro Gln Glu Ala Ile Asn Cys Leu Asn Ala Ala Ile Asp  
                   95                  100                  105  
 att tac aca gac atg gga agg ttt aca att gca gcc aag cac cac att 446  
 Ile Tyr Thr Asp Met Gly Arg Phe Thr Ile Ala Ala Lys His His Ile  
                   110                  115                  120                  125  
 act atg cag aga tct atg aga c 468  
 Thr Met Gln Arg Ser Met Arg  
                   130

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                   Met Tyr Thr Arg Ala Ala Asn Met Phe Lys Met Ala  
                   1                  5                  10  
 aaa aat tgg agt gct gca gga aac gca ttt tgt cag gca gcc aag ctc 160  
 Lys Asn Trp Ser Ala Ala Gly Asn Ala Phe Cys Gln Ala Ala Lys Leu  
                   15                  20                  25  
 cac atg cag ctt cag agc aaa cat gac tct gct acc agc ttt gtg gat 208  
 His Met Gln Leu Gln Ser Lys His Asp Ser Ala Thr Ser Phe Val Asp  
                   30                  35                  40  
 gct gga aat gct tac aaa aag gca gat ccc caa gag gct atc aac tgc 256  
 Ala Gly Asn Ala Tyr Lys Lys Ala Asp Pro Gln Glu Ala Ile Asn Cys  
                   45                  50                  55                  60  
 tta aat gca gcc atc gac att tac aca gac atg gga agg ttt aca att 304  
 Leu Asn Ala Ala Ile Asp Ile Tyr Thr Asp Met Gly Arg Phe Thr Ile

65 70 75 311  
 gca gca a  
 Ala Ala

<210> 1057  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 119..370

<400> 1057  
 ggaagtggcc ggtcagcgtc gctgccggtc tccggcggag acggactctg gagtttgggc 60  
 ggcccgggcg gccactagggt actctgatat tccgtactaa acacgtctgc aagtcaag 118  
 atg tgc cac ccg tcc ccc caa gcc aag ccc tcc aac ccc agt aac cct 166  
 Met Ser His Pro Ser Pro Gln Ala Lys Pro Ser Asn Pro Ser Asn Pro  
 1 5 10 15  
 cga gtc ttc ttt gac gtg gac atc gga ggg gag cga gtt ggt cga att 214  
 Arg Val Phe Phe Asp Val Asp Ile Gly Gly Glu Arg Val Gly Arg Ile  
 20 25 30  
 gtc tta gaa ttg ttt gca gat atc gta ccc aaa act gcg gaa aat ttt 262  
 Val Leu Glu Leu Phe Ala Asp Ile Val Pro Lys Thr Ala Glu Asn Phe  
 35 40 45  
 cgt gca ctg tgt aca gga gaa aaa ggc att gga cac acg act ggg aaa 310  
 Arg Ala Leu Cys Thr Gly Glu Lys Gly Ile Gly His Thr Thr Gly Lys  
 50 55 60  
 cct ctc cat ttc aaa gga tgc cct ttt cat cga att att aag aaa ttt 358  
 Pro Leu His Phe Lys Gly Cys Pro Phe His Arg Ile Ile Lys Lys Phe  
 65 70 75 80  
 atg att cag ggt g 371  
 Met Ile Gln Gly

<210> 1058  
 <211> 344  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 145..342

<400> 1058  
 asctcagccg taagtagttt ctctatcagt cgcgcastgt gttcgcggac tcaggtggaa 60  
 ggaatttctt ctcttcgttg acgttgctgg tggtcactgt ttggaattag tcaagtttcg 120  
 ggaatcaccg tcgctgccat caac atg tgc gtc cca agc gct ctc atg aag 171  
 Met Ser Val Pro Ser Ala Leu Met Lys  
 1 5  
 caa ccg ccc att cag tct acg gct ggg gcc gtc cca gtt cgc aat gag 219  
 Gln Pro Pro Ile Gln Ser Thr Ala Gly Ala Val Pro Val Arg Asn Glu  
 10 15 20 25

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<220>  
<221> CDS  
<222> 37..507
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723

<210> 1060  
 <211> 508  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 201..506

<400> 1060

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agcggccgag aagggcgagg cttccggcgg gtgacgcgcc cgggttcggc tacaaaagag      60
gacggctgcg gcgcgccggg cggaactttc cagaacgctc ggtgagaggc ggaggagcgg      120
taactacccc ggctgcgcac agctcggcgc tccttccgcg tccctcacac accggcctca      180
gccgcacccg gcagtagaag atg gtg aaa gaa aca act tac tac gat gtt ttg      233
                Met Val Lys Glu Thr Thr Tyr Tyr Asp Val Leu
                1             5             10
ggg gtc aaa ccc aat gct act cag gaa gaa ttg aaa aag gct tat agg      281
Gly Val Lys Pro Asn Ala Thr Gln Glu Glu Leu Lys Lys Ala Tyr Arg
                15             20             25
aaa ctg gcc ttg aag tac cat cct gat aag aac cca aat gaa gga gag      329
Lys Leu Ala Leu Lys Tyr His Pro Asp Lys Asn Pro Asn Glu Gly Glu
                30             35             40
aag ttt aaa cag att tct caa gct tac gaa gtt ctc tct gat gca aag      377
Lys Phe Lys Gln Ile Ser Gln Ala Tyr Glu Val Leu Ser Asp Ala Lys
                45             50             55
aaa agg gaa tta tat gac aaa gga gga gaa cag gca att aaa gag ggt      425
Lys Arg Glu Leu Tyr Asp Lys Gly Gly Glu Gln Ala Ile Lys Glu Gly
        60             65             70             75
gga gca ggt ggc ggt ttt ggc tcc ccc atg gac atc ttt gat atg ttt      473
Gly Ala Gly Gly Gly Phe Gly Ser Pro Met Asp Ile Phe Asp Met Phe
                80             85             90
ttt gga gga gga gga agg atg cag aga gaa agg ag      508
Phe Gly Gly Gly Gly Arg Met Gln Lys Pro Ala Pro Asp Phe Lys
                95             100

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<210> 1061  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 122..454

<400> 1061

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acgtcttggt tcgggccggg cataaaaggc ttcgcggccc agggctcact tggcgctgag      60
aacgcgggtc cacgcgtgtg atcgtccgtg cgtctagcct ttgccacgc agctttcagt      120
c atg gcc tcc ggt aac gcg cgc atc gga aag cca gcc cct gac ttc aag      169
    Met Ala Ser Gly Asn Ala Arg Ile Gly Lys Pro Ala Pro Asp Phe Lys
    1             5             10             15
gcc aca gcg gtg gtt gat ggc gcc ttc aaa gag gtg aag ctg tcg gac      217

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Ala	Thr	Ala	Val	Val	Asp	Gly	Ala	Phe	Lys	Glu	Val	Lys	Leu	Ser	Asp	
			20					25					30			
tac	aaa	ggg	aag	tac	gtg	gtc	ctc	ttt	ttc	tac	cct	ctg	gac	ttc	act	265
Tyr	Lys	Gly	Lys	Tyr	Val	Val	Leu	Phe	Phe	Tyr	Pro	Leu	Asp	Phe	Thr	
		35					40					45				
ttt	gtg	tgc	ccc	acc	gag	atc	atc	gcg	ttc	agc	aac	cgt	gca	gag	gac	313
Phe	Val	Cys	Pro	Thr	Glu	Ile	Ile	Ala	Phe	Ser	Asn	Arg	Ala	Glu	Asp	
		50				55					60					
ttc	cgc	aag	ctg	ggc	tgt	gaa	gtg	ctg	ggc	gtc	tcg	gtg	gac	tct	cag	361
Phe	Arg	Lys	Leu	Gly	Cys	Glu	Val	Leu	Gly	Val	Ser	Val	Asp	Ser	Gln	
		65			70				75					80		
ttc	acc	cac	ctg	gct	tgg	atc	aac	acc	ccc	cgg	aaa	gag	gga	ngc	ttg	409
Phe	Thr	His	Leu	Ala	Trp	Ile	Asn	Thr	Pro	Arg	Lys	Glu	Gly	Xaa	Leu	
			85					90					95			
ggc	ccc	ctg	aac	atc	ccc	ctg	ctt	gct	gac	gtg	acc	aga	cgc	ttg		454
Gly	Pro	Leu	Asn	Ile	Pro	Leu	Leu	Ala	Asp	Val	Thr	Arg	Arg	Leu		
		100						105					110			

<210> 1062  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 231..392

<400> 1062															
accggctgtc	gtaaaacggt	gaatggagag	cgagtkgkkg	gggggaaaaa	gggaggmcag		60								
ggggcgcgga	gtcagagtgg	cgcasaagtg	gccgcaggtk	gcgacggtgg	cgggggggtgg		120								
ggtgtgaggt	aatccagggg	tcgcggaaga	ggaggctgag	agggtcaaaa	gaaaactaaa		180								
gctgcagtcc	ggcctactgt	tccggggggc	gcggaccccc	acccgggggag	atg gac		236								
					Met Asp										
					1										
ctc aac cgg atc atc cag gcg ctg agg cac cat cga ccc gaa gtt gcg							284								
Leu Asn Arg Ile Ile Gln Ala Leu Arg His His Arg Pro Glu Val Ala															
	5			10		15									
gat tgc agc cga gaa cga gct caa cca gtc cta caa gat tat caa ttt							332								
Asp Cys Ser Arg Glu Arg Ala Gln Pro Val Leu Gln Asp Tyr Gln Phe															
	20			25		30									
tgc ccc cag ttt act tcg nat tat agt ctc tgr nca tgt gga ttc cag							380								
Cys Pro Gln Phe Thr Ser Xaa Tyr Ser Leu Xaa Xaa Cys Gly Phe Gln															
	35			40		45	50								
tac gac agg cag c															
Tyr Asp Arg Gln							393								

<210> 1063  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 87..482

<400> 1063

tntctcttcc tccccgcctc cagctgccgg caggaccttt ctctcgctgc cgctgggacc 60  
ccgtgtcatc gcccaggccg agcacg atg ccc cct aaa aag gga ggt gat gga 113  
Met Pro Pro Lys Lys Gly Gly Asp Gly  
1 5  
att aaa cca ccc cca atc att gga aga ttt gga acc tca ctg aaa att 161  
Ile Lys Pro Pro Pro Ile Ile Gly Arg Phe Gly Thr Ser Leu Lys Ile  
10 15 20 25  
ggt att gtt gga ttg cca aat gtt ggg aaa tct act ttc ttc aat gtg 209  
Gly Ile Val Gly Leu Pro Asn Val Gly Lys Ser Thr Phe Phe Asn Val  
30 35 40  
tta acc aat agt cag gct tca gca gaa aac ttc ccg ttc tgc act att 257  
Leu Thr Asn Ser Gln Ala Ser Ala Glu Asn Phe Pro Phe Cys Thr Ile  
45 50 55  
gat cct aat gag agc aga gta cct gtg cca gat gaa agg ttt gac ttt 305  
Asp Pro Asn Glu Ser Arg Val Pro Val Pro Asp Glu Arg Phe Asp Phe  
60 65 70  
ctt tgt caa tac cac aaa cca gca agc aaa att cct gcc ttt cta aat 353  
Leu Cys Gln Tyr His Lys Pro Ala Ser Lys Ile Pro Ala Phe Leu Asn  
75 80 85  
gtg gtg gat att gct ggc ctt gtg aaa gga gct cac aat ggg cag ggc 401  
Val Val Asp Ile Ala Gly Leu Val Lys Gly Ala His Asn Gly Gln Gly  
90 95 100 105  
ctg ggg aat gct ttt tta tct cat att agt gcc tgt gat ggc atc ttt 449  
Leu Gly Asn Ala Phe Leu Ser His Ile Ser Ala Cys Asp Gly Ile Phe  
110 115 120  
cat cta aca cgt gct ttt gaa gat gat gat atc a 483  
His Leu Thr Arg Ala Phe Glu Asp Asp Ile  
125 130

<210> 1064

<211> 254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..254

<400> 1064

aaaaagggca ggcacgcgg ggctggccac ttccgtactt ccgctttccg gcccagccag 60  
cgcccgcg atg act gcc act ctc cgc ccc tac ctg agt gcc gtg cgg gcc 110  
Met Thr Ala Thr Leu Arg Pro Tyr Leu Ser Ala Val Arg Ala  
1 5 10  
aca ttg cag gct gmc ctc tgc ctg gag aac ttc tcc tcc cag gtt gtg 158  
Thr Leu Gln Ala Xaa Leu Cys Leu Glu Asn Phe Ser Ser Gln Val Val  
15 20 25 30  
gaa cga cac aac aag ccg gaa gtg gaa gtc agg agt agc aaa gag ctc 206  
Glu Arg His Asn Lys Pro Glu Val Glu Val Arg Ser Ser Lys Glu Leu  
35 40 45



# DRAFT

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<220>  
<221> CDS  
<222> 103..351
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<210> 1066
<211> 494
<212> DNA
<213> Homo sapiens
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<400> 1066
agtagtactt tccggcggtt ttgaccctat tcccgtgct gcaccgcrsc cttttctctt      60
ccggttctag gcgcttcggg agccgcggct tatggtgcag ac atg gcc aag tcc      114
                                     Met Ala Lys Ser
                                     1
aag aac cac acc aca cac aac cag tcc cga aaa tgg cac aga aat ggt      162
Lys Asn His Thr Thr His Asn Gln Ser Arg Lys Trp His Arg Asn Gly
5          10          15          20
atc aag aaa ccc cga tca caa aga tac gaa tct ctt aag ggg gtg gac      210

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Ile Lys Lys Pro Arg Ser Gln Arg Tyr Glu Ser Leu Lys Gly Val Asp
      25                      30                      35
ccc aag ttc ctg agg aac atg cgc ttt gcc aag aag cac aac aaa aag      258
Pro Lys Phe Leu Arg Asn Met Arg Phe Ala Lys Lys His Asn Lys Lys
      40                      45                      50
ggc cta aag aag atg cag gcc aac aat gcc aag gcc atg agt gca cgt      306
Gly Leu Lys Lys Met Gln Ala Asn Asn Ala Lys Ala Met Ser Ala Arg
      55                      60                      65
gcc gag gct atc aag gcc ctc gta aag ccc aag gag gtt aag ccc aag      354
Ala Glu Ala Ile Lys Ala Leu Val Lys Pro Lys Glu Val Lys Pro Lys
      70                      75                      80
atc cca aag ggt gtc agc cgc aag ctc gat cga ctt gcc tac att gcc      402
Ile Pro Lys Gly Val Ser Arg Lys Leu Asp Arg Leu Ala Tyr Ile Ala
      85                      90                      95                      100
cac ccc aag ctt ggg aag cgt gct cgt gcc cgt att gcc aag ggg ctc      450
His Pro Lys Leu Gly Lys Arg Ala Arg Ala Arg Ile Ala Lys Gly Leu
      105                      110                      115
agg ctg tgc cgg cca aag gcc aag gcc aag gcc aag gcc aag ga      494
Arg Leu Cys Arg Pro Lys Ala Lys Ala Lys Ala Lys Lys
      120                      125                      130

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<210> 1067  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 134..358

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<400> 1067
acttagggac ctgctgggggt gcggggaaaaa ggcgagctct cggtgggatt gcgtgcagga      60
gggtcgtggt ctggctgtgg cggaggagca taagaagact ctgcggtgga gctgtggaag      120
ccaggcgcac agg atg caa gca gcc agg ccc agg gag gca gca gct gca      169
      Met Gln Ala Ala Arg Pro Arg Glu Ala Ala Ala
      1                      5                      10
tcc tca gag agg aag cca gga tgc ccc act ctg ctg ggg gta ctg cag      217
Ser Ser Glu Arg Lys Pro Gly Cys Pro Thr Leu Leu Gly Val Leu Gln
      15                      20                      25
ggg tgg ggc tgg agg ctg cag agc cca cag ccc tgc tca cca ggg cag      265
Gly Trp Gly Trp Arg Leu Gln Ser Pro Gln Pro Cys Ser Pro Gly Gln
      30                      35                      40
agc ccc ctt cag aac cca cag aga tcc gtc cac aaa agc gga aaa agg      313
Ser Pro Leu Gln Asn Pro Gln Arg Ser Val His Lys Ser Gly Lys Arg
      45                      50                      55                      60
ggc cag ccc cca aaa tgc tgg kga acg agc tat gca gcg tgt gtg gg      360
Gly Gln Pro Pro Lys Cys Trp Xaa Thr Ser Tyr Ala Ala Cys Val
      65                      70                      75

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<210> 1068  
 <211> 497  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 120..497

<400> 1068

ctctggcgag ctttgcggttc cctgtgcgcc ggaagtgatc ccctgcgtgg ctgggctgct	60
cgggttagat cgtcaggaaa agcctaaaga ttagactgta agaaaagaaa atagaagcc	119
atg ttt cga aga cct gta tta cag gta ctt cgt cag ttt gta aga cat	167
Met Phe Arg Arg Pro Val Leu Gln Val Leu Arg Gln Phe Val Arg His	
1 5 10 15	
gag tcc gaa aca act acc agt ttg gtt ctt gaa aga tcc ctg aat cgt	215
Glu Ser Glu Thr Thr Thr Ser Leu Val Leu Glu Arg Ser Leu Asn Arg	
20 25 30	
gtg cac tta ctt ggg cga gtg ggt cag gac cct gtc ttg aga cag gtg	263
Val His Leu Leu Gly Arg Val Gly Gln Asp Pro Val Leu Arg Gln Val	
35 40 45	
gaa gga aaa aat cca gtc aca ata ttt tct cta gca act aat gag atg	311
Glu Gly Lys Asn Pro Val Thr Ile Phe Ser Leu Ala Thr Asn Glu Met	
50 55 60	
tgg cga tca ggg gat agt gaa gtt tac caa ctg ggt gat gtc agt caa	359
Trp Arg Ser Gly Asp Ser Glu Val Tyr Gln Leu Gly Asp Val Ser Gln	
65 70 75 80	
aag aca aca tgg cac aga ata tca gta ttc cgg cca ggc ctc aga gac	407
Lys Thr Thr Trp His Arg Ile Ser Val Phe Arg Pro Gly Leu Arg Asp	
85 90 95	
gtg gca tat caa tat gtg aaa aag ggg tct cga att tat ttg gaa ggg	455
Val Ala Tyr Gln Tyr Val Lys Lys Gly Ser Arg Ile Tyr Leu Glu Gly	
100 105 110	
aaa ata gac tat ggt gaa tac atg gat aaa aat aat gtg agg	497
Lys Ile Asp Tyr Gly Glu Tyr Met Asp Lys Asn Asn Val Arg	
115 120 125	

<210> 1069  
 <211> 446  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 237..446

<400> 1069

gactccattt tgtaggccgc ttatttgtgt gcatccacgg cgattcttcc cgcagagttg	60
tgaagcgaaa ggcttacaat taaaaggaag aaaaaaaat aaagataatt cgggagtaca	120
attgacaaaag cgtgtgggtc gctcagcctc cagcagtaac tgctgatctc cagttcttgg	180
agggttccgg tgagaagaac gccctactg cgggtactgag gaagcggcag gaggag atg	239
Met	
1	
cgg ccc ctg gac ata gac gag gtg gaa gcg cct gag gaa gtg gag gtg	287
Arg Pro Leu Asp Ile Asp Glu Val Glu Ala Pro Glu Glu Val Glu Val	
5 10 15	

ctg gag ccc gag gag gat ttc gag cag ttc ctg ctc ccg gtc atc aac	335
Leu Glu Pro Glu Glu Asp Phe Glu Gln Phe Leu Leu Pro Val Ile Asn	
20 25 30	
gag atg cgc gag gac atc gcg tct ctt ata cgc gag cac ggg cgg gcg	383
Glu Met Arg Glu Asp Ile Ala Ser Leu Ile Arg Glu His Gly Arg Ala	
35 40 45	
tac ctg cgg acc agg agc aag ctg tgg gag atg gac aat atg ctt atc	431
Tyr Leu Arg Thr Arg Ser Lys Leu Trp Glu Met Asp Asn Met Leu Ile	
50 55 60 65	
cag atc aaa acg cag	446
Gln Ile Lys Thr Gln	
70	

<210> 1070  
 <211> 279  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 64..279

<400> 1070	
atttttttttg ttcgccgtta ctctgcgcac atcgctattg cggttccgag gcagtgggaa	60
gag atg cgg ccc ctg gac atc gtc gag ctg gcg gaa ccg gag gaa gtg	108
Met Arg Pro Leu Asp Ile Val Glu Leu Ala Glu Pro Glu Glu Val	
1 5 10 15	
gag gtg ctg gag ccc gag gag gat ttc gag cag ttt ctg ctc ccg gtc	156
Glu Val Leu Glu Pro Glu Glu Asp Phe Glu Gln Phe Leu Leu Pro Val	
20 25 30	
atc aac gag atg cgc gag gac atc gcg tgc ctg acg cgc gag cac ggg	204
Ile Asn Glu Met Arg Glu Asp Ile Ala Ser Leu Thr Arg Glu His Gly	
35 40 45	
cgg gcg tac ctg cgg aac cgg agc aag cag tgg gaa gag atg cgg ccc	252
Arg Ala Tyr Leu Arg Asn Arg Ser Lys Gln Trp Glu Glu Met Arg Pro	
50 55 60	
ctg gac atc gtc gaa skg gcg gaa acg	279
Leu Asp Ile Val Glu Xaa Ala Glu Thr	
65 70	

<210> 1071  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 64..291

<400> 1071	
atttttttttg ttcgccgtta ctctgcgcac atcgctattg cggttccgag gcagtgggaa	60
gag atg cgg ccc ctg gac atc gtc gag ctg gcg gaa ccg gag gaa gtg	108

Met	Arg	Pro	Leu	Asp	Ile	Val	Glu	Leu	Ala	Glu	Pro	Glu	Glu	Val		
1				5				10					15			
gag	gtg	ctg	gag	ccc	gag	gat	ttc	gag	cag	ttt	ctg	ctc	ccg	gtc		156
Glu	Val	Leu	Glu	Pro	Glu	Glu	Asp	Phe	Glu	Gln	Phe	Leu	Leu	Pro	Val	
			20					25				30				
atc	aac	gag	atg	cgc	gag	gac	atc	gcg	tcg	ctg	acg	cgc	gag	cac	ggg	204
Ile	Asn	Glu	Met	Arg	Glu	Asp	Ile	Ala	Ser	Leu	Thr	Arg	Glu	His	Gly	
		35						40				45				
cgg	gcg	tac	ctg	cgg	aac	cgg	agc	aag	ctg	tgg	gag	atg	gac	aat	atg	252
Arg	Ala	Tyr	Leu	Arg	Asn	Arg	Ser	Lys	Leu	Trp	Glu	Met	Asp	Asn	Met	
		50					55				60					
ctc	atc	cag	atc	aaa	acg	cag	gtg	gag	gcc	tcg	aag	gag	a			292
Leu	Ile	Gln	Ile	Lys	Thr	Gln	Val	Glu	Ala	Ser	Lys	Glu				
	65					70				75						

<210> 1072  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 179..391

<400>	1072															
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gttgaaaaag	ggtaaaagtt	ttcaggaata	ttcgggctct	ctattgctaa	gcatagcgag											120
tgctgggttt	ctctctccaa	cagacatcgc	tattgcgggt	ccgaggcagt	gggaagag											178
atg	cgg	ccc	ctg	gac	atc	gtc	gag	ctg	gcg	gaa	ccg	gag	gaa	gtg	gag	226
Met	Arg	Pro	Leu	Asp	Ile	Val	Glu	Leu	Ala	Glu	Pro	Glu	Glu	Val	Glu	
1			5					10					15			
gtg	ctg	gag	ccc	gag	gat	ttc	gag	cag	ttt	ctg	ctc	ccg	gtc	atc		274
Val	Leu	Glu	Pro	Glu	Glu	Asp	Phe	Glu	Gln	Phe	Leu	Leu	Pro	Val	Ile	
			20					25				30				
aac	gag	atg	cgc	gag	gac	atc	gcg	tcg	ctg	acg	cgc	gan	cac	ggg	cgg	322
Asn	Glu	Met	Arg	Glu	Asp	Ile	Ala	Ser	Leu	Thr	Arg	Xaa	His	Gly	Arg	
		35					40					45				
gcg	tac	ctg	cgg	aac	cgg	agc	aag	ctg	tgg	gag	atg	gac	aat	atg	ctc	370
Ala	Tyr	Leu	Arg	Asn	Arg	Ser	Lys	Leu	Trp	Glu	Met	Asp	Asn	Met	Leu	
	50					55				60						
atc	cag	atc	aaa	acg	cag	gtg										391
Ile	Gln	Ile	Lys	Thr	Gln	Val										
	65					70										

<210> 1073  
 <211> 472  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 76..471

**SECRET**

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<210> 1074
<211> 435
<212> DNA
<213> Homo sapiens
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<400> 1074																	
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Met Glu Val																	
1																	
aaa ggg aaa aag caa ttc aca gga aag art aca aag aca gca caa gaa																	106
Lys Gly Lys Lys Gln Phe Thr Gly Lys Xaa Thr Lys Thr Ala Gln Glu																	
5 10 15																	
aaa aac aga ttt cat aaa aat agt gat tct ggt tct tca aag aca ttt																	154
Lys Asn Arg Phe His Lys Asn Ser Asp Ser Gly Ser Ser Lys Thr Phe																	
20 25 30 35																	
cca aca agg aaa gtt gct aaa gaa ggt gga cct aaa gtc aca tct agg																	202
Pro Thr Arg Lys Val Ala Lys Glu Gly Gly Pro Lys Val Thr Ser Arg																	
40 45 50																	

aac ttt gag aaa agt atc aca aaa ctt ggg aaa aag ggt gta aag cag	250
Asn Phe Glu Lys Ser Ile Thr Lys Leu Gly Lys Lys Gly Val Lys Gln	
55 60 65	
ttc aag aat aag cag caa ggg gac aaa tca cca aag aac aaa ttc cag	298
Phe Lys Asn Lys Gln Gln Gly Asp Lys Ser Pro Lys Asn Lys Phe Gln	
70 75 80	
ccg gca aat aaa ttc aac aag aag aga aaa ttc cag cca gat ggt aga	346
Pro Ala Asn Lys Phe Asn Lys Lys Arg Lys Phe Gln Pro Asp Gly Arg	
85 90 95	
agc gat gaa tca gca gcc aag aag ccc aaa tgg gat gac ttc aaa aag	394
Ser Asp Glu Ser Ala Ala Lys Lys Pro Lys Trp Asp Asp Phe Lys Lys	
100 105 110 115	
aag aag aaa gaa ctg aag caa agc aga caa ctc agt gat aa	435
Lys Lys Lys Glu Leu Lys Gln Ser Arg Gln Leu Ser Asp	
120 125	

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 70..357

<400> 1075	
cgggggcggtg gttgcatcag attctaggaa gtgtctgtag ccgcagctgc ggggtccggga	60
ttcccagcc atg gca gat tcc tcc ggg cag cag ggc aaa ggc cgg cgt gtg	111
Met Ala Asp Ser Ser Gly Gln Gln Gly Lys Gly Arg Arg Val	
1 5 10	
cag ccc cag tgg tcc cct cct gct ggg acc cag cca tgc aga ctc cac	159
Gln Pro Gln Trp Ser Pro Pro Ala Gly Thr Gln Pro Cys Arg Leu His	
15 20 25 30	
ctt tac aac agc ctc acc agg aac aag gaa gtg ttc ata cct caa gat	207
Leu Tyr Asn Ser Leu Thr Arg Asn Lys Glu Val Phe Ile Pro Gln Asp	
35 40 45	
ggg aaa aag gtg acg tgg tat tgc tgt ggg cca acc gtc tat gac gca	255
Gly Lys Lys Val Thr Trp Tyr Cys Cys Gly Pro Thr Val Tyr Asp Ala	
50 55 60	
tct cac atg ggg cac gcc agg tcc tac atc tct ttt gat atc ttg aga	303
Ser His Met Gly His Ala Arg Ser Tyr Ile Ser Phe Asp Ile Leu Arg	
65 70 75	
aga gtg ttg aag gat tac ttc aaa ttt gat gtc ttt tat tgc rtg aac	351
Arg Val Leu Lys Asp Tyr Phe Lys Phe Asp Val Phe Tyr Cys Xaa Asn	
80 85 90	
att acg	357
Ile Thr	
95	

<210> 1076  
 <211> 462  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 280..462

<400> 1076

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atTTTTtTgc ttccatgacc aaagaagatt ctaaacttat agctctcata tggcccagtg      60
agtggcaaat gatacaaaag ctctttgttg tggatcatgt aattaaaatc acgaagaatt      120
gaagtgggag atgtaaacc ctcagaaaca cagtatatatt ctgagcccaa actctgtcca      180
gaatgcagag aaggcttatt gtgtcagcag cagagggacc tgcgtgaata cactcaagcc      240
accatctatg tccataaagt tgtggataat aaaaagggtg atg aag gat tgc gct      294
                                   Met Lys Asp Ser Ala
                                   1         5
ccg gaa ctg aat gtg agt agt tct gaa aca gag nwg gac aag gaa gaa      342
Pro Glu Leu Asn Val Ser Ser Ser Glu Thr Glu Xaa Asp Lys Glu Glu
                                   10        15        20
gct aaa cca gat gga gaa nna ant tna gat ttt aat caa agc aat ggt      390
Ala Lys Pro Asp Gly Glu Xaa Xaa Xaa Asp Phe Asn Gln Ser Asn Gly
                                   25        30        35
gga aca aag cgg caa aag ata tcc cat caa aat tat ata gcc tat caa      438
Gly Thr Lys Arg Gln Lys Ile Ser His Gln Asn Tyr Ile Ala Tyr Gln
                                   40        45        50
agc aag tta ttc gcc gaa gta tgc      462
Ser Lys Leu Phe Ala Glu Val Cys
                                   55        60

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<210> 1077  
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<400> 1077

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agtatgtagg catctttcat tcagaatgga cattaatatc ttgaatagag aagaaagctt      120
ttagaaatgt atcatttgtc aaaattgcat gccttttaaa aaatgataaa gagagatgct      180
gagtgttttg tatgttagca tgcactcttt ctttttatatt ctgttcagac tcaagttttt      240
agaagctaga atatagatcc cttaagaaa aaaaaaggaa gaaagaagaa tttgctgttg      300
acatcacttg ttagaagagc aactctgaaa gaaaacgagc aaattccaaa atatgaaaag      360
attcacaatt tcaaggtgca tacattcaga gggccacact ggtgtgaata ctgtgccaac      420
tttatgtggg gtctcattgc tcagggagtg aa atg tgc aga ttg tgg ttt gaa      473
                                   Met Cys Arg Leu Trp Phe Glu
                                   1         5
tgt tca aag cag tgt tcc aag atg gtc cca aat gac tgt aag cca gac      521
Cys Ser Lys Gln Cys Ser Lys Met Val Pro Asn Asp Cys Lys Pro Asp
                                   10        15        20
ttg aag cat gtc aaa aag gtg tac agc tgt gac ctt acg acg ctc gtg      569
Leu Lys His Val Lys Lys Val Tyr Ser Cys Asp Leu Thr Thr Leu Val
                                   25        30        35

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aaa gca cat acc act aag cgg cca atg gtg gta gac atg tgc atc agg      617
Lys Ala His Thr Thr Lys Arg Pro Met Val Val Asp Met Cys Ile Arg
40                      45                      50                      55
gag att gag tct aga ggt ctt aat tct gaa gga cta tac cga gta tca      665
Glu Ile Glu Ser Arg Gly Leu Asn Ser Glu Gly Leu Tyr Arg Val Ser
                      60                      65                      70
gga ttt agt gac cta att gaa gat gtc aag atg gct ttc gac aga gat      713
Gly Phe Ser Asp Leu Ile Glu Asp Val Lys Met Ala Phe Asp Arg Asp
                      75                      80                      85
ggt gag aag gca gat att tct gtg aac atg tat gaa gat atc aac att      761
Gly Glu Lys Ala Asp Ile Ser Val Asn Met Tyr Glu Asp Ile Asn Ile
                      90                      95                      100
atc act ggt
Ile Thr Gly
105

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<210> 1078
<211> 1126
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 479..1126

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<400> 1078
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agtatgtagg catctttcat tcagaatgga cattaatc ttgaatagag aagaaagctt      120
ttagaaatgt atcatttgct aaaattgcat gccttttaaa aaatgataaa gagagatgct      180
gagtgttttg tatgttagca tcgactcttt ctttttattt ctgttcagac tcaagttttt      240
agaagctaga atatagatcc ctttaagaaa aaaaaaggaa gaaagaagaa tttgctgggt      300
agtcgacctc tgtttaagaa gtgcttcac ctcctcctcc acctctccgt ggtgtttctc      360
tgcagctctc tgtaggttag gggtctgtgc tgctggcag aatgctcatg tgtagctga      420
atagatatca tcgacagaca tagaccacta taggttttct ttccttgtag attccaaa      478
atg cca tcc aaa gag tct tgg tca ggg agg aaa act aat agg gct gca      526
Met Pro Ser Lys Glu Ser Trp Ser Gly Arg Lys Thr Asn Arg Ala Ala
1                      5                      10                      15
gtt cac aaa tca aaa caa gag ggc cgt cag caa gat tta ttg ata gca      574
Val His Lys Ser Lys Gln Glu Gly Arg Gln Gln Asp Leu Leu Ile Ala
20                      25                      30
gcc ttg gga atg aaa ctg ggt tct cca aag tcg tct gtg aca atc tgg      622
Ala Leu Gly Met Lys Leu Gly Ser Pro Lys Ser Ser Val Thr Ile Trp
35                      40                      45
caa cct ctg aaa ctc ttt gct tat tcg cag ttg aca tca ctt gtt aga      670
Gln Pro Leu Lys Leu Phe Ala Tyr Ser Gln Leu Thr Ser Leu Val Arg
50                      55                      60
aga gca act ctg aaa gaa aac gag caa att cca aaa tat gaa aag att      718
Arg Ala Thr Leu Lys Glu Asn Glu Gln Ile Pro Lys Tyr Glu Lys Ile
65                      70                      75                      80
cac aat ttc aag gtg cat aca ttc aga ggg cca cac tgg tgt gaa tac      766
His Asn Phe Lys Val His Thr Phe Arg Gly Pro His Trp Cys Glu Tyr
85                      90                      95
tgt gcc aac ttt atg tgg ggt ctc att gct cag gga gtg aaa tgt gca      814

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Cys	Ala	Asn	Phe	Met	Trp	Gly	Leu	Ile	Ala	Gln	Gly	Val	Lys	Cys	Ala	
			100				105						110			
gat	tgt	ggt	ttg	aat	gtt	cat	aag	cag	tgt	tcc	aag	atg	gtc	cca	aat	862
Asp	Cys	Gly	Leu	Asn	Val	His	Lys	Gln	Cys	Ser	Lys	Met	Val	Pro	Asn	
			115				120						125			
gac	tgt	aag	cca	gac	ttg	aag	cat	gtc	aaa	aag	gtg	tac	agc	tgt	gac	910
Asp	Cys	Lys	Pro	Asp	Leu	Lys	His	Val	Lys	Lys	Val	Tyr	Ser	Cys	Asp	
			130				135						140			
ctt	acg	acg	ctc	gtg	aaa	gca	cat	acc	act	aag	cgg	cca	atg	gtg	gta	958
Leu	Thr	Thr	Leu	Val	Lys	Ala	His	Thr	Thr	Lys	Arg	Pro	Met	Val	Val	
			145				150						160			
gac	atg	tgc	atc	agg	gag	att	gag	tct	aga	ggg	ctt	aat	tct	gaa	gga	1006
Asp	Met	Cys	Ile	Arg	Glu	Ile	Glu	Ser	Arg	Gly	Leu	Asn	Ser	Glu	Gly	
			165							170			175			
cta	tac	cga	gta	tca	gga	ttt	agt	gac	cta	att	gaa	gat	gtc	aag	atg	1054
Leu	Tyr	Arg	Val	Ser	Gly	Phe	Ser	Asp	Leu	Ile	Glu	Asp	Val	Lys	Met	
			180				185						190			
gct	ttc	gac	aga	gat	ggg	gag	aag	gca	gat	att	tct	gtg	aac	atg	tat	1102
Ala	Phe	Asp	Arg	Asp	Gly	Glu	Lys	Ala	Asp	Ile	Ser	Val	Asn	Met	Tyr	
			195				200						205			
gaa	gat	atc	aac	att	atc	act	ggg									1126
Glu	Asp	Ile	Asn	Ile	Ile	Thr	Gly									
			210				215									

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<210> 1079
<211> 568
<212> DNA
<213> Homo sapiens
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<220>  
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<222> 202..567
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Lys	Trp	His	Asp	Lys	Gln	Tyr	Lys	Lys	Ala	His	Leu	Gly	Thr	Ala	Leu	
				25					30					35		
aag	gcc	aac	cct	ttt	gga	ggg	gct	tct	cat	gca	aaa	ggg	ttg	gcc	atc	198
Lys	Ala	Asn	Pro	Phe	Gly	Gly	Ala	Ser	His	Ala	Lys	Gly	Leu	Ala	Ile	
			40					45					50			
gct	tcc	cac	cct													210
Ala	Ser	His	Pro													
			55													

<210> 1082  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 118..414

<400> 1082																
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cctgctgtcg	ctcctggtcg	gcgcgtggct	caagctagga	aatggacagg	ctacagt											117
atg gtc caa ctg	cag ggt ggg aga	ttc ctg atg	gga aca aat	tct cca												165
Met Val Gln Leu	Gln Gly Gly Arg	Phe Leu Met	Gly Thr Asn	Ser Pro												
1	5	10	15													
gac agc aga gat	ggg gaa ggg cct	gtg cgg gag	gcg aca gtg	aaa ccc												213
Asp Ser Arg Asp	Gly Glu Gly Pro	Val Arg Glu	Ala Thr Val	Lys Pro												
	20	25	30													
ttt gcc atc gac	ata ttt cct	gtc acc aac	aaa gat ttc	agg gat ttt												261
Phe Ala Ile Asp	Ile Phe Pro	Val Thr Asn	Lys Asp Phe	Arg Asp Phe												
	35	40	45													
gtc agg gag aaa	aag tat cgg	aca gaa gct	gag atg ttt	gga tgg agc												309
Val Arg Glu Lys	Lys Tyr Arg	Thr Glu Ala	Glu Met Phe	Gly Trp Ser												
	50	55	60													
ttt gtc ttt gag	gac ttt gtc	tct gat gag	ctg aga aac	aaa gcc acc												357
Phe Val Phe Glu	Asp Phe Val	Ser Asp Glu	Leu Arg Asn	Lys Ala Thr												
	65	70	75	80												
cag cca atg aag	gtc aag ttt	acc cat ggg	gga act ggt	tcc agc caa												405
Gln Pro Met Lys	Val Lys Phe	Thr His Gly	Gly Thr Gly	Ser Ser Gln												
	85	90	95													
acc gca cca																414
Thr Ala Pro																

<210> 1083  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 38..457

<400> 1083

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                                Met Pro Gly Val Thr Val
                                1           5
aaa gac gtg aac cag cag gag ttc gtc aga gct ctg gca gcc ttc ctc      103
Lys Asp Val Asn Gln Gln Glu Phe Val Arg Ala Leu Ala Ala Phe Leu
                                10           15           20
aaa aag tcc ggg aag ctg aaa gtc ccc gaa tgg gtg gat acc gtc aag      151
Lys Lys Ser Gly Lys Leu Lys Val Pro Glu Trp Val Asp Thr Val Lys
                                25           30           35
ctg gcc aag cac aaa gag ctt gct ccc tac gat gag aac tgg ttc tac      199
Leu Ala Lys His Lys Glu Leu Ala Pro Tyr Asp Glu Asn Trp Phe Tyr
                                40           45           50
acg cga gct gct tcc aca gcg cgg cac ctg tac ctc cgg ggt ggc gct      247
Thr Arg Ala Ala Ser Thr Ala Arg His Leu Tyr Leu Arg Gly Gly Ala
55                                60           65           70
ggg gtt ggc tcc atg acc aag atc tat ggg gga cgt cag aga aac ggc      295
Gly Val Gly Ser Met Thr Lys Ile Tyr Gly Gly Arg Gln Arg Asn Gly
                                75           80           85
gtc atg ccc agc cac ttc agc cga ggc tcc aag agt gtg gcc cgc cgg      343
Val Met Pro Ser His Phe Ser Arg Gly Ser Lys Ser Val Ala Arg Arg
                                90           95           100
gtc ctc caa gcc ctg gag ggg ctg aaa atg gtg gaa aag gac caa gat      391
Val Leu Gln Ala Leu Glu Gly Leu Lys Met Val Glu Lys Asp Gln Asp
                                105           110           115
ggc ggc cgc aaa ctg aca cct cag gga caa aga gat ctg gac aga atc      439
Gly Gly Arg Lys Leu Thr Pro Gln Gly Gln Arg Asp Leu Asp Arg Ile
120           125           130
gcc gga cag tgg cag ctg c
Ala Gly Gln Trp Gln Leu
135           140

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<210> 1084  
 <211> 399  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 71..397

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<400> 1084
ctgggtgtca ttggctctgg gaagcggcag cagaggcagg gaccactcgg ggtctggtgt      60
cggcacagcc atg gcg ggc gcg ttg gtg cgg aaa gcg gcg gac tat gtc      109
          Met Ala Gly Ala Leu Val Arg Lys Ala Ala Asp Tyr Val
          1           5           10
cga agc aag gat ttc cgg gac tac ctc atg agt acg cac ttc tgg ggc      157
Arg Ser Lys Asp Phe Arg Asp Tyr Leu Met Ser Thr His Phe Trp Gly
15           20           25
cca gta gcc aac tgg ggt ctt ccc att gct gcc atc aat gat atg aaa      205
Pro Val Ala Asn Trp Gly Leu Pro Ile Ala Ala Ile Asn Asp Met Lys
30           35           40           45
aag tct cca gag att atc agt ggg cgg atg aca ttt gcc ctc tgt tgc      253
Lys Ser Pro Glu Ile Ile Ser Gly Arg Met Thr Phe Ala Leu Cys Cys

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	50		55		60	
tat tct ttg aca ttc atg aga ttt gcc tac aag gta cag cct cgg aac						301
Tyr Ser Leu Thr Phe Met Arg Phe Ala Tyr Lys Val Gln Pro Arg Asn						
	65		70		75	
tgg ctt ctg ttt gca tgc cac gca aca aat gaa gta gcc cag ctc atc						349
Trp Leu Leu Phe Ala Cys His Ala Thr Asn Glu Val Ala Gln Leu Ile						
	80		85		90	
cag gga ggg cgg ctt atc aaa cac gag atg act aaa acg gca tct gca						397
Gln Gly Gly Arg Leu Ile Lys His Glu Met Thr Lys Thr Ala Ser Ala						
	95		100		105	
ta						399

<210> 1085  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 265..594

<400> 1085  
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 attagtgaca aacagaggcc tggacagcag gttgcaactt gtgtgcgact tttaggtcgt 120  
 aattctaact ccaagaggct cttgggttat gtggcaactc tgaaggataa ttttggattt 180  
 attgaaacag ccaatcatga taaggaaatc tttttccatt acagtgagtt ctctggtgat 240  
 gttgatagcc tggaactggg ggac atg gtc gag tat agc ttg tcc aaa ggc 291  
 Met Val Glu Tyr Ser Leu Ser Lys Gly  
 1 5  
 aaa ggc aac aaa gtc agt gca gaa aaa gtg aac aaa aca cac tca gtg 339  
 Lys Gly Asn Lys Val Ser Ala Glu Lys Val Asn Lys Thr His Ser Val  
 10 15 20 25  
 aat ggc att act gag gaa gct gat ccc acc att tac tct ggc aaa gta 387  
 Asn Gly Ile Thr Glu Glu Ala Asp Pro Thr Ile Tyr Ser Gly Lys Val  
 30 35 40  
 att cgc ccc ctg agg agt gtt gat cca aca cag act gag tac caa gga 435  
 Ile Arg Pro Leu Arg Ser Val Asp Pro Thr Gln Thr Glu Tyr Gln Gly  
 45 50 55  
 atg att gag att gtg gag gag ggc gat atg aaa ggt gag gtc tat cca 483  
 Met Ile Glu Ile Val Glu Glu Gly Asp Met Lys Gly Glu Val Tyr Pro  
 60 65 70  
 ttt ggc atc gtt ggg atg gcc aac aaa ggg gat tgc ctg cag aaa ggg 531  
 Phe Gly Ile Val Gly Met Ala Asn Lys Gly Asp Cys Leu Gln Lys Gly  
 75 80 85  
 gag agc gtc aag ttc caa tts ygt gtc ctg ggc can nat cgm tgg rnc 579  
 Glu Ser Val Lys Phe Gln Xaa Xaa Val Leu Gly Xaa Xaa Arg Trp Xaa  
 90 95 100 105  
 tat ggc tta cac knc sa 596  
 Tyr Gly Leu His Xaa  
 110

<210> 1086  
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<212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 83..403

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 tttttctcaac atcctggcctt agtattgtgt gcaaaatcag agaggggtgc aagatcctga 60  
 tttttcagga gttcaagcga ca atg gca gcc caa tac ggc agt atg agc ttc 112  
 Met Ala Ala Gln Tyr Gly Ser Met Ser Phe  
 1 5 10  
 aac ccc agc aca cca ggg gcc agt tat ggg cct gga agg caa gag ccc 160  
 Asn Pro Ser Thr Pro Gly Ala Ser Tyr Gly Pro Gly Arg Gln Glu Pro  
 15 20 25  
 aga aat tcc caa ttg aga att gtg tta gtg ggt aaa acc gga gca gga 208  
 Arg Asn Ser Gln Leu Arg Ile Val Leu Val Gly Lys Thr Gly Ala Gly  
 30 35 40  
 aaa agt gca aca gga aac agc atc ctt ggc cgg aaa gtg ttt cat tct 256  
 Lys Ser Ala Thr Gly Asn Ser Ile Leu Gly Arg Lys Val Phe His Ser  
 45 50 55  
 ggc act gca gca aaa tcc att acc aag aag tgt gag aaa cgc agc agc 304  
 Gly Thr Ala Ala Lys Ser Ile Thr Lys Lys Cys Glu Lys Arg Ser Ser  
 60 65 70  
 tca tgg aag gaa aca gaa ctt gtc gta gtt gac aca cca ggc att ttc 352  
 Ser Trp Lys Glu Thr Glu Leu Val Val Val Asp Thr Pro Gly Ile Phe  
 75 80 85 90  
 gac aca gag gtg ccc aat gct gaa acg tcc aag gag att att cgc tgc 400  
 Asp Thr Glu Val Pro Asn Ala Glu Thr Ser Lys Glu Ile Ile Arg Cys  
 95 100 105  
 att ct 405  
 Ile

<210> 1087  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 17..340

<400> 1087  
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 Met Ser Gly Leu Ala Ala Thr Thr Phe His Trp Lys  
 1 5 10  
 aag tgc aga ttg gat ttg cca ggg cat gta gct ctc cag gct tgc aag 100  
 Lys Cys Arg Leu Asp Leu Pro Gly His Val Ala Leu Gln Ala Cys Lys  
 15 20 25  
 cga tta cca gat gaa cac aat gac gta cag aag aaa acc ttt acc aaa 148  
 Arg Leu Pro Asp Glu His Asn Asp Val Gln Lys Lys Thr Phe Thr Lys  
 30 35 40

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<220>  
<221> CDS  
<222> 143..340
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<210> 1089
<211> 536
<212> DNA
<213> Homo sapiens
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cgtgtagcgt cgccgttact ccgaggagat accagtcggt agaggagaag tcgagggttag 120  
 agggaaactgg gaggcacttt gctgtctgca atcgaagttg aggggtgcaaa a atg cag 177  
 Met Gln

1  
 agt aat aaa act ttt aac ttg gag aag caa aac cat act cca aga aag 225  
 Ser Asn Lys Thr Phe Asn Leu Glu Lys Gln Asn His Thr Pro Arg Lys  
 5 10 15

cat cat caa cat cac cac cag cag cag cac cac cag cag caa cag cag 273  
 His His Gln His His His Gln Gln Gln His His Gln Gln Gln Gln Gln  
 20 25 30

cag ccg cca cca ccg cca ata cct gca aat ggg caa cag gcc agc agc 321  
 Gln Pro Pro Pro Pro Pro Ile Pro Ala Asn Gly Gln Gln Ala Ser Ser  
 35 40 45 50

caa aat gaa ggc ttg act att gac ctg aag aat ttt aga aaa cca gga 369  
 Gln Asn Glu Gly Leu Thr Ile Asp Leu Lys Asn Phe Arg Lys Pro Gly  
 55 60 65

gag aag acc ttc acc caa cga agc cgt ctt ttt gtg gga aat ctt cct 417  
 Glu Lys Thr Phe Thr Gln Arg Ser Arg Leu Phe Val Gly Asn Leu Pro  
 70 75 80

ccc gac atc act gag gaa gaa atg agg waa cta ttt gag aaa tat gga 465  
 Pro Asp Ile Thr Glu Glu Glu Met Arg Xaa Leu Phe Glu Lys Tyr Gly  
 85 90 95

aag gca ggc gaa gtc wtc att cat aag gwt aaa gga ttt ggc ttw atc 513  
 Lys Ala Gly Glu Val Xaa Ile His Lys Xaa Lys Gly Phe Gly Xaa Ile  
 100 105 110

cgc ttg gaa acc cga acc cta gc 536  
 Arg Leu Glu Thr Arg Thr Leu  
 115 120

<210> 1090  
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 <212> DNA  
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 agggaaactgg gaggcacttt gctgtctgca atcgaagttg agaggcccag tatttaggcg 180  
 acagtgaatt tattactctg aagagggttc tgcacatatt tccaaattat attggtggtc 240  
 atcagaagta ggtgatagga agaaatactt ctcaagggtg caaaa atg cag agt aat 297  
 Met Gln Ser Asn

1  
 aaa act ttt aac ttg gag aag caa aac cat act cca aga aag cat cat 345  
 Lys Thr Phe Asn Leu Glu Lys Gln Asn His Thr Pro Arg Lys His His  
 5 10 15 20

caa cat cac cac cag cag cag cac cac cag cag caa cag cag cag ccg 393  
 Gln His His His Gln Gln Gln His His Gln Gln Gln Gln Gln Pro  
 25 30 35

cca sca mcg cca ata cct gca aat ggg caa cag gcc agc agc caa aat 441

Pro	Xaa	Xaa	Pro	Ile	Pro	Ala	Asn	Gly	Gln	Gln	Ala	Ser	Ser	Gln	Asn	
			40					45					50			
gaa	ggc	ttg	act	att	gac	ctg	aag	aat	ttt	aga	aaa	cca	gga	gag	aag	489
Glu	Gly	Leu	Thr	Ile	Asp	Leu	Lys	Asn	Phe	Arg	Lys	Pro	Gly	Glu	Lys	
		55					60					65				
acc	ttc	acc	caa	cga	agc	cgt	ctt	ttt	gtg	gga	aat	ctt	cct	ccc	gac	537
Thr	Phe	Thr	Gln	Arg	Ser	Arg	Leu	Phe	Val	Gly	Asn	Leu	Pro	Pro	Asp	
	70					75				80						
atc	act	gag	gaa	gaa	atg	agg	waa	cta	ttt	gag	aaa	tat	gga	aag	gca	585
Ile	Thr	Glu	Glu	Glu	Met	Arg	Xaa	Leu	Phe	Glu	Lys	Tyr	Gly	Lys	Ala	
85					90					95					100	
ggc	gaa	gtc	wtc	att	cat	aag	gwt	aaa	gga	ttt	ggc	ttw	atc	cgc	ttg	633
Gly	Glu	Val	Xaa	Ile	His	Lys	Xaa	Lys	Gly	Phe	Gly	Xaa	Ile	Arg	Leu	
			105						110					115		
gaa	acc	cga	acc	cta	gc											650
Glu	Thr	Arg	Thr	Leu												
			120													

<210> 1091  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 83..445

<400> 1091																
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cagtcggtag	aggggtgcaa	aa	atg	cag	agt	aat	aaa	act	ttt	aac	ttg	gag				112
			Met	Gln	Ser	Asn	Lys	Thr	Phe	Asn	Leu	Glu				
			1				5				10					
aag	caa	aac	cat	act	cca	aga	aag	cat	cat	caa	cat	cac	cac	cag	cag	160
Lys	Gln	Asn	His	Thr	Pro	Arg	Lys	His	His	Gln	His	His	His	Gln	Gln	
			15					20					25			
cag	cac	cac	cag	cag	caa	cag	cag	cag	ccg	cca	cca	ccg	cca	ata	cct	208
Gln	His	His	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ile	Pro	
			30				35					40				
gca	aat	ggg	caa	cag	gcc	agc	agc	caa	aat	gaa	ggc	ttg	act	att	gac	256
Ala	Asn	Gly	Gln	Gln	Ala	Ser	Ser	Gln	Asn	Glu	Gly	Leu	Thr	Ile	Asp	
	45					50					55					
ctg	aag	aat	ttt	aga	aaa	cca	gga	gag	aag	acc	ttc	acc	caa	cga	agc	304
Leu	Lys	Asn	Phe	Arg	Lys	Pro	Gly	Glu	Lys	Thr	Phe	Thr	Gln	Arg	Ser	
	60				65					70						
cgt	ctt	ttt	gtg	gga	aat	ctt	cct	ccc	gac	atc	act	gag	gaa	gaa	atg	352
Arg	Leu	Phe	Val	Gly	Asn	Leu	Pro	Pro	Asp	Ile	Thr	Glu	Glu	Glu	Met	
	75				80					85					90	
agg	waa	cta	ttt	gag	aaa	tat	gga	aag	gca	ggc	gaa	gtc	wtc	att	cat	400
Arg	Xaa	Leu	Phe	Glu	Lys	Tyr	Gly	Lys	Ala	Gly	Glu	Val	Xaa	Ile	His	
			95				100							105		
aag	gwt	aaa	gga	ttt	ggc	ttw	atc	cgc	ttg	gaa	acc	cga	acc	cta	gc	447
Lys	Xaa	Lys	Gly	Phe	Gly	Xaa	Ile	Arg	Leu	Glu	Thr	Arg	Thr	Leu		
			110				115							120		

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 279..641

<400> 1092  
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 cgtgtagcgt cgccgttatc cgaggagata ccagtcggta gaggagaagt cgaggtaga 120  
 gggaaactggg aggcactttg ctgtctgcaa tcgaagtga gatggagttt cactcttgtg 180  
 caatggcaca atctcggctc acggcaacct ccgcctccca ggttcaagtg attctcctgg 240  
 ctcagcctcc tgagtaactg ggattacagg gtgcaaaa atg cag agt aat aaa act 296  
 Met Gln Ser Asn Lys Thr  
 1 5  
 ttt aac ttg gag aag caa aac cat act cca aga aag cat cat caa cat 344  
 Phe Asn Leu Glu Lys Gln Asn His Thr Pro Arg Lys His His Gln His  
 10 15 20  
 cac cac cag cag cag cac cac cag cag caa cag cag cag ccg cca cca 392  
 His His Gln Gln Gln His His Gln Gln Gln Gln Gln Gln Pro Pro Pro  
 25 30 35  
 ccg cca ata cct gca aat ggg caa cag gcc agc agc caa aat gaa ggc 440  
 Pro Pro Ile Pro Ala Asn Gly Gln Gln Ala Ser Ser Gln Asn Glu Gly  
 40 45 50  
 ttg act att gac ctg aag aat ttt aga aaa cca gga gag aag acc ttc 488  
 Leu Thr Ile Asp Leu Lys Asn Phe Arg Lys Pro Gly Glu Lys Thr Phe  
 55 60 65 70  
 acc caa cga agc cgt ctt ttt gtg gga aat ctt cct ccc gac atc act 536  
 Thr Gln Arg Ser Arg Leu Phe Val Gly Asn Leu Pro Pro Asp Ile Thr  
 75 80 85  
 gag gaa gaa atg agg waa cta ttt gag aaa tat gga aag gca ggc gaa 584  
 Glu Glu Glu Met Arg Xaa Leu Phe Glu Lys Tyr Gly Lys Ala Gly Glu  
 90 95 100  
 gtc wtc att cat aag gwt aaa gga ttt ggc ttw atc cgc ttg gaa acc 632  
 Val Xaa Ile His Lys Xaa Lys Gly Phe Gly Xaa Ile Arg Leu Glu Thr  
 105 110 115  
 cga acc cta gc 643  
 Arg Thr Leu  
 120

<210> 1093  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 247..609

&lt;400&gt; 1093

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agtcggtaga ggagaagtcg aggttagagg gaactgggag gcactttgct gtctgcaatc      120
gaagttgaga tggagtttca ctcttggtgca atggcacaat ctcgggtcac ggcaacctcc      180
gcctcccagg ttcaagtgat tctcctggct cagcctcctg agtaactggg attacagggg      240
gcaaaa atg cag agt aat aaa act ttt aac ttg gag aag caa aac cat      288
      Met Gln Ser Asn Lys Thr Phe Asn Leu Glu Lys Gln Asn His
          1             5             10
act cca aga aag cat cat caa cat cac cac cag cag cag cac cac cag      336
Thr Pro Arg Lys His His Gln His His His Gln Gln Gln His His Gln
15             20             25             30
cag caa cag cag cag ccg cca cca ccg cca ata cct gca aat ggg caa      384
Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Ile Pro Ala Asn Gly Gln
          35             40             45
cag gcc agc agc caa aat gaa ggc ttg act att gac ctg aag aat ttt      432
Gln Ala Ser Ser Gln Asn Glu Gly Leu Thr Ile Asp Leu Lys Asn Phe
          50             55             60
aga aaa cca gga gag aag acc ttc acc caa cga agc cgt ctt ttt gtg      480
Arg Lys Pro Gly Glu Lys Thr Phe Thr Gln Arg Ser Arg Leu Phe Val
          65             70             75
gga aat ctt cct ccc gac atc act gag gaa gaa atg agg waa cta ttt      528
Gly Asn Leu Pro Pro Asp Ile Thr Glu Glu Glu Met Arg Xaa Leu Phe
          80             85             90
gag aaa tat gga aag gca ggc gaa gtc wtc att cat aag gwt aaa gga      576
Glu Lys Tyr Gly Lys Ala Gly Glu Val Xaa Ile His Lys Xaa Lys Gly
          95             100             105             110
ttt ggc ttw atc cgc ttg gaa acc cga acc cta gc      611
Phe Gly Xaa Ile Arg Leu Glu Thr Arg Thr Leu
          115             120

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&lt;210&gt; 1094

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 18..710

&lt;400&gt; 1094

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gatttgatat caaatca atg gca ggg aac att att cct gct att gct act      50
      Met Ala Gly Asn Ile Ile Pro Ala Ile Ala Thr
          1             5             10
act aat gca gta att gct ggg ttg ata gta ntg gaa gga ttg aag att      98
Thr Asn Ala Val Ile Ala Gly Leu Ile Val Xaa Glu Gly Leu Lys Ile
          15             20             25
tta tca gga aaa ata gac cag tgc aga aca att ttt ttg aat aaa caa      146
Leu Ser Gly Lys Ile Asp Gln Cys Arg Thr Ile Phe Leu Asn Lys Gln
          30             35             40
cca aac cca aga aag aag ctt ctt gtg cct tgt gca ctg gat cct ccc      194
Pro Asn Pro Arg Lys Lys Leu Leu Val Pro Cys Ala Leu Asp Pro Pro
          45             50             55
aac ccc aat tgt tat gta tgt gcc agc aag cca gag gtg act gtg cgg      242

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Asn	Pro	Asn	Cys	Tyr	Val	Cys	Ala	Ser	Lys	Pro	Glu	Val	Thr	Val	Arg		
60					65					70					75		
ctg	aat	gtc	cat	aaa	gtg	act	gtt	ctc	acc	tta	caa	gac	aag	ata	gtg		290
Leu	Asn	Val	His	Lys	Val	Thr	Val	Leu	Thr	Leu	Gln	Asp	Lys	Ile	Val		
			80						85					90			
aaa	gaa	aaa	ttt	gct	atg	gta	gca	cca	gat	gtc	caa	att	gaa	gat	ggg		338
Lys	Glu	Lys	Phe	Ala	Met	Val	Ala	Pro	Asp	Val	Gln	Ile	Glu	Asp	Gly		
			95					100					105				
aaa	gga	aca	atc	cta	ata	tct	tcc	gaa	gag	gga	gag	acg	gaa	gct	aat		386
Lys	Gly	Thr	Ile	Leu	Ile	Ser	Ser	Glu	Glu	Gly	Glu	Thr	Glu	Ala	Asn		
		110					115					120					
aat	cac	aag	aag	ttg	tca	gaa	ttt	gga	att	aga	aat	ggc	agc	cgg	ctt		434
Asn	His	Lys	Lys	Leu	Ser	Glu	Phe	Gly	Ile	Arg	Asn	Gly	Ser	Arg	Leu		
		125				130					135						
caa	gca	gat	gac	ttc	ctc	cag	gac	tat	act	tta	ttg	atc	aac	atc	ctt		482
Gln	Ala	Asp	Asp	Phe	Leu	Gln	Asp	Tyr	Thr	Leu	Leu	Ile	Asn	Ile	Leu		
140				145						150					155		
cat	agt	gaa	gac	cta	gga	aag	gac	gtt	gaa	ttt	gaa	gtt	gtt	ggt	gat		530
His	Ser	Glu	Asp	Leu	Gly	Lys	Asp	Val	Glu	Phe	Glu	Val	Val	Gly	Asp		
			160					165						170			
gcc	ccg	gaa	aaa	gtg	ggg	ccc	aaa	caa	gct	gaa	gat	gct	gcc	aaa	agc		578
Ala	Pro	Glu	Lys	Val	Gly	Pro	Lys	Gln	Ala	Glu	Asp	Ala	Ala	Lys	Ser		
			175				180					185					
ata	acc	aat	ggc	agt	gat	gat	gga	gct	cag	ccc	tcc	acc	tcc	aca	gct		626
Ile	Thr	Asn	Gly	Ser	Asp	Asp	Gly	Ala	Gln	Pro	Ser	Thr	Ser	Thr	Ala		
		190				195					200						
caa	gag	caa	gat	gac	gtt	ctc	ata	gtt	gat	tcg	gat	gaa	gaa	gat	tct		674
Gln	Glu	Gln	Asp	Asp	Val	Leu	Ile	Val	Asp	Ser	Asp	Glu	Glu	Asp	Ser		
		205				210				215							
tca	aat	aat	gcc	gac	gtc	agt	gaa	gaa	gag	aga	agc	c					711
Ser	Asn	Asn	Ala	Asp	Val	Ser	Glu	Glu	Glu	Arg	Ser						
220					225					230							

&lt;210&gt; 1095

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 202..378

&lt;400&gt; 1095

agttctgctt	taggacccgc	ccccagcac	gctcctcgac	gctgcgaggt	cccgccccgc		60
gtgctggccg	cggtaaaagt	ggtagcagcg	gaggcgagcg	gagggtttcc	cgcgccggat		120
ttctgacagt	cagacttgtc	cacaagaact	caactggcaa	ggctgctttt	ctgtgctaaa		180
actggggagc	tagtgggcac	s atg aag atc ttc tgc agt cgg gcc aat ccg					231
		Met Lys Ile Phe Cys Ser Arg Ala Asn Pro					
		1	5		10		
acc acg ggg tct gtg gag tgg ctg gag gag gat gaa cac tat gat tac							279
Thr Thr Gly Ser Val Glu Trp Leu Glu Glu Asp Glu His Tyr Asp Tyr							
		15	20		25		
cac cag gag att gca agg tca tct tat gca gat atg cta cat gas aaa							327

His Gln Glu Ile Ala Arg Ser Ser Tyr Ala Asp Met Leu His Xaa Lys  
 30 35 40  
 gac aga mat gta aaa tac tac caa ggt atc cgg gct gcc gtg wgc agg 375  
 Asp Arg Xaa Val Lys Tyr Tyr Gln Gly Ile Arg Ala Ala Val Xaa Arg  
 45 50 55  
 gaa gg 380  
 Glu

<210> 1096  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 74..370

<400> 1096  
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 acacaacaaa agt atg gat atg gga aac caa cat cct tct att agt agg 109  
 Met Asp Met Gly Asn Gln His Pro Ser Ile Ser Arg  
 1 5 10  
 ctt cag gaa atc caa aag gaa gta aaa agt gta gaa cag caa gtt atc 157  
 Leu Gln Glu Ile Gln Lys Glu Val Lys Ser Val Glu Gln Gln Val Ile  
 15 20 25  
 ggc ttc agt ggt ctg tca gat gac aag aat tac aag aaa ctg gag agg 205  
 Gly Phe Ser Gly Leu Ser Asp Asp Lys Asn Tyr Lys Lys Leu Glu Arg  
 30 35 40  
 att cta aca aaa cag ctt ttt gaa ata gac tct gta gat act gaa gga 253  
 Ile Leu Thr Lys Gln Leu Phe Glu Ile Asp Ser Val Asp Thr Glu Gly  
 45 50 55 60  
 aaa gga gat att cag caa gct agg aag cgg gca gca cag gag aca gaa 301  
 Lys Gly Asp Ile Gln Gln Ala Arg Lys Arg Ala Ala Gln Glu Thr Glu  
 65 70 75  
 cgt ctt ctc aaa gag ttg gag cag aat gca aac cac cca cac cgg att 349  
 Arg Leu Leu Lys Glu Leu Glu Gln Asn Ala Asn His Pro His Arg Ile  
 80 85 90  
 gaa ata cag aac att ttt gag a 371  
 Glu Ile Gln Asn Ile Phe Glu  
 95

<210> 1097  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 198..398

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tggagctgtg	ctgtaaaaac	aagagtaaca	tttttatatt	aaagttaa	aaagttacaa	120
ctttgaagag	agtttctgca	agacatgaca	caaagctgct	agcagaaaat	caaaacgctg	180
attaaaagaa	gcacggt	atg atg acc	aaa cat	aaa aag	tgt ttt ata att	230
	Met Met	Thr Lys	His Lys	Lys Cys	Phe Ile Ile	
	1		5		10	
ggt ggt ggt	tta ata aca	act aat	att att	act ctg	ata gtt aaa cta	278
Val Gly Val	Leu Ile Thr	Thr Asn	Ile Ile	Thr Leu	Ile Val Lys Leu	
	15		20		25	
act cga gat	tct cag agt	tta tgc	ccc tat	gat tgg	att ggt ttc caa	326
Thr Arg Asp	Ser Gln Ser	Leu Cys	Pro Tyr	Asp Trp	Ile Gly Phe Gln	
	30		35		40	
aac aaa tgc	tat tat ttc	tct aaa	gaa gaa	ggm gat	tgg rat tca agt	374
Asn Lys Cys	Tyr Tyr Phe	Ser Lys	Glu Glu	Gly Asp	Trp Xaa Ser Ser	
	45		50		55	
aaa tac aac	tgt tcc act	caa cat	gc			400
Lys Tyr Asn	Cys Ser Thr	Gln His				
60		65				

<210> 1098  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 11..364

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	Met Ala Ala Leu Gly Val Leu Glu Ser Asp Leu Pro Ser
	1 5 10
gcc gtg aca	ctt ctg aaa aat ctc cag gag caa gtg atg gct gta act
Ala Val Thr	Leu Leu Lys Asn Leu Gln Glu Gln Val Met Ala Val Thr
	15 20 25
gca caa gtg	aaa tca ctg aca caa aaa gtt caa gct ggt gcc tat cct
Ala Gln Val	Lys Ser Leu Thr Gln Lys Val Gln Ala Gly Ala Tyr Pro
	30 35 40 45
aca gaa aag	ggt ctc agc ttc ttg gaa gtg aaa gac cag ctg ctg ctc
Thr Glu Lys	Gly Leu Ser Phe Leu Glu Val Lys Asp Gln Leu Leu Leu
	50 55 60
atg tac ctt	atg gat ttg acc cac ctc att ctg gac aaa gcc tca gga
Met Tyr Leu	Met Asp Leu Thr His Leu Ile Leu Asp Lys Ala Ser Gly
	65 70 75
gga tct ctt	cag gga cat gat gca gtt ttg aga ctg gtg gag att cgc
Gly Ser Leu	Gln Gly His Asp Ala Val Leu Arg Leu Val Glu Ile Arg
	80 85 90
acg gtt ttg	gaa aag ctt cgt ccc ttg gac caa aag ctg aag tat caa
Thr Val Leu	Glu Lys Leu Arg Pro Leu Asp Gln Lys Leu Lys Tyr Gln
	95 100 105
atn gac aag	ctg atc aag act gca gtg ac
Xaa Asp Lys	Leu Ile Lys Thr Ala Val
110	115

<210> 1099  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 27..248

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 Met Ser Glu Glu Thr Arg Gln Ser Lys  
 1 5  
 ttg gcc gca gcg aag aaa aag ttg aga gaa tat cag cag agn aat agc 101  
 Leu Ala Ala Ala Lys Lys Lys Leu Arg Glu Tyr Gln Gln Xaa Asn Ser  
 10 15 20 25  
 cct ggt gtt cct aca gga gcg aaa aag aag aaa ata aaa aat ggc 149  
 Pro Gly Val Pro Thr Gly Ala Lys Lys Lys Lys Lys Ile Lys Asn Gly  
 30 35 40  
 agt aac cct gag aca acc act tct ggt ggt tgc cac tca cct gag gat 197  
 Ser Asn Pro Glu Thr Thr Thr Ser Gly Gly Cys His Ser Pro Glu Asp  
 45 50 55  
 gtg agt ctt gga tgg cca ggc tcc tgg gga cag ggg gcc caa ggg gca 245  
 Val Ser Leu Gly Trp Pro Gly Ser Trp Gly Gln Gly Ala Gln Gly Ala  
 60 65 70  
 gta g 249  
 Val

<210> 1100  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 99..449

<400> 1100  
 aaaaagttgg agaaggtgtg gcagtcctca tttctgtgga atctgaagaa gcccacgcag 60  
 attttaattc ccactctaga ttctgtatct agatcacc atg gcg act gga cag aag 116  
 Met Ala Thr Gly Gln Lys  
 1 5  
 ttg atg aga gct gtt aga gtt ttt gaa ttt ggt gga cca gaa gtc ctg 164  
 Leu Met Arg Ala Val Arg Val Phe Glu Phe Gly Gly Pro Glu Val Leu  
 10 15 20  
 aaa ttg cga tca gat att gca gta ccg att cca aaa gac cat cag gtt 212  
 Lys Leu Arg Ser Asp Ile Ala Val Pro Ile Pro Lys Asp His Gln Val  
 25 30 35  
 cta atc aag gtc cat gca tgt ggt gtc aac ccc gtg gag aca tac att 260  
 Leu Ile Lys Val His Ala Cys Gly Val Asn Pro Val Glu Thr Tyr Ile  
 40 45 50  
 cgc tct ggt ant tat agt aga aaa cca ctc tta ccc tat act cct ggc 308



Arg	Ser	Gly	Xaa	Tyr	Ser	Arg	Lys	Pro	Leu	Leu	Pro	Tyr	Thr	Pro	Gly	
55					60				65						70	
tca	gat	gtg	gct	ggg	gtg	ata	gaa	gct	gtt	gga	gat	aat	gca	tct	gct	356
Ser	Asp	Val	Ala	Gly	Val	Ile	Glu	Ala	Val	Gly	Asp	Asn	Ala	Ser	Ala	
			75						80					85		
ttc	aag	aaa	ggg	gac	aga	gtt	ttc	act	agc	agc	acg	atc	tct	ggg	ggg	404
Phe	Lys	Lys	Gly	Asp	Arg	Val	Phe	Thr	Ser	Ser	Thr	Ile	Ser	Gly	Gly	
			90					95					100			
tat	gca	gag	tat	gct	ctt	gca	gca	gac	cac	act	gtt	tac	aaa	cta	c	450
Tyr	Ala	Glu	Tyr	Ala	Leu	Ala	Ala	Asp	His	Thr	Val	Tyr	Lys	Leu		
		105					110					115				

<210> 1101  
 <211> 278  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 43..276

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	Met Val Gln Lys
	1
aag ttg gag gag ctg cag tct atg aag caa cac ctt ctc ttt cag caa	102
Lys Leu Glu Glu Leu Gln Ser Met Lys Gln His Leu Leu Phe Gln Gln	
5	10 15 20
gaa gaa gag cgg caa gcc cag ttc atg atg agg cag gag acg tta gct	150
Glu Glu Glu Arg Gln Ala Gln Phe Met Met Arg Gln Glu Thr Leu Ala	
	25 30 35
cag caa cag tta cag ctt gag cag atc caa cag ctg caa caa cag ctt	198
Gln Gln Gln Leu Gln Leu Glu Gln Ile Gln Gln Leu Gln Gln Gln Leu	
	40 45 50
cac cag cag ctg gag gag caa aag att cgg cag atc tac cag tat aac	246
His Gln Gln Leu Glu Glu Gln Lys Ile Arg Gln Ile Tyr Gln Tyr Asn	
	55 60 65
tat gac cct tct gga act gct tct cca caa ac	278
Tyr Asp Pro Ser Gly Thr Ala Ser Pro Gln	
	70 75

<210> 1102  
 <211> 211  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 58..210

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atg gag acg gta cag ctg agg aac ccg ccg cgc cgg cag ctg aaa aag	105
Met Glu Thr Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys	
1 5 10 15	
ttg gat gaa gat agt tta acc aaa caa cca gaa gaa gta ttt gat gtc	153
Leu Asp Glu Asp Ser Leu Thr Lys Gln Pro Glu Glu Val Phe Asp Val	
20 25 30	
tta gag aaa ctt gga gaa ggg tcc tat ggc agc gta tac aaa gct att	201
Leu Glu Lys Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile	
35 40 45	
cat aaa gag a	211
His Lys Glu	
50	

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Met Trp Ser Glu Gly Arg Tyr Glu Tyr	
1 5	
gaa aga att ccg aga gaa cga gca cct cct cga agt cat ccc agt gat	162
Glu Arg Ile Pro Arg Glu Arg Ala Pro Pro Arg Ser His Pro Ser Asp	
10 15 20 25	
ggc tac aat aga cta gtt aat att gtg cca aag aaa cca cca ctg cta	210
Gly Tyr Asn Arg Leu Val Asn Ile Val Pro Lys Lys Pro Pro Leu Leu	
30 35 40	
gac aga cct ggt gaa gga agc tac aat aga tat tac agt cat gtt att	258
Asp Arg Pro Gly Glu Gly Ser Tyr Asn Arg Tyr Tyr Ser His Val Ile	
45 50 55	
acc gag act atg acg agg gcc gca gtt ttt ctc atg atc gaa gaa gtg	306
Thr Glu Thr Met Thr Arg Ala Ala Val Phe Leu Met Ile Glu Glu Val	
60 65 70	
gtc cac ctc aca gag gag atg aat ctg gtt	336
Val His Leu Thr Glu Glu Met Asn Leu Val	
75 80	

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 Met Pro Ser Lys Gly Pro Leu Gln Ser Val Gln Val Phe Gly Arg  
 1 5 10 15  
 aag aag aca gcg aca gct gtg gcg cac tgc aaa cgc ggc aat ggt ctc 157  
 Lys Lys Thr Ala Thr Ala Val Ala His Cys Lys Arg Gly Asn Gly Leu  
 20 25 30  
 atc aag gtg aac ggg cgg ccc ctg gag atg att gag ccg cgc acg cta 205  
 Ile Lys Val Asn Gly Arg Pro Leu Glu Met Ile Glu Pro Arg Thr Leu  
 35 40 45  
 cag tac aag ctg ctg gag cca gtt ctg ctt ctc ggc aag gag cga ttt 253  
 Gln Tyr Lys Leu Leu Glu Pro Val Leu Leu Leu Gly Lys Glu Arg Phe  
 50 55 60  
 gct ggt gta gac atc cgt gtc cgt gta aag ggt ggt ggt cac gtg gcc 301  
 Ala Gly Val Asp Ile Arg Val Arg Val Lys Gly Gly Gly His Val Ala  
 65 70 75  
 cag att tat gct atc cgt cag tcc atc tcc aaa gcc ctg gtg gcc tat 349  
 Gln Ile Tyr Ala Ile Arg Gln Ser Ile Ser Lys Ala Leu Val Ala Tyr  
 80 85 90 95  
 tac cag aaa tat gtg gat gag gct tcc aag aag gag atc aaa gac atc 397  
 Tyr Gln Lys Tyr Val Asp Glu Ala Ser Lys Lys Glu Ile Lys Asp Ile  
 100 105 110  
 ctc atc cag tat gac cgg acc ctg ctg gta gct gac cct cgt cgc tgc 445  
 Leu Ile Gln Tyr Asp Arg Thr Leu Leu Val Ala Asp Pro Arg Arg Cys  
 115 120 125  
 gag tcc aaa aag ttt gga ggt ctg gtg ccc gcg ctc gct acc aga aat 493  
 Glu Ser Lys Lys Phe Gly Gly Leu Val Pro Ala Leu Ala Thr Arg Asn  
 130 135 140  
 cct acc gat aag cc 507  
 Pro Thr Asp Lys  
 145

<210> 1105  
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 Met Ala Cys Ala Ala Ala  
 1 5  
 cgg tcc ccg gcc gac cag gac agg ttt att tgt atc tat cct gct tat 163  
 Arg Ser Pro Ala Asp Gln Asp Arg Phe Ile Cys Ile Tyr Pro Ala Tyr  
 10 15 20  
 tta aat aat aag aag acc atc gca gag gga agg cga atc ccc ata agt 211  
 Leu Asn Asn Lys Lys Thr Ile Ala Glu Gly Arg Arg Ile Pro Ile Ser  
 25 30 35

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aag gct gtt gaa aat cct aca gct aca gag att caa gat gta tgt tca      259
Lys Ala Val Glu Asn Pro Thr Ala Thr Glu Ile Gln Asp Val Cys Ser
  40                      45                      50
gca gtt gga ctt aac gta ttt ctt gag aaa aat aaa atg tac tct aga      307
Ala Val Gly Leu Asn Val Phe Leu Glu Lys Asn Lys Met Tyr Ser Arg
  55                      60                      65                      70
gaa tgg aat cgt gat gtc caa tac aga ggc aga gtc cgg gtc cag ctc      355
Glu Trp Asn Arg Asp Val Gln Tyr Arg Gly Arg Val Arg Val Gln Leu
                      75                      80                      85
aaa cag gaa gat ggg agc ctc tgc ctt gta cag ttc cca tca cgt aag      403
Lys Gln Glu Asp Gly Ser Leu Cys Leu Val Gln Phe Pro Ser Arg Lys
                      90                      95                      100
tca gta atg ttg tat gca gca gaa atg ata cct a      437
Ser Val Met Leu Tyr Ala Ala Glu Met Ile Pro
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<210> 1106  
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<220>  
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tttaaggcgc c atg agg ggt gac aga ggc cgt ggt cgt ggt ggg cgc ttt      110
          Met Arg Gly Asp Arg Gly Arg Gly Arg Gly Gly Arg Phe
                1                5                10
ggt tcc aga gga ggc cca gga gga ggg ttc agg ccc ttt gta cca cat      158
Gly Ser Arg Gly Gly Pro Gly Gly Gly Phe Arg Pro Phe Val Pro His
  15                20                25
atc cca ttt gac ttc tat ttg tgt gaa atg gcc ttt ccc cgg gtc aag      206
Ile Pro Phe Asp Phe Tyr Leu Cys Glu Met Ala Phe Pro Arg Val Lys
  30                35                40                45
cca gca cct gat gaa act tcc ttc agt gag gcc ttg ctg aag agg aat      254
Pro Ala Pro Asp Glu Thr Ser Phe Ser Glu Ala Leu Leu Lys Arg Asn
                      50                      55                      60
cag gac ctg gct ccc aat tct gct gaa cag gca tct atc ctt tct ctg      302
Gln Asp Leu Ala Pro Asn Ser Ala Glu Gln Ala Ser Ile Leu Ser Leu
                      65                      70                      75
gtg aca aaa ata aac aat gtg att gat aat ctg att gtg gct cca ggg      350
Val Thr Lys Ile Asn Asn Val Ile Asp Asn Leu Ile Val Ala Pro Gly
                      80                      85                      90
aca ttt gaa gtg caa att gwa gaa gtt cga cag gtg ggt cct ata      395
Thr Phe Glu Val Gln Ile Xaa Glu Val Arg Gln Val Gly Pro Ile
                      95                      100                      105

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<210> 1107  
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<220>  
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 <222> 117..404

<400> 1107

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ccctgcaaag aaacaagagt gcttatccca gctaagctcc agggaaccat aaatcc atg	119
	Met
	1
gct aac ctt gac aaa tac act gaa aca ttc aag atg ggt agc aac agt	167
Ala Asn Leu Asp Lys Tyr Thr Glu Thr Phe Lys Met Gly Ser Asn Ser	
	5 10 15
acc agc act gct gag att tac tgt aat gtc act aat gtg aaa ttt caa	215
Thr Ser Thr Ala Glu Ile Tyr Cys Asn Val Thr Asn Val Lys Phe Gln	
	20 25 30
tac tcc ctc tat gca acc acc tat atc ctc ata ttc att cct ggt ctt	263
Tyr Ser Leu Tyr Ala Thr Thr Tyr Ile Leu Ile Phe Ile Pro Gly Leu	
	35 40 45
ctg gct aac agt gca gcc ttg tgg gtt ctg tgc cgc ttc atc agc aag	311
Leu Ala Asn Ser Ala Ala Leu Trp Val Leu Cys Arg Phe Ile Ser Lys	
	50 55 60 65
aaa aat aaa gcc atc att ttc atg atc aac ctc tct gtg gct gac ctt	359
Lys Asn Lys Ala Ile Ile Phe Met Ile Asn Leu Ser Val Ala Asp Leu	
	70 75 80
gct cat gta tta tct tta ccc ctc cgg att tac tat tac atc agc ca	406
Ala His Val Leu Ser Leu Pro Leu Arg Ile Tyr Tyr Tyr Ile Ser	
	85 90 95

<210> 1108  
 <211> 438  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 232..438

<400> 1108

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ccccacccaa tgcgagacgt ggccagatcc catccaacac acgggtttaat tttcatgggg	120
ctctgggatac aaaagaacag aaacagcaac aacaaaaagcc cagccgctgt ctgattttaa	180
gctggcaaag tgggaaaaat aaagtgttga gtaaacagac caagttggat c atg ggg	237
	Met Gly
	1
aat ttc aga ggt cat gcc ctc cct gga acc ttc ttt ttt att att ggt	285
Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile Ile Gly	
	5 10 15
ctt tgg tgg tgt aca aag agt att ctg aag tat atc tgc aaa aag caa	333
Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys Lys Gln	
	20 25 30
aag cga acc tgc tat ctt ggt tcc aaa aca tta ttc tat cga ttg gaa	381

Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg Leu Glu  
 35 40 45 50  
 att ttg gag gga att aca ata gtt ggc atg gct tta act ggc atg gct 429  
 Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly Met Ala  
 55 60 65  
 ggg gag cag 438  
 Gly Glu Gln

<210> 1109  
 <211> 458  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 38..457

<400> 1109  
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 Met Ser Gly Glu Ser Ala  
 1 5  
 agg agc ttg ggg aag gga agc gcg ccc ccg ggg ccg gtc ccg gag gnc 103  
 Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro Gly Pro Val Pro Glu Xaa  
 10 15 20  
 tcg atc cgc atc tac agc atg agg ttc tgc ccg ttt gct gag agg acg 151  
 Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys Pro Phe Ala Glu Arg Thr  
 25 30 35  
 cgt cta gtc ctg aag gcc aag gga atc agg cat gaa gtc atc aat atc 199  
 Arg Leu Val Leu Lys Ala Lys Gly Ile Arg His Glu Val Ile Asn Ile  
 40 45 50  
 aac ctg aaa aat aag cct gag tgg ttc ttt aag aaa aat ccc ttt ggt 247  
 Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe Lys Lys Asn Pro Phe Gly  
 55 60 65 70  
 ctg gtg cca gtt ctg gaa aac agt cag ggt cag ctg atc tac gag tct 295  
 Leu Val Pro Val Leu Glu Asn Ser Gln Gly Gln Leu Ile Tyr Glu Ser  
 75 80 85  
 gcc atc acc tgt gag tac ctg gat gaa gca tac cca ggg aag aag ctg 343  
 Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala Tyr Pro Gly Lys Lys Leu  
 90 95 100  
 ttg ccg gat gac ccc tat gag aaa gct tgc cag aag atg atc tta gag 391  
 Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys Gln Lys Met Ile Leu Glu  
 105 110 115  
 ttg ttt tct aag gtg cca tcc ttg gta gga agc ttt att aga agc sra 439  
 Leu Phe Ser Lys Val Pro Ser Leu Val Gly Ser Phe Ile Arg Ser Xaa  
 120 125 130  
 aat waa gaa gac tat gat g 458  
 Asn Xaa Glu Asp Tyr Asp  
 135 140

<210> 1110  
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 <212> DNA  
 <213> Homo sapiens

[illegible]

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			1				5					10				
gaa	ggg	aga	agg	cga	aca	ttt	cat	gtt	tgg	cgg	gca	tgt	gag	tgc	aca	98
Glu	Gly	Arg	Arg	Arg	Thr	Phe	His	Val	Trp	Arg	Ala	Cys	Glu	Cys	Thr	
		15					20					25				
aga	tgg	aaa	gag	cga	ttg	gag	cat	cct	ggt	ata	att	acc	ccc	att	gtg	146
Arg	Trp	Lys	Glu	Arg	Leu	Glu	His	Pro	Gly	Ile	Ile	Thr	Pro	Ile	Val	
		30				35					40					
ctc	tta	atg	gaa	att	tca	aag	gac	ggg	agt	att	ctg	ttg	gtt	ggt	gtc	194
Leu	Leu	Met	Glu	Ile	Ser	Lys	Asp	Gly	Ser	Ile	Leu	Leu	Val	Gly	Val	
		45			50					55					60	
cag	gtt	tgt	ggc	act	gtt	cca	aga	ggc	ctt	aca	cac	aca	c			234
Gln	Val	Cys	Gly	Thr	Val	Pro	Arg	Gly	Leu	Thr	His	Thr				
			65					70								

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757

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 <212> DNA  
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<220>  
 <221> CDS  
 <222> 69..380

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 ggggcact atg aac gaa gag gag cag ttt gta aac att gat ttg aat gat 110  
 Met Asn Glu Glu Glu Gln Phe Val Asn Ile Asp Leu Asn Asp  
 1 5 10  
 gac aac att tgc agt gtt tgt aaa ctg gga aca gac aaa gaa aca ctc 158  
 Asp Asn Ile Cys Ser Val Cys Lys Leu Gly Thr Asp Lys Glu Thr Leu  
 15 20 25 30  
 tcc ttc tgc cac att tgt ttt gag cta aat att gag ggg gta cca aag 206  
 Ser Phe Cys His Ile Cys Phe Glu Leu Asn Ile Glu Gly Val Pro Lys  
 35 40 45  
 tct gat ctc ttg cac acc aaa tca tta agg ggc cat aaa gac tgc ttt 254  
 Ser Asp Leu Leu His Thr Lys Ser Leu Arg Gly His Lys Asp Cys Phe  
 50 55 60  
 gaa aaa tac cat tta att gca aac cag ggt tgt cct cga tct aag ctt 302  
 Glu Lys Tyr His Leu Ile Ala Asn Gln Gly Cys Pro Arg Ser Lys Leu  
 65 70 75  
 tca aaa agt act tat gaa gaa gtt aaa acc att ttg agt aag aag ata 350  
 Ser Lys Ser Thr Tyr Glu Glu Val Lys Thr Ile Leu Ser Lys Lys Ile  
 80 85 90  
 aac tgg att gtg cag tat gca caa aat aag 380  
 Asn Trp Ile Val Gln Tyr Ala Gln Asn Lys  
 95 100

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 <211> 376  
 <212> DNA  
 <213> Homo sapiens

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 <222> 155..376

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 ccttcggcac ttagctttg ggtggtgggc tgcagattaa ttttgtaacc accttaagaa 120  
 aaatacggaa ctctaactcc ttgccactca agaa atg tcc tcc ctt tca gaa tat 175  
 Met Ser Ser Leu Ser Glu Tyr  
 1 5  
 gcc ttc cgc atg tct cgt ctc agt gcc cgg cta ttt ggt gaa gtc acc 223  
 Ala Phe Arg Met Ser Arg Leu Ser Ala Arg Leu Phe Gly Glu Val Thr  
 10 15 20  
 agg cct act aat tcc aag tct atg aaa gtg gtg aaa ctg ttt agt gaa 271



Arg	Pro	Thr	Asn	Ser	Lys	Ser	Met	Lys	Val	Val	Lys	Leu	Phe	Ser	Glu		
25						30					35						
ctg	ccc	ttg	gcc	aag	aag	aag	gag	act	tat	gat	tgg	tat	cca	aat	cac	319	
Leu	Pro	Leu	Ala	Lys	Lys	Lys	Glu	Thr	Tyr	Asp	Trp	Tyr	Pro	Asn	His		
40				45						50					55		
cac	act	tac	gct	gaa	ctc	atg	cag	acg	ctc	cga	ttt	ctt	gga	ctc	tac	367	
His	Thr	Tyr	Ala	Glu	Leu	Met	Gln	Thr	Leu	Arg	Phe	Leu	Gly	Leu	Tyr		
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aga	gat	gag														376	
Arg	Asp	Glu															

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 <222> 80..328

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		Met Ser Ser	Leu Ser Glu	Tyr Ala Phe	Arg Met												
		1	5	10													
tct cgt ctc	agt gcc cgg	cta ttt ggt	gaa gtc acc	agg cct act	aat											160	
Ser Arg Leu	Ser Ala Arg	Leu Phe Gly	Glu Val Thr	Arg Pro Thr	Asn												
	15	20	25														
tcc aag tct	atg aaa gtg	gtg aaa ctg	ttt agt gaa	ctg ccc ttg	gcc											208	
Ser Lys Ser	Met Lys Val	Val Lys Leu	Phe Ser Glu	Leu Pro Leu	Ala												
	30	35	40														
aag aag aag	gag act tat	gat tgg tat	cca aat cac	cac act tac	gct											256	
Lys Lys Lys	Glu Thr Tyr	Asp Trp Tyr	Pro Asn His	His Thr Tyr	Ala												
	45	50	55														
gaa ctc atg	cag acg ctc	cga ttt ctt	gga ctc tac	aga gat gag	cat											304	
Glu Leu Met	Gln Thr Leu	Arg Phe Leu	Gly Leu Tyr	Arg Asp Glu	His												
	60	65	70		75												
cag gat ttt	atg gat gag	caa aaa														328	
Gln Asp Phe	Met Asp Glu	Gln Lys															
		80															

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 ggctgaaggt ttagcgggtg ccgcctctaa agagagcaat cactacatt atg gct 176  
 Met Ala

1  
 ggg att ttg cgc tta gta gtt caa tgg ccc cca ggc aga cta cag acc 224  
 Gly Ile Leu Arg Leu Val Val Gln Trp Pro Pro Gly Arg Leu Gln Thr  
 5 10 15

gtg aca aaa ggt gtg gag tct ctt att tgt aca gat tgg att cgt cac 272  
 Val Thr Lys Gly Val Glu Ser Leu Ile Cys Thr Asp Trp Ile Arg His  
 20 25 30

aaa ttc acc aga tca aga att cca gaa aaa gtg ttt cag gcc tca cct 320  
 Lys Phe Thr Arg Ser Arg Ile Pro Glu Lys Val Phe Gln Ala Ser Pro  
 35 40 45 50

gaa gat cat gaa aaa tac ggt ggg gat cca cag aac cct cat aaa ctg 368  
 Glu Asp His Glu Lys Tyr Gly Gly Asp Pro Gln Asn Pro His Lys Leu  
 55 60 65

cat att gtt acc aga ata aaa ag 391  
 His Ile Val Thr Arg Ile Lys  
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<210> 1116  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> 132..326

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 ccaccaagtg a atg cct gaa tct cta cta ggc tgg ttt gaa cct gtt gtg 170  
 Met Pro Glu Ser Leu Leu Gly Trp Phe Glu Pro Val Val  
 1 5 10

tgt acc tta aga atg aaa aat act aga cat ctg tca ctt cat cca att 218  
 Cys Thr Leu Arg Met Lys Asn Thr Arg His Leu Ser Leu His Pro Ile  
 15 20 25

aag tcc tac ctt ggt tta tta ata gaa cta aga gcc tca cat agg tca 266  
 Lys Ser Tyr Leu Gly Leu Leu Ile Glu Leu Arg Ala Ser His Arg Ser  
 30 35 40 45

cct gac tcc ttc ttc agt aga tgc cat ttc aat aga ttt tgc aat ccc 314  
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tct gat acc agc gc 328  
 Ser Asp Thr Ser  
 65

<210> 1117  
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 <212> DNA  
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<220>  
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				1				5								
tta	ctg	aaa	aat	act	ata	aat	gac	ccc	aaa	gct	ttg	acc	agc	aaa	gat	104
Leu	Leu	Lys	Asn	Thr	Ile	Asn	Asp	Pro	Lys	Ala	Leu	Thr	Ser	Lys	Asp	
			10					15					20			
atg	agg	ttc	tgt	ctg	aac	acc	ctc	cag	cac	gag	tgg	ttc	cgc	gtg	tcc	152
Met	Arg	Phe	Cys	Leu	Asn	Thr	Leu	Gln	His	Glu	Trp	Phe	Arg	Val	Ser	
		25					30				35					
agt	cag	aag	tca	gcc	att	cca	gcc	atg	gtg	ggg	gac	tac	ata	gct	gct	200
Ser	Gln	Lys	Ser	Ala	Ile	Pro	Ala	Met	Val	Gly	Asp	Tyr	Ile	Ala	Ala	
	40					45				50						
ttt	gag	gcc	att	tcc	cca	gat	gtc	ctc	cgc	tat	gtc	atc	aac	ttg	gca	248
Phe	Glu	Ala	Ile	Ser	Pro	Asp	Val	Leu	Arg	Tyr	Val	Ile	Asn	Leu	Ala	
55				60					65					70		
gac	ggc	aac	ggc	aac	aca	gcc	ctc	cat	tac	agc	gtg	tcc	cac	tcc	aac	296
Asp	Gly	Asn	Gly	Asn	Thr	Ala	Leu	His	Tyr	Ser	Val	Ser	His	Ser	Asn	
			75					80					85			
ttc	gag	att	gtk	aag	ctg	ctg	tta	gat	gcc	gat	gtg	tgt	aat	gtg	gat	344
Phe	Glu	Ile	Val	Lys	Leu	Leu	Leu	Asp	Ala	Asp	Val	Cys	Asn	Val	Asp	
		90					95					100				
cac	cag	aac	aag	gca	ggc	tac	acc	c								369
His	Gln	Asn	Lys	Ala	Gly	Tyr	Thr									
		105					110									

<210> 1118  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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			Met	Ala	Thr	Arg	Asn	Pro	Pro	Pro	Gln	Asp				
			1				5				10					
tat	gaa	agt	gat	gac	gac	tct	tat	gaa	gtg	ttg	gat	tta	act	gag	tat	160
Tyr	Glu	Ser	Asp	Asp	Asp	Ser	Tyr	Glu	Val	Leu	Asp	Leu	Thr	Glu	Tyr	
			15					20				25				
gca	aga	aga	cac	cag	tgg	tgg	aat	cga	gtg	ttt	ggc	cac	agt	tcg	gga	208
Ala	Arg	Arg	His	Gln	Trp	Trp	Asn	Arg	Val	Phe	Gly	His	Ser	Ser	Gly	
			30				35				40					
cct	atg	gta	gaa	aaa	tac	tca	gta	gct	acc	cag	att	gta	atg	ggg	ggc	256
Pro	Met	Val	Glu	Lys	Tyr	Ser	Val	Ala	Thr	Gln	Ile	Val	Met	Gly	Gly	

45	50	55	
gtt act ggc tgg tgt gca gga ttt ctr ttc cag aaa gtt gga aaa ctt			304
Val Thr Gly Trp Cys Ala Gly Phe Leu Phe Gln Lys Val Gly Lys Leu			
60	65	70	
gca gca act gca gta ggt ggt ggc ttt ctt ctt ctt cag att gct agt			352
Ala Ala Thr Ala Val Gly Gly Gly Phe Leu Leu Leu Gln Ile Ala Ser			
75	80	85	90
cat agt ggc tat gtg cag att gac tgg aag aga gtt gaa aaa gat gta			400
His Ser Gly Tyr Val Gln Ile Asp Trp Lys Arg Val Glu Lys Asp Val			
95	100	105	
aat aaa gca aaa aga cag att aag aaa cga nng aac aaa gca gca c			446
Asn Lys Ala Lys Arg Gln Ile Lys Lys Arg Xaa Asn Lys Ala Ala			
110	115	120	

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 217..420

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ttgtagtgcc gcgagttgag ctctctttgc ctaagtggtc gcgccccctt taagagcagc	120
gattgtaagg agaggcggtc ccggtgtcct cgggtcccag gtgattgtga agtgctgacc	180
aattgccact ggacatactt gaaacaaaat aggaaa atg gca gca aac tct tca	234
	Met Ala Ala Asn Ser Ser
	1 5
gga caa ggt ttt caa aac aaa aat aga gtt gca atc ttg gca gaa ctg	282
Gly Gln Gly Phe Gln Asn Lys Asn Arg Val Ala Ile Leu Ala Glu Leu	
10	15
aca aag aga aaa gaa aac tac tta tgc aga acc agt ctt caa caa atc	330
Thr Lys Arg Lys Glu Asn Tyr Leu Cys Arg Thr Ser Leu Gln Gln Ile	
25	30
atc ctg gar cta ggt att gac act ata atg tgg gtt tnn tgt ntg ttt	378
Ile Leu Glu Leu Gly Ile Asp Thr Ile Met Trp Val Xaa Cys Xaa Phe	
40	45
tgt ttt gtt ttg ttt tgt ttt gag acg gag tct cgc cct gtc	420
Cys Phe Val Leu Phe Cys Phe Glu Thr Glu Ser Arg Pro Val	
55	60

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 <211> 244  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 38..244

<400> 1120

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				1			5									
tgt	cat	act	tgt	aac	acc	aca	gat	cga	aat	gcc	ata	tgt	gtg	aac	tgc	103
Cys	His	Thr	Cys	Asn	Thr	Thr	Asp	Arg	Asn	Ala	Ile	Cys	Val	Asn	Cys	
			10				15					20				
att	aag	aag	tgc	cat	cag	gga	cat	gat	gta	gag	ttt	att	aga	cat	gat	151
Ile	Lys	Lys	Cys	His	Gln	Gly	His	Asp	Val	Glu	Phe	Ile	Arg	His	Asp	
			25				30				35					
agg	ttt	ttc	tgt	gac	tgt	ggg	gct	gga	aca	ctg	tct	aat	cct	tgt	aca	199
Arg	Phe	Phe	Cys	Asp	Cys	Gly	Ala	Gly	Thr	Leu	Ser	Asn	Pro	Cys	Thr	
	40					45				50						
tta	gct	ggg	gag	cct	aca	cat	gat	aca	gat	aca	cta	tat	gac	tct		244
Leu	Ala	Gly	Glu	Pro	Thr	His	Asp	Thr	Asp	Thr	Leu	Tyr	Asp	Ser		
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<210> 1121

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 41..454

<400> 1121

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				Met	Trp	Ser	Leu	Gly								
				1			5									
tgc	atc	acg	gcg	gag	ttg	tac	acg	ggc	tac	ccc	ctg	ttc	ccc	ggg	gag	103
Cys	Ile	Thr	Ala	Glu	Leu	Tyr	Thr	Gly	Tyr	Pro	Leu	Phe	Pro	Gly	Glu	
			10					15					20			
aat	gag	gtg	gag	cag	ctg	gcc	tgc	atc	atg	gag	gtg	ctg	ggg	ctg	ccg	151
Asn	Glu	Val	Glu	Gln	Leu	Ala	Cys	Ile	Met	Glu	Val	Leu	Gly	Leu	Pro	
			25				30					35				
cca	gcc	ggc	ttc	att	cag	aca	gcc	tcc	agg	aga	cag	aca	ttc	ttt	gat	199
Pro	Ala	Gly	Phe	Ile	Gln	Thr	Ala	Ser	Arg	Arg	Gln	Thr	Phe	Phe	Asp	
	40					45					50					
tcc	aaa	ggg	ttt	cct	aaa	aat	ata	acc	aac	aac	agg	ggg	aaa	aaa	aga	247
Ser	Lys	Gly	Phe	Pro	Lys	Asn	Ile	Thr	Asn	Asn	Arg	Gly	Lys	Lys	Arg	
	55				60				65							
tac	cca	gat	tcc	aag	gac	ctc	acg	atg	gtg	ctg	aaa	acc	tat	gac	acc	295
Tyr	Pro	Asp	Ser	Lys	Asp	Leu	Thr	Met	Val	Leu	Lys	Thr	Tyr	Asp	Thr	
	70				75				80				85			
agc	ttc	ctg	gac	ttt	ctc	aga	agg	tgt	ttg	gta	tgg	gaa	cct	tct	ctt	343
Ser	Phe	Leu	Asp	Phe	Leu	Arg	Arg	Cys	Leu	Val	Trp	Glu	Pro	Ser	Leu	
			90					95				100				
cgc	atg	acc	ccg	gac	cag	gcc	ctc	aag	cat	gct	tgg	att	cat	cag	tct	391
Arg	Met	Thr	Pro	Asp	Gln	Ala	Leu	Lys	His	Ala	Trp	Ile	His	Gln	Ser	
			105				110					115				
cgg	aac	ctc	aag	cca	cag	ccc	agg	ccc	cag	acc	ctg	agg	aaa	tcc	aat	439
Arg	Asn	Leu	Lys	Pro	Gln	Pro	Arg	Pro	Gln	Thr	Leu	Arg	Lys	Ser	Asn	

120 125 130 454  
tcc ttt ttc ccc tct  
Ser Phe Phe Pro Ser  
135

<210> 1122  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 62..262

<400> 1122  
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a atg ctc ata tca gtc aca aat cta gga tgt act gtc ttg ttg tat gtg 109  
Met Leu Ile Ser Val Thr Asn Leu Gly Cys Thr Val Leu Leu Tyr Val  
1 5 10 15  
agc ttt gta gag att ttt aaa aat ata agc atc acc ttc cca ttg aag 157  
Ser Phe Val Glu Ile Phe Lys Asn Ile Ser Ile Thr Phe Pro Leu Lys  
20 25 30  
agt gga gag agt cta ctg gat gac tgg cca gga act ttc tct ctg aat 205  
Ser Gly Glu Ser Leu Leu Asp Asp Trp Pro Gly Thr Phe Ser Leu Asn  
35 40 45  
cgg aca ttt gga tgt ctt ctt tct tcc aag aaa tgg tgg ttc aca tta 253  
Arg Thr Phe Gly Cys Leu Leu Ser Ser Lys Lys Trp Trp Phe Thr Leu  
50 55 60  
aag tat cat 262  
Lys Tyr His  
65

<210> 1123  
<211> 413  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 226..411

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gacttttttaa gaaatctcaa tgaactatgt gtagagaatc actgatccgg cctgcaagca 120  
ttttgcacgg caaaaatata gatcagtgtt aagtgaagat cacattttat atgcgatctt 180  
gacttttttg tcttacatta tatttttata gattttgtta taaac atg gtg ctg gga 237  
Met Val Leu Gly  
1  
aag gtg aag agt ttg aca ata agc ttt gac tgt ctt aat gac agc aat 285  
Lys Val Lys Ser Leu Thr Ile Ser Phe Asp Cys Leu Asn Asp Ser Asn  
5 10 15 20  
gtc cct gtg tat tct agt ggg gat acc gtc tca gga agg gta aat tta 333

Val	Pro	Val	Tyr	Ser	Ser	Gly	Asp	Thr	Val	Ser	Gly	Arg	Val	Asn	Leu	
				25					30					35		
gaa	gtt	act	ggg	gaa	atc	aga	gta	aaa	tct	ctt	aaa	att	crt	gca	aga	381
Glu	Val	Thr	Gly	Glu	Ile	Arg	Val	Lys	Ser	Leu	Lys	Ile	Xaa	Ala	Arg	
			40					45					50			
ggr	cat	gcg	aaa	gta	cgc	tgg	act	gaa	tct	ag						413
Gly	His	Ala	Lys	Val	Arg	Trp	Thr	Glu	Ser							
			55					60								

<210> 1124  
 <211> 544  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 333..542

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ggagtgtctg	ggctttgaac	tccgagagga	ggtggaccag	aacttttgga	actagtgccg											180	
gcggctctcc	acccccccagt	ataaaagaac	gtgtggatca	ctttgctgag	tacatccaag											240	
atttgaagaa	ctgaaataaaa	tcagctttta	acctgctttt	taaaaatatc	tgggttgga											300	
tttgccctg	acaaataata	aaatgatgag	tg atg caa	gtg aca tgt	tgg ctg											353	
			Met Gln	Val Thr	Cys Trp	Leu											
			1		5												
cag cgt tgg	agc aga tgg	atg ggt atc	ata gca ggt	tct aag gct	ctg											401	
Gln Arg Trp	Ser Arg Trp	Met Gly Ile	Ile Ala Gly	Ser Lys Ala	Leu												
	10		15		20												
gaa tat tcc	aat ggg att	ttt gat tgc	caa tct ccc	acc tct cca	ttc											449	
Glu Tyr Ser	Asn Gly Ile	Phe Asp Cys	Gln Ser Pro	Thr Ser Pro	Phe												
	25		30		35												
atg gga agt	ttg cga gct	ctg cac ctt	gtg gaa gac	ctg cgt gga	ttg											497	
Met Gly Ser	Leu Arg Ala	Leu His Leu	Val Glu Asp	Leu Arg Gly	Leu												
	40		45		50											55	
tta gag atg	atg gaa aca	gat gag aaa	gaa ggc ttg	aga tgc cag	at											544	
Leu Glu Met	Met Glu Thr	Asp Glu Lys	Glu Gly Leu	Arg Cys Gln													
	60		65		70												

<210> 1125  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 75..254

<400> 1125																	
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gaggtattct	attg atg	ggc tta	ggt cac	gag caa	gga ttt	gga gcc	cct									110	

	Met	Gly	Leu	Gly	His	Glu	Gln	Gly	Phe	Gly	Ala	Pro	
	1				5					10			
tgt tta aaa tgc aaa gaa aaa tgt gaa gga ttc gaa ctg cac ttc tgg													158
Cys Leu Lys Cys Lys Glu Lys Cys Glu Gly Phe Glu Leu His Phe Trp													
	15				20					25			
aga aaa ata tgt cgt aac tgc aag tgt ggc caa gaa gag cat gat gtc													206
Arg Lys Ile Cys Arg Asn Cys Lys Cys Gly Gln Glu Glu His Asp Val													
	30				35					40			
ctc ttg agc aat gaa gag gat cga aaa gtg gga aaa ctt ttt gaa gac													254
Leu Leu Ser Asn Glu Glu Asp Arg Lys Val Gly Lys Leu Phe Glu Asp													
45				50				55				60	

<210> 1126  
 <211> 293  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 46..291

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gca gaa att ctc cct gct cag gaa aag gta gag gca agg att gac tta													105
Ala Glu Ile Leu Pro Ala Gln Glu Lys Val Glu Ala Arg Ile Asp Leu													
5				10				15				20	
aag atg ggt aag aag cgt gtt act gat cat aag cta amt gtg gac aaa													153
Lys Met Gly Lys Lys Arg Val Thr Asp His Lys Leu Xaa Val Asp Lys													
				25				30				35	
gta att aaa aat att aac aca att tct tcg gag ttg aag aag ata aaa													201
Val Ile Lys Asn Ile Asn Thr Ile Ser Ser Glu Leu Lys Lys Ile Lys													
				40				45				50	
gag ctc tcc cag tta ttg ctt tgk gac ctt atc cta cat ttt aat cat													249
Glu Leu Ser Gln Leu Leu Leu Xaa Asp Leu Ile Leu His Phe Asn His													
				55				60				65	
ccc atc aag act gag aac tta gca gaa gca gaa aga aac aac cc													293
Pro Ile Lys Thr Glu Asn Leu Ala Glu Ala Glu Arg Asn Asn													
	70				75							80	

<210> 1127  
 <211> 532  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 107..532

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Met Leu Arg  
1  
gtc gcg tgg agg acg ctg agt ttg att cgg acc cgg gca gtt acc cag 163  
Val Ala Trp Arg Thr Leu Ser Leu Ile Arg Thr Arg Ala Val Thr Gln  
5 10 15  
gtc cta gta ccc ggg ctg ccg ggc ggt ggg agc gcc aag ttt cct ttc 211  
Val Leu Val Pro Gly Leu Pro Gly Gly Gly Ser Ala Lys Phe Pro Phe  
20 25 30 35  
aac cag tgg ggc ctg cag cct cga agt ctc ctc ctc cag gcc gcg cgc 259  
Asn Gln Trp Gly Leu Gln Pro Arg Ser Leu Leu Leu Gln Ala Ala Arg  
40 45 50  
gga tat gtc gtc cgg aaa cca gcc cag tct agg ctg gat gat gac cca 307  
Gly Tyr Val Val Arg Lys Pro Ala Gln Ser Arg Leu Asp Asp Asp Pro  
55 60 65  
cct cct tct acg ctg ctc aaa gac tac cag aat gtc cct gga att gag 355  
Pro Pro Thr Leu Leu Lys Asp Tyr Gln Asn Val Pro Gly Ile Glu  
70 75 80  
aag gtt gat gat gtc gtg aaa aga ctc ttg tct ttg gaa atg gcc aac 403  
Lys Val Asp Asp Val Val Lys Arg Leu Leu Ser Leu Glu Met Ala Asn  
85 90 95  
aag aag gag atg cta aaa atc aag caa gaa cag ttt atg aag aag att 451  
Lys Lys Glu Met Leu Lys Ile Lys Gln Glu Gln Phe Met Lys Lys Ile  
100 105 110 115  
gtt gca aac cca gag gac acc aga tcc ctg gag gct cga att att gcc 499  
Val Ala Asn Pro Glu Asp Thr Arg Ser Leu Glu Ala Arg Ile Ile Ala  
120 125 130  
ttg tct gtc aag atc cgc agt tat gaa gaa cac 532  
Leu Ser Val Lys Ile Arg Ser Tyr Glu Glu His  
135 140

<210> 1128  
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<212> DNA  
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<222> 162..467

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ctcatctgcg ccacttgctc gcttcacact ccgcccgcac c atg gtg aag ctc gcg 176  
Met Val Lys Leu Ala  
1 5  
aag gca ggt aaa aat caa ggt gac ccc aag aaa atg gct cct cct cca 224  
Lys Ala Gly Lys Asn Gln Gly Asp Pro Lys Lys Met Ala Pro Pro Pro  
10 15 20  
aag gag gta gaa gaa gat agt gaa gat gag gaa atg tca gaa gat gaa 272  
Lys Glu Val Glu Glu Asp Ser Glu Asp Glu Glu Met Ser Glu Asp Glu  
25 30 35  
gaa gat gat agc agt gga gaa gag gtc gtc ata cct cag aag aaa ggc 320

004220"666E1560

Glu	Asp	Asp	Ser	Ser	Gly	Glu	Glu	Val	Val	Ile	Pro	Gln	Lys	Lys	Gly		
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aag	aag	gct	gct	gca	acc	tca	gca	aag	aag	gtg	gtc	gtt	tcc	cca	aca		368
Lys	Lys	Ala	Ala	Ala	Thr	Ser	Ala	Lys	Lys	Val	Val	Val	Ser	Pro	Thr		
	55					60				65							
aaa	aag	gtt	gca	gtt	gcc	aca	cca	gcc	aag	aaa	gca	gct	gtc	act	cca		416
Lys	Lys	Val	Ala	Val	Ala	Thr	Pro	Ala	Lys	Lys	Ala	Ala	Val	Thr	Pro		
70					75					80				85			
ggc	aaa	aag	gca	gca	gca	aca	cct	gcc	aag	aag	aca	gtt	aca	cca	gcc		464
Gly	Lys	Lys	Ala	Ala	Ala	Thr	Pro	Ala	Lys	Lys	Thr	Val	Thr	Pro	Ala		
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aaa																	467
Lys																	

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 97..375

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				Met	Gly	Glu	Lys	Ser	Glu								
				1				5									
aac	tgt	ggg	gtt	cca	gag	gat	ctg	tta	aat	ggt	ttg	aag	gtt	aca	gat		162
Asn	Cys	Gly	Val	Pro	Glu	Asp	Leu	Leu	Asn	Gly	Leu	Lys	Val	Thr	Asp		
			10				15						20				
act	cag	gaa	gcc	gag	tgt	gct	ggc	cct	cca	gtt	cct	gat	ccc	aaa	aat		210
Thr	Gln	Glu	Ala	Glu	Cys	Ala	Gly	Pro	Pro	Val	Pro	Asp	Pro	Lys	Asn		
		25					30					35					
cag	cat	tcc	cag	agt	aag	ctg	ctc	agg	gat	gat	gag	gcc	cat	ctc	cag		258
Gln	His	Ser	Gln	Ser	Lys	Leu	Leu	Arg	Asp	Asp	Glu	Ala	His	Leu	Gln		
	40				45					50							
gag	gac	cag	gga	gaa	gag	gag	tgt	ttt	cat	gac	tgc	agt	gcc	tca	ttt		306
Glu	Asp	Gln	Gly	Glu	Glu	Glu	Cys	Phe	His	Asp	Cys	Ser	Ala	Ser	Phe		
55				60				65						70			
gag	gag	gag	cca	gga	gcg	gac	aag	gtt	gag	aac	aaa	tct	aat	gaa	gat		354
Glu	Glu	Glu	Pro	Gly	Ala	Asp	Lys	Val	Glu	Asn	Lys	Ser	Asn	Glu	Asp		
				75				80						85			
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Val	Asn	Ser	Ser	Glu	Leu	Asp											
				90													

<210> 1130  
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 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 106..411

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                               Met Asn Lys Lys
                               1
aag aaa ccg ttc cta ggg atg ccc gcg ccc ctc ggc tac gtg ccg ggg      165
Lys Lys Pro Phe Leu Gly Met Pro Ala Pro Leu Gly Tyr Val Pro Gly
5                               10                               15                               20
ctg ggc cgg ggc gcc act ggc ttc acc acg cgg tca gac att ggg ccc      213
Leu Gly Arg Gly Ala Thr Gly Phe Thr Thr Arg Ser Asp Ile Gly Pro
                               25                               30                               35
gcc cgt gat gca aat gac cct gtg gat gat cgc cat gca ccc cca ggc      261
Ala Arg Asp Ala Asn Asp Pro Val Asp Asp Arg His Ala Pro Pro Gly
                               40                               45                               50
aag aga acc gtt ggg gac cag atg aag aaa aat cag gct gct gac gat      309
Lys Arg Thr Val Gly Asp Gln Met Lys Lys Asn Gln Ala Ala Asp Asp
                               55                               60                               65
gac gac gag gat cta aat gac acc aat tac gat gag ttt aat ggc tat      357
Asp Asp Glu Asp Leu Asn Asp Thr Asn Tyr Asp Glu Phe Asn Gly Tyr
                               70                               75                               80
gct ggg arc ctc ttc tca agt gga ccc tac gag aaa gat gat gag gaa      405
Ala Gly Xaa Leu Phe Ser Ser Gly Pro Tyr Glu Lys Asp Asp Glu Glu
85                               90                               95                               100
gca gat
Ala Asp
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<210> 1131  
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<212> DNA  
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<220>  
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<222> 263..505

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gaatccgagt tgggccagma tcacgtacgg tggtttcttg tgcattgact gttccgggggt      180
gcaccgctcc ctgggcgtcc atctgagctt catcaggtcc acagagttgg attccaactg      240
gaactgggtc cagctgaggt gt atg cag gtc ggc ggg aat gcc aat gcg acg      292
                               Met Gln Val Gly Gly Asn Ala Asn Ala Thr
                               1                               5                               10
gct ttt ttt cgc caa cat gga tgc aca gcc aat gat gcc aac acc aaa      340
Ala Phe Phe Arg Gln His Gly Cys Thr Ala Asn Asp Ala Asn Thr Lys
                               15                               20                               25
tat aat agc cga gct gcc cag atg tac cgg gag aag atc cgg cag ctg      388
Tyr Asn Ser Arg Ala Ala Gln Met Tyr Arg Glu Lys Ile Arg Gln Leu
                               30                               35                               40

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ggg agt gcg gcc ctg gct agg cat ggc act gat ctt tgg ata gac aac 436  
 Gly Ser Ala Ala Leu Ala Arg His Gly Thr Asp Leu Trp Ile Asp Asn  
           45                          50                          55  
 atg agt agt gnc gtt cct aat cac tcc cca gag aag aag gac tct gat 484  
 Met Ser Ser Xaa Val Pro Asn His Ser Pro Glu Lys Lys Asp Ser Asp  
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 Phe Phe Thr Glu His Thr Gln  
           75                          80

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 <213> Homo sapiens

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 ttcccgatca caaatctcac ctccactaca actctcttta tacttttctt gcagaaataa 180  
 taatagaaat aaggaggtgg tgggggtttcc aaaaatctta accttcaacc atctggggaa 240  
 aaggcaaaaa tcccatctac cgcaactctc agttcgagag taaagggttc ccaacagtga 300  
 tgtcacaaga ttgaccacat tgatcacaat atg gag tct gga gaa cgg tta cca 354  
   Met Glu Ser Gly Glu Arg Leu Pro  
   1                          5  
 tcc tca gca gcc tcc tct act aca cca act tca tct tcc gac acc ttc 402  
 Ser Ser Ala Ala Ser Ser Thr Thr Pro Thr Ser Ser Ser Asp Thr Phe  
           10                          15                          20  
 tgt ggc ttc agt agt ttc aaa aag tgg cct ttc cca ctg gag ttg ctt 450  
 Cys Gly Phe Ser Ser Phe Lys Lys Trp Pro Phe Pro Leu Glu Leu Leu  
           25                          30                          35                          40  
 cac tta gct cta caa acc cat gtg gac att tat tc 488  
 His Leu Ala Leu Gln Ser Thr His Val Asp Ile Tyr  
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<220>  
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 ccgaggagga ttaacacact ggctgaacac ygggaaggaa ctggcacttg gagtccggac 180  
 atctgaaact tgaattgaca agccgacatc agtctccaga gtgaatccaa ggagtggacc 240

caagacattt	gtgttctgtg	atgtggtggc	atgttacctg	tcattctccga	tcgataactc	300
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aggccaacta	gtcatcagtt	tatttc	atg gat gcc agt	gaa att tgg tgc cgt		412
			Met Asp Ala Ser	Glu Ile Trp Cys Arg		
			1	5		
gac tcg gat	cgg gga agc tcc	ctt agg aga tca	atc ccc tgt cct cct		460	
Asp Ser Asp	Arg Gly Ser Ser	Leu Arg Arg Ser	Ile Pro Cys Pro Pro			
10	15	20	25			
gct ctt tgt	ttc gtg agg aag	atc cac cta cga	cct ctg gtc ctc agr		508	
Ala Leu Cys	Phe Val Arg Lys	Ile His Leu Arg	Pro Leu Val Leu Arg			
	30	35	40			
cca acc agc	cca agg anc atc	tca cca att tta	aat ccg ttc ctt tcc		556	
Pro Thr Ser	Pro Arg Xaa Ile	Ser Pro Ile Leu	Asn Pro Phe Leu Ser			
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ttt cct ggt	aga gac gaa gga	gac gc			582	
Phe Pro Gly	Arg Asp Glu Gly	Asp				
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 <213> Homo sapiens

<220>  
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tggaacacga	ctgtcttctt	ctgccaaa	atg tca gga	att gga aat	aaa aga	112
			Met Ser Gly Ile	Gly Asn Lys Arg		
			1	5		
gca gct gga	gaa cct ggc acc	tcc atg cct cct	gag aag aag	gca gct		160
Ala Ala Gly	Glu Pro Gly Thr	Ser Met Pro Pro	Glu Lys Lys	Ala Ala		
10	15	20				
gtt gaa gat	tca ggg acc aca	gtg gaa aca	att aag cta	gga ggt gtc		208
Val Glu Asp	Ser Gly Thr Thr	Val Glu Thr	Ile Lys Leu	Gly Gly Val		
25	30	35	40			
tct tca acg	gag gaa cta gac	att aga aca	ctg caa acc	aaa aat cgc		256
Ser Ser Thr	Glu Glu Leu Asp	Ile Arg Thr	Leu Gln Thr	Lys Asn Arg		
	45	50	55			
aag ctg gca	gaa atg ttg gat	cag cgg cag	gcc att gaa	gat gaa ctt		304
Lys Leu Ala	Glu Met Leu Asp	Gln Arg Gln	Ala Ile Glu	Asp Glu Leu		
	60	65	70			
cgt gag cac	att gaa aaa	ctg gaa cg				330
Arg Glu His	Ile Glu Lys	Leu Glu				
	75	80				

<210> 1135  
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 <212> DNA  
 <213> Homo sapiens

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gctgcccgggt	gaaatcgtag gacagtgaaag atg ctg ctg gaa ttg tcc gag gag															54
	Met Leu Leu Glu Leu Ser Glu Glu															
	1 5															
cat aag gaa cac ctg gcc ttc ctg cct caa gtk gac agc gcg gtg gtc																102
His Lys Glu His Leu Ala Phe Leu Pro Gln Val Asp Ser Ala Val Val																
	10 15 20															
gcc gag ttt ggg cgg att gct gtg gaa ttc ctg aga cgc ggc gca aac																150
Ala Glu Phe Gly Arg Ile Ala Val Glu Phe Leu Arg Arg Gly Ala Asn																
	25 30 35 40															
cca aaa atc tac gaa ggc gcc gcc aga aaa ctc aat gtg agt agt gac																198
Pro Lys Ile Tyr Glu Gly Ala Ala Arg Lys Leu Asn Val Ser Ser Asp																
	45 50 55															
act gtc cag cat ggt gtg gaa gga tta acg tat ctc ctc act gag agc																246
Thr Val Gln His Gly Val Glu Gly Leu Thr Tyr Leu Leu Thr Glu Ser																
	60 65 70															
tca aag ctc atg att tct gaa ctg gat ttc caa gac tct gtt ttt gtt																294
Ser Lys Leu Met Ile Ser Glu Leu Asp Phe Gln Asp Ser Val Phe Val																
	75 80 85															
ctg gga ttc tct gaa gaa tta aac aaa ttg ttg ctt cag ctt tat ctg																342
Leu Gly Phe Ser Glu Glu Leu Asn Lys Leu Leu Leu Gln Leu Tyr Leu																
	90 95 100															
gac aac aga aaa gag atc aga acg att ctg agt gaa ttg gca cca agc																390
Asp Asn Arg Lys Glu Ile Arg Thr Ile Leu Ser Glu Leu Ala Pro Ser																
	105 110 115 120															
ctt ccc agt tat cat aac ctt gaa tgg cga cta gat gta cag aac aac																438
Leu Pro Ser Tyr His Asn Leu Glu Trp Arg Leu Asp Val Gln Asn Asn																
	125 130 135															
aaa aaa gtg atg gaa ctg gat gct ctc cca gtc tta cat ttc																480
Lys Lys Val Met Glu Leu Asp Ala Leu Pro Val Leu His Phe																
	140 145 150															

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<221> CDS
<222> 98..271
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cactagagca gagtacgagt ctgaggcgga gggagta atg gca gga caa gcg ttt      115
                               Met Ala Gly Gln Ala Phe
                               1           5
aga aag ttt ctt cca ctc ttt gac cga gta ttg gtt gaa agg agt gct      163
Arg Lys Phe Leu Pro Leu Phe Asp Arg Val Leu Val Glu Arg Ser Ala

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10	15	20	
gct gaa act gta acc aaa gga ggc att atg ctt cca gaa aat ggt gac			211
Ala Glu Thr Val Thr Lys Gly Gly Ile Met Leu Pro Glu Asn Gly Asp			
25	30	35	
act cca tgg myg aga gag att cag atc tct cct tcc ccc aag cca cac			259
Thr Pro Trp Xaa Arg Glu Ile Gln Ile Ser Pro Ser Pro Lys Pro His			
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gcc tcc ctg cct cc			273
Ala Ser Leu Pro			
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	Met Ala
	1
gag cag gag ccc aca gcc gag cag ctg gcc cag att gca gcg gag aac	166
Glu Gln Glu Pro Thr Ala Glu Gln Leu Ala Gln Ile Ala Ala Glu Asn	
5	10
gag gag gat gag cac tcg gtc aac tac aag ccc ccg gcc cag aag agc	214
Glu Glu Asp Glu His Ser Val Asn Tyr Lys Pro Pro Ala Gln Lys Ser	
20	25
atc cag gag atc cag gag ctg gac aag gac gac gag agc ctg cga aag	262
Ile Gln Glu Ile Gln Glu Leu Asp Lys Asp Asp Glu Ser Leu Arg Lys	
35	40
tac aag gag gcc ctg ctg ggc cgc gtg gcc gtt tcc gca gac ccc aac	310
Tyr Lys Glu Ala Leu Leu Gly Arg Val Ala Val Ser Ala Asp Pro Asn	
55	60
gtc ccc aac gtc gtg gtg act ggc ctg acc ctg gtg tgc agc tcg gcc	358
Val Pro Asn Val Val Val Thr Gly Leu Thr Leu Val Cys Ser Ser Ala	
70	75
ccg ggc ccc ctg gag ctg gac ctg acg ggc gac ctg gag agc ttc aag	406
Pro Gly Pro Leu Glu Leu Asp Leu Thr Gly Asp Leu Glu Ser Phe Lys	
85	90
aag cag tcg ttt gtg ctg aag gag ggt gtg gag tac cgg ata aaa atc	454
Lys Gln Ser Phe Val Leu Lys Glu Gly Val Glu Tyr Arg Ile Lys Ile	
100	105
tct ttc cgg gtt aac cga gag ata gtg tcc ggc atg aag tac atc cag	502
Ser Phe Arg Val Asn Arg Glu Ile Val Ser Gly Met Lys Tyr Ile Gln	
115	120
cat acg tnc a	125
His Thr Xaa	130
	512

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 <222> 17..376

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                   Met Ala Asp Gly Glu Glu Pro Glu Lys Lys Arg Arg  
                   1                  5                  10  
 aga ata gag gag ctg ctg gct gag aaa atg gct gtt gat ggt ggg tgt 100  
 Arg Ile Glu Glu Leu Leu Ala Glu Lys Met Ala Val Asp Gly Gly Cys  
                   15                  20                  25  
 ggg gac act gga gac tgg gaa ggt cgc tgg aac cat gta aag aag ttc 148  
 Gly Asp Thr Gly Asp Trp Glu Gly Arg Trp Asn His Val Lys Lys Phe  
                   30                  35                  40  
 ctc gag cga tct gga ccc ttc aca cac cct gat ttc gaa ccg agc act 196  
 Leu Glu Arg Ser Gly Pro Phe Thr His Pro Asp Phe Glu Pro Ser Thr  
                   45                  50                  55                  60  
 gaa tct ctc cag ttc ttg tta gat aca tgt aaa gtt cta gtc att gga 244  
 Glu Ser Leu Gln Phe Leu Leu Asp Thr Cys Lys Val Leu Val Ile Gly  
                   65                  70                  75  
 gct ggc ggc tta gga tgt gag ctc ctg aaa aat ctg gcc ttg tct ggt 292  
 Ala Gly Gly Leu Gly Cys Glu Leu Leu Lys Asn Leu Ala Leu Ser Gly  
                   80                  85                  90  
 ttt aga cag att cat gtt ata gat atg gac act ata gat gtt tcc aat 340  
 Phe Arg Gln Ile His Val Ile Asp Met Asp Thr Ile Asp Val Ser Asn  
                   95                  100                  105  
 cta aat agg cag ttt tta ttt agg cct aaa gat att g 377  
 Leu Asn Arg Gln Phe Leu Phe Arg Pro Lys Asp Ile  
                   110                  115                  120

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 agagggagtc ctcgcggacg tcagccaaga ttccaga atg act act atc ttg act 115  
                   Met Thr Thr Ile Leu Thr  
                   1                  5  
 tac ccc ttt aaa aat ctt ccc act gca tca aaa tgg gcc ctc aga ttt 163  
 Tyr Pro Phe Lys Asn Leu Pro Thr Ala Ser Lys Trp Ala Leu Arg Phe  
                   10                  15                  20  
 tcc ata aga cct ctg agc tgt tcc tcc cag cta cga gct gcc cca gct 211



Ser	Ile	Arg	Pro	Leu	Ser	Cys	Ser	Ser	Gln	Leu	Arg	Ala	Ala	Pro	Ala		
	25						30					35					
gtc	cag	acc	aaa	acg	aag	aag	acg	tta	gcc	aaa	ccc	aat	ata	agg	aat		259
Val	Gln	Thr	Lys	Thr	Lys	Lys	Thr	Leu	Ala	Lys	Pro	Asn	Ile	Arg	Asn		
	40					45					50						
ggt	gtg	gtg	gtg	gat	ggg	ggt	cgc	act	cca	ttt	ttg	ctg	tct	ggc	act		307
Val	Val	Val	Val	Asp	Gly	Val	Arg	Thr	Pro	Phe	Leu	Leu	Ser	Gly	Thr		
55					60					65				70			
tca	tat	aaa	gac	ctg	atg	cca	cat	gat	ttg	gct	aga	gca	gcg	ctt	acg		355
Ser	Tyr	Lys	Asp	Leu	Met	Pro	His	Asp	Leu	Ala	Arg	Ala	Ala	Leu	Thr		
				75				80						85			
ggg	ttg	ttg	cat	mga	acc	agt	gtc	cct	aag	gaa	gta	gtt	gat	tat	rtc		403
Gly	Leu	Leu	His	Arg	Thr	Ser	Val	Pro	Lys	Glu	Val	Val	Asp	Tyr	Xaa		
			90				95						100				
atc	ttt	ggg	aca	ggt	att	cag	gaa	gtg	aaa	aca	agc	aat	gtg	gct	aga		451
Ile	Phe	Gly	Thr	Val	Ile	Gln	Glu	Val	Lys	Thr	Ser	Asn	Val	Ala	Arg		
	105					110					115						
gag	gct	gcc	ctt	gga	gct	ggc	ttc	tct	gac	aag	act	cct	gct	cac	act		499
Glu	Ala	Ala	Leu	Gly	Ala	Gly	Phe	Ser	Asp	Lys	Thr	Pro	Ala	His	Thr		
	120					125					130						
gtc	acc	atg	gct	tgt	atc	tct	gcc	aac	caa	gcc	atg	asc	aca	ggg	gtt		547
Val	Thr	Met	Ala	Cys	Ile	Ser	Ala	Asn	Gln	Ala	Met	Xaa	Thr	Gly	Val		
	135				140					145					150		
ggc	ttg	att	gct	tct	ggc	cag	tgt	gat	gtg	atc	gtg	gca	ggg	ggg	gtt		595
Gly	Leu	Ile	Ala	Ser	Gly	Gln	Cys	Asp	Val	Ile	Val	Ala	Gly	Gly	Val		
			155					160						165			
gag	ttg	atg	tcc	gat	gtc	cct	att	cgt	cac	tca	agg	aaa	atg	aga	aaa		643
Glu	Leu	Met	Ser	Asp	Val	Pro	Ile	Arg	His	Ser	Arg	Lys	Met	Arg	Lys		
			170					175						180			
ctg	atg	ctt	gat	ctc	aat	aag	gcc	aaa	tct	atg	ggc	cag	cga	ctg	tct		691
Leu	Met	Leu	Asp	Leu	Asn	Lys	Ala	Lys	Ser	Met	Gly	Gln	Arg	Leu	Ser		
	185					190						195					
tta	atc	tct	aaa	ttc	cga	ttt	aag	tgc	cta	gca	cct	gag	ct				732
Leu	Ile	Ser	Lys	Phe	Arg	Phe	Lys	Cys	Leu	Ala	Pro	Glu					
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 <212> DNA  
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 <222> 166..330

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cctatagttg	gggtgagtgg	ggacccacag	gctcaggagg	ctgag atg	ggc cag	ggg											177
					Met Gly Gln Gly												
					1												
cac att cca	ttt ccg	aga gcc	ccc ata	ggc tgc	cca ccc	tgc cct	ggg										225
His Ile Pro	Phe Pro	Arg Ala	Pro Ile	Gly Cys	Pro Pro	Cys Pro	Gly										

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5           10           15           20
gtc tgg ggc cca ggg tct ggt gcg gag agg gcc cac agt gga ctt ggt      273
Val Trp Gly Pro Gly Ser Gly Ala Glu Arg Ala His Ser Gly Leu Gly
           25           30           35
gac gct gta tgc cct cac cgc tca gcc cct ggg gct ggc ttg gca gac      321
Asp Ala Val Cys Pro His Arg Ser Ala Pro Gly Ala Gly Leu Ala Asp
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agt aca gca tc
Ser Thr Ala
           55

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<220>  
 <221> CDS  
 <222> 14..316

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           Met Ser Leu Lys Met Asp Asn Arg Asp Val Ala Gly
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aag gct aac cgg tgg ttt ggg gtt gct ccc cct aaa tct gga aaa atg      97
Lys Ala Asn Arg Trp Phe Gly Val Ala Pro Pro Lys Ser Gly Lys Met
           15           20           25
aac atg aac atc ctt cac cag gaa gag ctc atc gct cag aag aaa cgg      145
Asn Met Asn Ile Leu His Gln Glu Glu Leu Ile Ala Gln Lys Lys Arg
           30           35           40
gaa att gaa gcc aaa atg gaa cag aaa gcc aag cag aat cag gtg gcc      193
Glu Ile Glu Ala Lys Met Glu Gln Lys Ala Lys Gln Asn Gln Val Ala
           45           50           55           60
agc cct cag ccc cca cat cct ggc gaa atc aca aat gca cac aac tct      241
Ser Pro Gln Pro Pro His Pro Gly Glu Ile Thr Asn Ala His Asn Ser
           65           70           75
ncc tgc att tcc aac aag ttt gcc aac gat ggt agc ttc ttg cag cag      289
Xaa Cys Ile Ser Asn Lys Phe Ala Asn Asp Gly Ser Phe Leu Gln Gln
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Phe Leu Lys Leu Gln Lys Ala Xaa Thr
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 tcattctcaa attcttagga cggtcggggc ctggaaggaa cgctctcgga attggccgcg 180  
 gaaaccgatc tgcccgttgt gtttgtgaaa cagagaaaga taggcggcca tggccaacc 240  
 ttgaaggctt atcaggaggg cagacttcaa aagctactaa aa atg aac ggc cct 294  
 Met Asn Gly Pro

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 gaa gat ctt ccc aag tcc tat gac tat gac ctt atc atc att gga ggt 342  
 Glu Asp Leu Pro Lys Ser Tyr Asp Tyr Asp Leu Ile Ile Ile Gly Gly  
 5 10 15 20  
 ggc tca gga ggt ctg gca gct gct aag gag gca gcc caa tat ggc aag 390  
 Gly Ser Gly Gly Leu Ala Ala Ala Lys Glu Ala Ala Gln Tyr Gly Lys  
 25 30 35  
 aag gtg atg gtc ctg gac ttt gtc act ccc acc cct ctt gga act aga 438  
 Lys Val Met Val Leu Asp Phe Val Thr Pro Thr Pro Leu Gly Thr Arg  
 40 45 50  
 tgg ggt ctc gga gga aca tgt gtg aat gtg ggt tgc ata cct aaa aaa 486  
 Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys  
 55 60 65  
 ctg atg cat caa gca gct ttg tta gga caa gcc ctg caa gac tct cga 534  
 Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu Gln Asp Ser Arg  
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 tccatttttaa tctgcgggga gccctgcct taccagggcg ttctctccgc ccgcgggtgg 180  
 atgctccgcg cctgcctcc gcagcctcgc tcagcagtc tgcgttgggg tctgcgcct 240  
 aggatgcact gag atg gta cat cag gat aac tgc tgc tat cag gca cag 289  
 Met Val His Gln Asp Asn Cys Ser Tyr Gln Ala Gln  
 1 5 10  
 aaa aat gag aga gag tct atc aga cag aag ttg gca ctt gga agc ttc 337  
 Lys Asn Glu Arg Glu Ser Ile Arg Gln Lys Leu Ala Leu Gly Ser Phe  
 15 20 25  
 ttt gat gat ggc cca gga att tat acc agc tgt agc aaa agt ggg aag 385  
 Phe Asp Asp Gly Pro Gly Ile Tyr Thr Ser Cys Ser Lys Ser Gly Lys  
 30 35 40  
 cca agc ctt tcc tcc cga ctg cag agt ggg atg aac ttg cag ata tgc 433  
 Pro Ser Leu Ser Ser Arg Leu Gln Ser Gly Met Asn Leu Gln Ile Cys  
 45 50 55 60

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Phe Val Asn Asp Ser Gly Ser Asp Lys Asp Ser Asp Ala Asp Asp Ser	
65 70 75	
aag act gaa acc agc ttg gac acc ccc ttg tct ccc atg agc aaa cag	529
Lys Thr Glu Thr Ser Leu Asp Thr Pro Leu Ser Pro Met Ser Lys Gln	
80 85 90	

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ccaggctctc cttcggaag atg tgc gac acg gca gta gct gat acc cgg cgc	173
Met Ser Asp Thr Ala Val Ala Asp Thr Arg Arg	
1 5 10	
ctt aac tgc aag ccg cag gac ctg acc gac gct tac ggg ccg cca agt	221
Leu Asn Ser Lys Pro Gln Asp Leu Thr Asp Ala Tyr Gly Pro Pro Ser	
15 20 25	
aac ttc ctg gag atc gac atc ttt aat cct cag acg gtg ggc gtg gga	269
Asn Phe Leu Glu Ile Asp Ile Phe Asn Pro Gln Thr Val Gly Val Gly	
30 35 40	
cgc gcg cgc ttc acc acc tat gag gtt cgc atg cgg aca aac cta cct	317
Arg Ala Arg Phe Thr Thr Tyr Glu Val Arg Met Arg Thr Asn Leu Pro	
45 50 55	
atc ttc aag cta aag gag tcc tgc gta cgg cgg cgc tac agt gac ttt	365
Ile Phe Lys Leu Lys Glu Ser Cys Val Arg Arg Arg Tyr Ser Asp Phe	
60 65 70 75	
gag tgg ctg aaa aat gag ctg gag aga gat agc aag att gta gta cca	413
Glu Trp Leu Lys Asn Glu Leu Glu Arg Asp Ser Lys Ile Val Val Pro	
80 85 90	
cca ctg cct ggg aaa gcc ttg aag cgg ct	442
Pro Leu Pro Gly Lys Ala Leu Lys Arg	
95 100	

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 <212> DNA  
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caggccaggt catctttggg tgggtggagtg caaaggaggc gacctgcaac agaggagtcc 120  
 cggtcaccag caacc atg acg gac cag cag gct gag gcc agg tcc tac ctc 171  
                   1                  5                  10  
 agc gaa gag atg atc gct gag ttc aag gct gcc ttt gac atg ttt gat 219  
 Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp  
                   15                  20                  25  
 gct gat ggt ggt ggg gac atc agc gtc aag gag ttg ggc acg gtg atg 267  
 Ala Asp Gly Gly Gly Asp Ile Ser Val Lys Glu Leu Gly Thr Val Met  
                   30                  35                  40  
 agg atg ctg ggc cag aca ccc acc aag gag gag ctg gac gcc atc atc 315  
 Arg Met Leu Gly Gln Thr Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile  
                   45                  50                  55                  60  
 gag gag gtg gat gag gac ggc agc ggc acc atc gac ttc gag gag ttc 363  
 Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe  
                   65                  70                  75  
 ttg gtc atg atg gtg cgc cag atg aaa gag gac gcg waa ggg aag agc 411  
 Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Xaa Gly Lys Ser  
                   80                  85                  90  
 gan gag gag ckg gga gtg caa gag aaa aac agg gag ggc ca 452  
 Xaa Glu Glu Xaa Gly Val Gln Glu Lys Asn Arg Glu Gly  
                   95                  100                  105

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 <212> DNA  
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 <222> 77..346

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 gccacgcggc agcagg atg agt gcg gag gca agc gcc cgg cct ctg cgg gtg 112  
                   1                  5                  10  
 ggc tcc cgt gta gag gtg att gga aaa ggc cac cga ggc act gtg gcc 160  
 Gly Ser Arg Val Glu Val Ile Gly Lys Gly His Arg Gly Thr Val Ala  
                   15                  20                  25  
 tat gtt gga gcc aca ctg ttt gcc act ggc aaa tgg gta ggc gtg att 208  
 Tyr Val Gly Ala Thr Leu Phe Ala Thr Gly Lys Trp Val Gly Val Ile  
                   30                  35                  40  
 ctg gat gaa gca aag ggc aaa aat gat gga act gtt caa ggc agg aag 256  
 Leu Asp Glu Ala Lys Gly Lys Asn Asp Gly Thr Val Gln Gly Arg Lys  
                   45                  50                  55                  60  
 tac ttc act tgt gat gaa ggg cat ggc atc ttt gtg cgc cag tcc cag 304  
 Tyr Phe Thr Cys Asp Glu Gly His Gly Ile Phe Val Arg Gln Ser Gln  
                   65                  70                  75  
 atc cag gta ttt gaa gat gga gca gat act act ccc cag aga c 347  
 Ile Gln Val Phe Glu Asp Gly Ala Asp Thr Thr Pro Gln Arg  
                   80                  85                  90

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 86..433

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 gctagaattt tgaggctccc ttctg atg aaa att gag ctg tcc atg cag cca 112  
 Met Lys Ile Glu Leu Ser Met Gln Pro  
 1 5  
 tgg aac ccg ggt tac agc agt gag ggg gcc acg gct caa gaa act tac 160  
 Trp Asn Pro Gly Tyr Ser Ser Glu Gly Ala Thr Ala Gln Glu Thr Tyr  
 10 15 20 25  
 aca tgt cca aaa atg att gag atg gag cag gcg gag gcc cag ctt gct 208  
 Thr Cys Pro Lys Met Ile Glu Met Glu Gln Ala Glu Ala Gln Leu Ala  
 30 35 40  
 gag tta gac ctg cta gcc agt atg ttc cct ggt gag aat gag ctc ata 256  
 Glu Leu Asp Leu Leu Ala Ser Met Phe Pro Gly Glu Asn Glu Leu Ile  
 45 50 55  
 gtg aat gac cag ctg gct gta gca gaa ctg aaa gat tgt att gaa aag 304  
 Val Asn Asp Gln Leu Ala Val Ala Glu Leu Lys Asp Cys Ile Glu Lys  
 60 65 70  
 awk aca atg gag ggg cga tct tca aaa gtc tac ttt act atc aat atg 352  
 Xaa Thr Met Glu Gly Arg Ser Ser Lys Val Tyr Phe Thr Ile Asn Met  
 75 80 85  
 aac ctg gat gta tct gac gaa aaa atg act cag aaa att aaa ctg gaa 400  
 Asn Leu Asp Val Ser Asp Glu Lys Met Thr Gln Lys Ile Lys Leu Glu  
 90 95 100 105  
 gag aat ttt aat tcg cca tcg aga aga cat tcc tt 435  
 Glu Asn Phe Asn Ser Pro Ser Arg Arg His Ser  
 110 115

<210> 1148  
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 <212> DNA  
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 <222> 61..339

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 atg gcc cat ttc tcc agc gag gac cag gcg atg ctg cag gcg atg ctg 108  
 Met Ala His Phe Ser Ser Glu Asp Gln Ala Met Leu Gln Ala Met Leu  
 1 5 10 15  
 agg cgg ttg ttc cag agc gtg aag gag aaa atc acg ggt gcc cct tcc 156  
 Arg Arg Leu Phe Gln Ser Val Lys Glu Lys Ile Thr Gly Ala Pro Ser

ctg gag tgt gcc gaa gag att ctt tta cat ctg gag gaa act gat gaa	20	25	30	204
Leu Glu Cys Ala Glu Glu Ile Leu Leu His Leu Glu Glu Thr Asp Glu				
	35	40	45	
aat ttt cac aac tat gaa ttt gtg aaa tac ctc agg cag cat ata ggc				252
Asn Phe His Asn Tyr Glu Phe Val Lys Tyr Leu Arg Gln His Ile Gly				
	50	55	60	
aac act ttg ggt tct atg att gan gaa gaa atg gaa aaa tgc aca tct				300
Asn Thr Leu Gly Ser Met Ile Xaa Glu Glu Met Glu Lys Cys Thr Ser				
	65	70	75	80
gat cgg aat cag ggt gaa gaa tgc ggc tat gat aca gtt gt				341
Asp Arg Asn Gln Gly Glu Glu Cys Gly Tyr Asp Thr Val				
	85	90		

<210> 1149  
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 <212> DNA  
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<220>  
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 <222> 79..477

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caccttctctc tgtctgcc atg gac caa caa gca ata tat gct gag tta aac	111
Met Asp Gln Gln Ala Ile Tyr Ala Glu Leu Asn	
	1
tta ccc aca gac tca ggc cca gaa agt tct tca cct tca tct ctt cct	159
Leu Pro Thr Asp Ser Gly Pro Glu Ser Ser Ser Pro Ser Ser Leu Pro	
	15
cgg gat gtc tgt cag ggt tca cct tgg cat caa ttt gcc ctg aaa ctt	207
Arg Asp Val Cys Gln Gly Ser Pro Trp His Gln Phe Ala Leu Lys Leu	
	30
akc tgt gct ggg att att ctc ctt gtc ttg gtt gtt act ggg ttg agt	255
Xaa Cys Ala Gly Ile Ile Leu Leu Val Leu Val Thr Gly Leu Ser	
	45
gtt tca gtg aca tcc tta ata cag aaa tca tca ata gaa aaa tgc agt	303
Val Ser Val Thr Ser Leu Ile Gln Lys Ser Ser Ile Glu Lys Cys Ser	
	60
gtg gac att caa cag agc agg aat aaa aca aca gag aga ccg ggt ctc	351
Val Asp Ile Gln Gln Ser Arg Asn Lys Thr Thr Glu Arg Pro Gly Leu	
	80
tta aac tgc cca ata tat tgg cag caa ctc cga gag aaa tgc ttg tta	399
Leu Asn Cys Pro Ile Tyr Trp Gln Gln Leu Arg Glu Lys Cys Leu Leu	
	95
ttt tct cac act gtc aac cct tgg aat aac agt cta gct gat tgt tcc	447
Phe Ser His Thr Val Asn Pro Trp Asn Asn Ser Leu Ala Asp Cys Ser	
	110
acc aaa gaa tcc agc ctg ctg ctt att cga ga	479
Thr Lys Glu Ser Ser Leu Leu Leu Ile Arg	
	125
	130

<210> 1150  
 <211> 560  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 200..559

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 ccggccctcc gtagccgctc gactgtcgcg ctgcaccagc ttcctcctcg gcgttcccca 120  
 cgcctatattg ggcggattct tggcgccgga ggaagaggca gggtcaccct ctctccacgt 180  
 cagagacctg actgtggag atg gcg gct cag aag ata aac gag ggg ctg gaa 232  
 Met Ala Ala Gln Lys Ile Asn Glu Gly Leu Glu  
 1 5 10  
 cac ctc gcc aaa gca gag aaa tac ctg aaa act ggt ttt tta aaa tgg 280  
 His Leu Ala Lys Ala Glu Lys Tyr Leu Lys Thr Gly Phe Leu Lys Trp  
 15 20 25  
 aag cca gat tat gac agt gcc gct tct gaa tat gga aaa gca gct gtt 328  
 Lys Pro Asp Tyr Asp Ser Ala Ala Ser Glu Tyr Gly Lys Ala Ala Val  
 30 35 40  
 gct ttt aaa aat gcc aaa cag ttt gag caa gca aaa gat gcc tgc ctg 376  
 Ala Phe Lys Asn Ala Lys Gln Phe Glu Gln Ala Lys Asp Ala Cys Leu  
 45 50 55  
 agg gaa gct gtt gcc cat gaa aat aat agg gct ctt ttt cat gct gcc 424  
 Arg Glu Ala Val Ala His Glu Asn Asn Arg Ala Leu Phe His Ala Ala  
 60 65 70 75  
 aaa gct tat gag caa gct gga atg atg ttg aag gag atg cag aaa cta 472  
 Lys Ala Tyr Glu Gln Ala Gly Met Met Leu Lys Glu Met Gln Lys Leu  
 80 85 90  
 cca gag gcc gtt cag cta att gag aag gcc agc atg atg tat cta gaa 520  
 Pro Glu Ala Val Gln Leu Ile Glu Lys Ala Ser Met Met Tyr Leu Glu  
 95 100 105  
 aac ggc acc cca gac aca gca gcc atg gct ttg gag cga g 560  
 Asn Gly Thr Pro Asp Thr Ala Ala Met Ala Leu Glu Arg  
 110 115 120

<210> 1151  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 132..548

<400> 1151  
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 gtacttattt gctgtgctat ttgacctctt gggttcagag agctccctgg accatctaata 120  
 ggctatggga g atg ata aaa gct tcg atg atg aag aat cag tgg atg gaa 170  
 Met Ile Lys Ala Ser Met Met Lys Asn Gln Trp Met Glu

004220" 6667560



	1		5		10	
ata ggc cat cat cag ctg cat cag cct tca agg ttc ctg cac cta aaa						218
Ile Gly His His Gln Leu His Gln Pro Ser Arg Phe Leu His Leu Lys						
15		20		25		
cat ccg gaa atc ctg cca aca gtg caa gga agc ctg gtt cag cag gtg						266
His Pro Glu Ile Leu Pro Thr Val Gln Gly Ser Leu Val Gln Gln Val						
30		35		40		45
gcc cta agg ttg gag cgt gct tct aag gaa gga ggt gct gga gca gtt						314
Ala Leu Arg Leu Glu Arg Ala Ser Lys Glu Gly Gly Ala Gly Ala Val						
50		55		60		
gat gaa gat gat ttt ata aaa gct ttt aca gat gtc cct tct att cag						362
Asp Glu Asp Asp Phe Ile Lys Ala Phe Thr Asp Val Pro Ser Ile Gln						
65		70		75		
att tat tct agt cga gaa ctc gaa gaa aca tta aat aaa atc agg gaa						410
Ile Tyr Ser Ser Arg Glu Leu Glu Glu Thr Leu Asn Lys Ile Arg Glu						
80		85		90		
att ttg tca gat gat aaa cat gac tgg gat cag cgt gcc aat gca ctg						458
Ile Leu Ser Asp Asp Lys His Asp Trp Asp Gln Arg Ala Asn Ala Leu						
95		100		105		
aag aaa att cga tca ctg ctt gtt gct gga gct gca cag tat gat tgc						506
Lys Lys Ile Arg Ser Leu Leu Val Ala Gly Ala Ala Gln Tyr Asp Cys						
110		115		120		125
ttt ttt caa cat tta cga ttg ttg gat gga gca ctt aaa ctt tc						550
Phe Phe Gln His Leu Arg Leu Leu Asp Gly Ala Leu Lys Leu						
130		135				

<210> 1152  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 112..393

<400> 1152  
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 tctcctcccg ggagtcttct gcctactccc agaagaggag ggaagcacag t atg aag 117  
 Met Lys  
 1  
 act ttg gag act caa ccg tta gct ccg gac tgc tgt cct tca gac cag 165  
 Thr Leu Glu Thr Gln Pro Leu Ala Pro Asp Cys Cys Pro Ser Asp Gln  
 5 10 15  
 gac cca gct cca gcc cat cct tct ccc cac gct tcc ccg atg aat aaa 213  
 Asp Pro Ala Pro Ala His Pro Ser Pro His Ala Ser Pro Met Asn Lys  
 20 25 30  
 aat gcg gac tct gaa ctg atg cca ccg cct ccc gaa agg ggg gat ccg 261  
 Asn Ala Asp Ser Glu Leu Met Pro Pro Pro Pro Glu Arg Gly Asp Pro  
 35 40 45 50  
 ccc cgg ttg tcc cca gat cct gtg gct ggc tca gct gtg tcc cag gag 309  
 Pro Arg Leu Ser Pro Asp Pro Val Ala Gly Ser Ala Val Ser Gln Glu  
 55 60 65  
 cta cgg gag ggg gac cca gtt tct ctc tcc act ccc ctg gaa aca gag 357

Leu Arg Glu Gly Asp Pro Val Ser Leu Ser Thr Pro Leu Glu Thr Glu  
 70 75 80  
 ttt ggt tcc cct agt gag ttg agt cct cga atc aag 393  
 Phe Gly Ser Pro Ser Glu Leu Ser Pro Arg Ile Lys  
 85 90

<210> 1153  
 <211> 656  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 200..655

<400> 1153  
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 actattgggc gctaggagac gaactattgg tacggggcta gagaggaagg ctttgggatt 120  
 gccggggagc agcgagcgac cgacttccgt ttccagttac caaggcacga ggtccgggtg 180  
 ttccaacca gggggaaaa atg cgg cct ttg act gaa gag gag acc cgt gtc 232  
 Met Arg Pro Leu Thr Glu Glu Glu Thr Arg Val  
 1 5 10  
 atg ttt gag aag ata gcg aaa tac att ggg gag aat ctt caa ctg ctg 280  
 Met Phe Glu Lys Ile Ala Lys Tyr Ile Gly Glu Asn Leu Gln Leu Leu  
 15 20 25  
 gtg gac cgg ccc gat ggc acc tac tgt ttc cgt ctg cac aac gac cgg 328  
 Val Asp Arg Pro Asp Gly Thr Tyr Cys Phe Arg Leu His Asn Asp Arg  
 30 35 40  
 gtg tac tat gtg agt gag aag att atg aag ctg gcc gcc aat att tcc 376  
 Val Tyr Tyr Val Ser Glu Lys Ile Met Lys Leu Ala Ala Asn Ile Ser  
 45 50 55  
 ggg gac aag ctg gtg tgc ctg ggg acc tgc ttt gga aaa ttc act aaa 424  
 Gly Asp Lys Leu Val Ser Leu Gly Thr Cys Phe Gly Lys Phe Thr Lys  
 60 65 70 75  
 acc cac aag ttt mrg ttg cac gtc aca gct ctg gat tac ctt gca cct 472  
 Thr His Lys Phe Xaa Leu His Val Thr Ala Leu Asp Tyr Leu Ala Pro  
 80 85 90  
 tat gcc aag tat aaa gtt tgg ata aag cct ggt gca gag cag tcc ttc 520  
 Tyr Ala Lys Tyr Lys Val Trp Ile Lys Pro Gly Ala Glu Gln Ser Phe  
 95 100 105  
 ctg tat ggg aac cat gtg ttg aaa tct ggt ctg ggt cga atc act gaa 568  
 Leu Tyr Gly Asn His Val Leu Lys Ser Gly Leu Gly Arg Ile Thr Glu  
 110 115 120  
 aat act tct cag tac cag ggc gtg gtg gtg tac tcc atg gca gac atc 616  
 Asn Thr Ser Gln Tyr Gln Gly Val Val Val Tyr Ser Met Ala Asp Ile  
 125 130 135  
 cct ttg ggt ttt ggg gtg gca gcc aaa tct aca caa gac t 656  
 Pro Leu Gly Phe Gly Val Ala Ala Lys Ser Thr Gln Asp  
 140 145 150

<210> 1154  
 <211> 472  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 262..471

<400> 1154

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ttccagaaaag	agctatttta	acagaagcaa	ctcaaagata	tcccttcgac	agaagtggaa	180
gtgctgaaaa	atgctcatct	ctcacacaga	cttttgatgg	acaggagttt	ctaagtatca	240
tgcttaccaa	caagctgtaa	a atg atc acc	ctg aac aat	caa gat caa	cct	291
		Met Ile Thr	Leu Asn Asn	Gln Asp Gln	Pro	
		1	5	10		
gtc cct ntt	aac agc tca	cat cca gat	gaa tac aaa	att gca gcc	ctt	339
Val Pro Xaa	Asn Ser Ser	His Pro Asp	Glu Tyr Lys	Ile Ala Ala	Leu	
	15	20	25			
gtc ttc tat	agc tgt atc	ttc ata att	gga tta ttt	gtt aac atc	act	387
Val Phe Tyr	Ser Cys Ile	Phe Ile Ile	Gly Leu Phe	Val Asn Ile	Thr	
	30	35	40			
gca tta tgg	gtt ttc agt	tgt acc acc	aag aag aga	acc acg gta	acc	435
Ala Leu Trp	Val Phe Ser	Cys Thr Thr	Lys Lys Arg	Thr Thr Val	Thr	
	45	50	55			
atc tat atg	atg aat gtg	gca tta gtg	gac ttg ata	t		472
Ile Tyr Met	Met Asn Val	Ala Leu Val	Asp Leu Ile			
60	65	70				

<210> 1155

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 144..425

<400> 1155

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ccgtccccag	ctcagtgaca	aaa atg ctg	agt ttc ttc	cgt aga aca	cta ggg	173
		Met Leu Ser	Phe Phe Arg	Arg Thr Leu	Gly	
		1	5	10		
cgt cgg tct	atg cgt aaa	cat gca gag	aag gaa cga	ctc cga gaa	gca	221
Arg Arg Ser	Met Arg Lys	His Ala Glu	Lys Glu Arg	Leu Arg Glu	Ala	
	15	20	25			
caa cgc gcc	gcc aca cat	att cct gca	gct gga gat	tct aag tcc	atc	269
Gln Arg Ala	Ala Thr His	Ile Pro Ala	Ala Gly Asp	Ser Lys Ser	Ile	
	30	35	40			
atc acg tgt	cgg gtg tcc	ctt ctg gat	ggg act gat	gtt agt gtg	gac	317
Ile Thr Cys	Arg Val Ser	Leu Leu Asp	Gly Thr Asp	Val Ser Val	Asp	
	45	50	55			
ttg cca aaa	aaa gcc aaa	gga caa gag	ttg ttt gat	cag att atg	tac	365

Leu	Pro	Lys	Lys	Ala	Lys	Gly	Gln	Glu	Leu	Phe	Asp	Gln	Ile	Met	Tyr	
60						65				70						
cac	ctg	gac	ctg	att	gaa	agc	gac	tat	ttt	ggc	ctg	aga	ttt	atg	gat	413
His	Leu	Asp	Leu	Ile	Glu	Ser	Asp	Tyr	Phe	Gly	Leu	Arg	Phe	Met	Asp	
75					80					85				90		
tca	gca	caa	gta	gc												427
Ser	Ala	Gln	Val													

<210> 1156  
 <211> 604  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 174..602

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taaaaaaaaaac attaaaagca aaatgtaagt atataaggaa taccaaataca aatttataga	120
ctaattctttt tcnawtnagk attttaagag tcttttttctt ctttatagga aaa atg	176
	Met
	1
ctt tct gaa agc agc tcc ttt ttg aag ggt gtg atg ctt gga agc att	224
Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser Ile	
	5 10 15
ttc tgt gct ttg atc act atg cta gga cac att agg att ggt cat gga	272
Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly His Gly	
	20 25 30
aat aga atg cac cac cat gag cat cat cac cta caa gct cct aac aaa	320
Asn Arg Met His His His Glu His His His Leu Gln Ala Pro Asn Lys	
	35 40 45
gaa gat atc ttg aaa att tca gag gat gag cgc atg gag ctc agt aag	368
Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser Lys	
	50 55 60 65
agc ttt cga gta tac tgt att atc ctt gta aaa ccc aaa gat gtg agt	416
Ser Phe Arg Val Tyr Cys Ile Ile Leu Val Lys Pro Lys Asp Val Ser	
	70 75 80
ctt tgg gct gca gta aag gag act tgg acc aaa cac tgt gac aaa gca	464
Leu Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys Ala	
	85 90 95
gag ttc ttc agt tct gaa aat gtt aaa gtg ttt gag tca att aat atg	512
Glu Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn Met	
	100 105 110
gac aca aat gac atg tgg tta atg atg aga aag ctt aca aat acg cct	560
Asp Thr Asn Asp Met Trp Leu Met Met Arg Lys Leu Thr Asn Thr Pro	
	115 120 125
ttg ata agt ata gag acc aat aca act ggt tct tcc ttg cac gc	604
Leu Ile Ser Ile Glu Thr Asn Thr Thr Gly Ser Ser Leu His	
	130 135 140

<210> 1157  
 <211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 175..603

<400> 1157

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cctgcagcta gaacagcctg gtcaggagcg taacggagtg gatgcgccaa cgtgagagga 120  
aaccgtgcg cggctgcgct ttcctgtccc caagccgttc tagacgcggg aaaa atg 177  
Met  
1  
ctt tct gaa agc agc tcc ttt ttg aag ggt gtg atg ctt gga agc att 225  
Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser Ile  
5 10 15  
ttc tgt gct ttg atc act atg cta gga cac att agg att ggt cat gga 273  
Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly His Gly  
20 25 30  
aat aga atg cac cac cat gag cat cat cac cta caa gct cct aac aaa 321  
Asn Arg Met His His His Glu His His His Leu Gln Ala Pro Asn Lys  
35 40 45  
gaa gat atc ttg aaa att tca gag gat gag cgc atg gag ctc agt aag 369  
Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser Lys  
50 55 60 65  
agc ttt cga gta tac tgt att atc ctt gta aaa ccc aaa gat gtg agt 417  
Ser Phe Arg Val Tyr Cys Ile Ile Leu Val Lys Pro Lys Asp Val Ser  
70 75 80  
ctt tgg gct gca gta aag gag act tgg acc aaa cac tgt gac aaa gca 465  
Leu Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys Ala  
85 90 95  
gag ttc ttc agt tct gaa aat gtt aaa gtg ttt gag tca att aat atg 513  
Glu Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn Met  
100 105 110  
gac aca aat gac atg tgg tta atg atg aga aag ctt aca aat acg cct 561  
Asp Thr Asn Asp Met Trp Leu Met Met Arg Lys Leu Thr Asn Thr Pro  
115 120 125  
ttg ata agt ata gag acc aat aca act ggt tct tcc ttg cac gc 605  
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<210> 1158

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 13..414

<400> 1158

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Ser Asn Ser Gly Ser Tyr Ser Gly Asp Ala Ser Gly Ala Val Thr Val														
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tgg gag gtg gtc tca ctc ttg gga aaa ctg ctg ggc acc gtc gtc gcg														147
Trp Glu Val Val Ser Leu Leu Gly Lys Leu Leu Gly Thr Val Val Ala														
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ctg aag gtg gtt ctg tac ctg ctc cga gtg tgc tta gcg atg gcc tgg														195
Leu Lys Val Val Leu Tyr Leu Leu Arg Val Cys Leu Ala Met Ala Trp														
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aaa tcc ggc ggc gcc agc cac tcg gag cta atc cac aat ctc cgc aaa														243
Lys Ser Gly Gly Ala Ser His Ser Glu Leu Ile His Asn Leu Arg Lys														
					65					70			75	
aat gga atc atc aag aca gat aaa gta ttt gaa gtg atg ctg gct aca														291
Asn Gly Ile Ile Lys Thr Asp Lys Val Phe Glu Val Met Leu Ala Thr														
					80					85			90	
gay cgc tcc cac tat gca aaa tgt aac cca tac atg gat tct cca caa														339
Asp Arg Ser His Tyr Ala Lys Cys Asn Pro Tyr Met Asp Ser Pro Gln														
					95					100			105	
tca ata ggt ttc caa gca aca atc agt gct cca cac atg cat gca tat														387
Ser Ile Gly Phe Gln Ala Thr Ile Ser Ala Pro His Met His Ala Tyr														
					110					115			120	125
gcg cta gaa ctt cta ttt gat cag ttg c														415
Ala Leu Glu Leu Leu Phe Asp Gln Leu														
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 <212> DNA  
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 <222> 113..277

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 Met Glu  
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 ttt caa gca gta gtg atg gca gta ggt gga gga tct cgg atg aca gac 166  
 Phe Gln Ala Val Val Met Ala Val Gly Gly Gly Ser Arg Met Thr Asp  
 5 10 15  
 cta act tcc agc att ccc aaa cct ctg ctt cca gtt ggg aac aaa cct 214  
 Leu Thr Ser Ser Ile Pro Lys Pro Leu Leu Pro Val Gly Asn Lys Pro  
 20 25 30  
 tta att tgg tac cca ttg aac ctg ctt gag cgt gtg gat ttg aag aag 262  
 Leu Ile Trp Tyr Pro Leu Asn Leu Leu Glu Arg Val Asp Leu Lys Lys  
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 Ser Leu Trp Leu Gln  
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 Met Asp Lys Asp Cys Glu Met  
 1 5  
 aaa cgc acc aca ctg gac agc ccy ttg ggg aag ctg gag ctg tct ggt 162  
 Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly  
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 Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser  
 25 30 35  
 gca gct gat gcc gtg gag gtc cca gcc ccc gct gcg gtt ctc gga ggt 258  
 Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly  
 40 45 50 55  
 ccg gag ccc ctg atg cag tgc aca gcc tgg ctg aat gcc tat ttc cac 306  
 Pro Glu Pro Leu Met Gln Cys Thr Ala Trp Leu Asn Ala Tyr Phe His  
 60 65 70  
 cag ccc gag gct atc gaa gag ttc ccc gtg ccg gct ctt cac cat ccc 354  
 Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro  
 75 80 85  
 gtt ttc cag caa gag tgc ttc acc aga cag gtg tta tgg aag ctg ctg 402  
 Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu  
 90 95 100  
 aag gtt gtg aaa ttc gga gaa gtg att tct tac cag caa tta gca gcm 450  
 Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala  
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 Xaa Ala Gly  
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Leu Ala Val Glu Tyr Val Asp Ser Leu Leu Pro Glu Asn Pro Leu Gln
15          20          25          30
gaa cca ttt aaa aat gct tgg aac tat atg ttg aat aat tat aca aag 266
Glu Pro Phe Lys Asn Ala Trp Asn Tyr Met Leu Asn Asn Tyr Thr Lys
      35          40          45
ttc cag att gca aca tgg gga tcc ctt ata gtt cat gaa gcc ctt tat 314
Phe Gln Ile Ala Thr Trp Gly Ser Leu Ile Val His Glu Ala Leu Tyr
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ttc tta ttc tgt tta cct gga ttt tta ttt caa ttt atr cct tat atg 362
Phe Leu Phe Cys Leu Pro Gly Phe Leu Phe Gln Phe Xaa Pro Tyr Met
      65          70          75
aaa aaa tac aaa att caa aag gat aag cca gag aca tgg gaa aac caa 410
Lys Lys Tyr Lys Ile Gln Lys Asp Lys Pro Glu Thr Trp Glu Asn Gln
      80          85          90
tgg aag tgt ttc aaa gtt ctt ctc ttt aat cac ttc tgt atc cag ctg 458
Trp Lys Cys Phe Lys Val Leu Leu Phe Asn His Phe Cys Ile Gln Leu
95          100          105          110
cct ttg att tgt gga a
Pro Leu Ile Cys Gly
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<212> DNA  
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<220>  
<221> CDS  
<222> 77..361

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atacctctc tgaaaa atg gca gaa gca gtt ttc cat gcc cca aag agg aaa 112
      Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys
      1          5          10
aga aga gtg tat gag act tac gag tct cca ttg cca atc cct ttt ggt 160
Arg Arg Val Tyr Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly
15          20          25
cag gac cat ggt cct ctg aaa gaa ttc aag ata ttc cgt gct gaa atg 208
Gln Asp His Gly Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met
30          35          40
att aac aac aat gtg att gtg agg aat gcg gag gac att gag cag ctc 256
Ile Asn Asn Asn Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu
45          50          55          60
tat ggg aaa ggt tat ttt gga aaa ggt att ctt tca aga agc cgt cca 304
Tyr Gly Lys Gly Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro
65          70          75
agc ttc aca att tca gat cct aaa ctg gtt gct aaa tgg aaa gat atg 352
Ser Phe Thr Ile Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met

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80 85 90 362  
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Lys Thr Asn  
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<210> 1163  
<211> 266  
<212> DNA  
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<220>  
<221> CDS  
<222> 7..264

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Asn Leu Lys Lys Thr Pro Lys Lys Lys Met Lys Met Val Thr Gly Ala  
15 20 25 30  
gta gcg tcg gtg ctg gaa gac gag gcc aca gac act tct gat agt gaa 144  
Val Ala Ser Val Leu Glu Asp Glu Ala Thr Asp Thr Ser Asp Ser Glu  
35 40 45  
gga agc tgt gga tcg gaa aag gac cac ttt tat tct gat gat gac gca 192  
Gly Ser Cys Gly Ser Glu Lys Asp His Phe Tyr Ser Asp Asp Asp Ala  
50 55 60  
ata gaa gct gac agt gag ggt gat gct gag ccc tgt gac aaa gaa aat 240  
Ile Glu Ala Asp Ser Glu Gly Asp Ala Glu Pro Cys Asp Lys Glu Asn  
65 70 75  
gaa aat gat gga gaa tca agt gtt gg 266  
Glu Asn Asp Gly Glu Ser Ser Val  
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<210> 1164  
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<212> DNA  
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<220>  
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ccggtctctc cctgcaggmt cgggtcaacgc agccgtcgcc gccctctgca cccagcccag 180  
gtcgccactg cttcagtcgg gttctcaaag cctcagcacc atctttttatc cccgagcagc 240  
ctggatcgtc gttccctcag tccggacgcc actgctaggt ccgaccaccg ccgcttctga 300  
tatttcgggtg agtcttttcc tgtggagggt tgggtctcccg atctctgtgg tagccacctt 360  
aggcgtgtac ggtcctttga aaa atg gcc gag tca gag aac cgc aar gag ctg 413  
Met Ala Glu Ser Glu Asn Arg Lys Glu Leu

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Ser	Glu	Ser	Ser	Gln	Glu	Glu	Ala	Gly	Asn	Gln	Ile	Met	Val	Glu	Gly					
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ctc	ggg	gaa	cat	ctg	gag	cgc	ggt	gaa	gat	gcc	gct	gct	ggg	ctt	gga					509
Leu	Gly	Glu	His	Leu	Glu	Arg	Gly	Glu	Asp	Ala	Ala	Ala	Gly	Leu	Gly					
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gac	gat	ggg	aag	tgc	ggt	gaa	gaa	gct	gcc	gct	ggg	ctt	ggg	gaa	gaa					557
Asp	Asp	Gly	Lys	Cys	Gly	Glu	Glu	Ala	Ala	Ala	Gly	Leu	Gly	Glu	Glu					
		45				50					55									
ggg	gnn	aac	ggt	gaa	gat	act	gct	gct	ggg	tcc	ggg	gaa	gat	ggg	aaa					605
Gly	Xaa	Asn	Gly	Glu	Asp	Thr	Ala	Ala	Gly	Ser	Gly	Glu	Asp	Gly	Lys					
	60				65				70											
aaa	rgt	ggc	gat	act	gat	gag	gac													629
Lys	Xaa	Gly	Asp	Thr	Asp	Glu	Asp													
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&lt;210&gt; 1165

&lt;211&gt; 488

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 193..486

&lt;400&gt; 1165

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gcctgagact	taagggttatt	gcttgccgc	ggcctggtat	tccggcgatt	cgtttcttgc															120
tcggcttct	ggagctgtgg	tccgtgtggg	cttccacctc	agacagttgc	gctggctcag															180
cggggcccga	ac atg gct gcg tcc ggt ctg gat cat ctc aaa aat ggc tac																			231
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aga aga aga ttt tgt cga cct tcc agg gca cgt gac att aac aca gag																				279
Arg Arg Arg Phe Cys Arg Pro Ser Arg Ala Arg Asp Ile Asn Thr Glu																				
	15			20				25												
caa ggc cag aat gtt ctg gaa atc tta caa gac tgt ttt gaa gaa aaa																				327
Gln Gly Gln Asn Val Leu Glu Ile Leu Gln Asp Cys Phe Glu Glu Lys																				
	30			35				40				45								
agt ctt gcc aat gat ttt art aca aat tct aca aaa tca gtg cct aat																				375
Ser Leu Ala Asn Asp Phe Xaa Thr Asn Ser Thr Lys Ser Val Pro Asn																				
	50			55				60												
tca aca cgc aaa ata aaa gac act tgt att cag tca cca agc aaa gag																				423
Ser Thr Arg Lys Ile Lys Asp Thr Cys Ile Gln Ser Pro Ser Lys Glu																				
	65			70				75												
tgc aga aat cac atc caa agt cag ttc cag ttt ctt caa aga aga aag																				471
Cys Arg Asn His Ile Gln Ser Gln Phe Gln Phe Leu Gln Arg Arg Lys																				
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aag ctc tct aca gtt tg																				488
Lys Leu Ser Thr Val																				
	95																			

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<220>  
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 <222> 81..368

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 Met Glu Ser Asp Phe Tyr Leu Arg Tyr Tyr Val  
 1 5 10  
 ggg cac aag ggc aag ttc ggc cac gag ttc ctg gag ttt gag ttt cga 161  
 Gly His Lys Gly Lys Phe Gly His Glu Phe Leu Glu Phe Glu Phe Arg  
 15 20 25  
 ccg gac ggg aag tta aga tat gcc aac aac agc aat tac aag aat gat 209  
 Pro Asp Gly Lys Leu Arg Tyr Ala Asn Asn Ser Asn Tyr Lys Asn Asp  
 30 35 40  
 gtc atg atc aga aaa gag gag ctt gaa atc gtc att gga gat gaa cac 257  
 Val Met Ile Arg Lys Glu Glu Leu Glu Ile Val Ile Gly Asp Glu His  
 45 50 55  
 att tct ttt aca aca tca aaa att ggt tcc ctt att gat gtc aat caa 305  
 Ile Ser Phe Thr Thr Ser Lys Ile Gly Ser Leu Ile Asp Val Asn Gln  
 60 65 70 75  
 tcc aag gat cca gaa ggc tta cga gta ttt tat tat ctt gtc cag gac 353  
 Ser Lys Asp Pro Glu Gly Leu Arg Val Phe Tyr Tyr Leu Val Gln Asp  
 80 85 90  
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 Leu Lys Cys Leu Val  
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 <212> DNA  
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 <222> 81..479

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 Met Glu Ser Asp Phe Tyr Leu Arg Tyr Tyr Val  
 1 5 10  
 ggg cac aag ggc aag ttc ggc cac gag ttc ctg gag ttt gag ttt cga 161  
 Gly His Lys Gly Lys Phe Gly His Glu Phe Leu Glu Phe Glu Phe Arg  
 15 20 25  
 ccg gac ggg aag tta aga tat gcc aac aac agc aat tac aag aat gat 209  
 Pro Asp Gly Lys Leu Arg Tyr Ala Asn Asn Ser Asn Tyr Lys Asn Asp  
 30 35 40

gtc atg atc aga aaa gag gct tat gta cat aaa agc gtg atg gag gaa	257
Val Met Ile Arg Lys Glu Ala Tyr Val His Lys Ser Val Met Glu Glu	
45 50 55	
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Leu Lys Arg Ile Ile Asp Asp Ser Glu Ile Thr Lys Glu Asp Asp Ala	
60 65 70 75	
ttg tgg cct cct cct gac cga gtg ggc cgg cag gag ctt gaa atc gtc	353
Leu Trp Pro Pro Pro Asp Arg Val Gly Arg Gln Glu Leu Glu Ile Val	
80 85 90	
att gga gat gaa cac att tct ttt aca aca tca aaa att ggt tcc ctt	401
Ile Gly Asp Glu His Ile Ser Phe Thr Thr Ser Lys Ile Gly Ser Leu	
95 100 105	
att gat gtc aat caa tcc aag gat cca gaa ggc tta cga gta ttt tat	449
Ile Asp Val Asn Gln Ser Lys Asp Pro Glu Gly Leu Arg Val Phe Tyr	
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Tyr Leu Val Gln Asp Leu Lys Cys Leu Val	
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Lys Leu Arg Leu Gln Lys Trp Tyr Leu Ala Thr Ser Asp Lys Glu Arg	
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Lys Lys Met Val Arg Glu Leu Met Gln Val Val Leu Ala Arg Lys Pro	
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Lys Met Cys Ser Phe Leu Glu Trp Arg Asp Leu Lys Val Val Tyr Lys	
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Arg Tyr Ala Ser Leu Tyr Phe Cys Cys Ala Ile Glu Gly Gln Asp Asn	
65 70 75	
gag ctc atc aca ctg gag ctg atc cac cga tac gtg gag ctc tta gac	349
Glu Leu Ile Thr Leu Glu Leu Ile His Arg Tyr Val Glu Leu Leu Asp	
80 85 90	
aaa tac ttt ggc agt gtg tgc gag ctg gac atc atc ttc aac ttt gag	397
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 Val Cys Arg Arg Leu Trp Gln Gly Leu Gly Asn Phe Ser Val Asn Thr  
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 Ser Lys Gly Asn Thr Ala Lys Asn Gly Gly Leu Leu Leu Ser Thr Asn  
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 Met Lys Trp Val Gln Phe Ser Xaa Leu His Val Asp Val Pro Lys Asp  
 45 50 55  
 ttg acc aaa cct gtg gta aca atc tct gat gaa cca gac ata tta tat 245  
 Leu Thr Lys Pro Val Val Thr Ile Ser Asp Glu Pro Asp Ile Leu Tyr  
 60 65 70  
 aag cgc ctc tcg gtt ttg gtg aaa ggt cac gat aag gct gta ttg gac 293  
 Lys Arg Leu Ser Val Leu Val Lys Gly His Asp Lys Ala Val Leu Asp  
 75 80 85  
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 aaaatggtgg cttgcttctg tttctctttt tttccccaca catagcagta ccaat atg 178  
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 aag tgg gta cag ttt tca aac cta cac gtt gat gtt cca aag gat ttg 226  
 Lys Trp Val Gln Phe Ser Asn Leu His Val Asp Val Pro Lys Asp Leu  
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Thr	Lys	Pro	Val	Val	Thr	Ile	Ser	Asp	Glu	Pro	Asp	Ile	Leu	Tyr	Lys	
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cgc	ctc	tcg	gtt	ttg	gtg	aaa	ggg	cac	gat	aag	gct	gta	ttg	gac	agt	322
Arg	Leu	Ser	Val	Leu	Val	Lys	Gly	His	Asp	Lys	Ala	Val	Leu	Asp	Ser	
	35					40					45					
tat	gaa	tat	ttt	gct	gtg	ctt	gct	gct	aaa	gaa	ctt	ggg	atc			364
Tyr	Glu	Tyr	Phe	Ala	Val	Leu	Ala	Ala	Lys	Glu	Leu	Gly	Ile			
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Arg	Leu	Ser	Arg	Pro	Glu	Arg	Pro	Asp	Leu	Val	Phe	Glu	Glu	Glu	Asp	
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Leu	Pro	Tyr	Glu	Glu	Glu	Ile	Met	Arg	Asn	Gln	Phe	Ser	Val	Lys	Cys	
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Trp	Leu	Arg	Tyr	Ile	Glu	Phe	Lys	Gln	Gly	Ala	Pro	Lys	Pro	Arg	Leu	
	40						45					50				
aat	cag	cta	tac	gag	cgg	gca	ctc	aag	ctg	ctg	ccc	tgc	agc	tac	aaa	248
Asn	Gln	Leu	Tyr	Glu	Arg	Ala	Leu	Lys	Leu	Leu	Pro	Cys	Ser	Tyr	Lys	
	55					60					65					
ctc	tgg	tac	cga	tac	ctg	aag	gcg	cgt	cgg	gca	cag	gtg	aag	cat	cgc	296
Leu	Trp	Tyr	Arg	Tyr	Leu	Lys	Ala	Arg	Arg	Ala	Gln	Val	Lys	His	Arg	
70					75				80					85		
tgt	gtg	acc	gac	cct	gcc	tat	gaa	gat	gtc	aac	aac	tgt	cat	gag	agg	344
Cys	Val	Thr	Asp	Pro	Ala	Tyr	Glu	Asp	Val	Asn	Asn	Cys	His	Glu	Arg	
				90					95					100		
gcc	ttt	gtg	ttc	atg	cac	aag	atg	cct	cgt	ctg	tgg	cta	gat	tac	tgc	392
Ala	Phe	Val	Phe	Met	His	Lys	Met	Pro	Arg	Leu	Trp	Leu	Asp	Tyr	Cys	
			105					110					115			
cag	tcc	tca	tg													403
Gln	Ser	Ser														
			120													

<210> 1172  
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<220>

004220"666E7560

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<222> 56..358

<400> 1172

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											1					
gct	aaa	cat	cat	cct	gat	ttg	atc	ttt	tgc	cgc	aag	cag	gct	ggg	gtt	106
Ala	Lys	His	His	Pro	Asp	Leu	Ile	Phe	Cys	Arg	Lys	Gln	Ala	Gly	Val	
			5					10					15			
gcc	atc	gga	aga	ctg	tgt	gaa	aaa	tgt	gat	ggc	aag	tgt	gtg	att	tgt	154
Ala	Ile	Gly	Arg	Leu	Cys	Glu	Lys	Cys	Asp	Gly	Lys	Cys	Val	Ile	Cys	
		20				25						30				
gac	tcc	tat	gtg	cgt	ccc	tgc	act	ctg	gtg	cgc	ata	tgt	gat	gag	tgt	202
Asp	Ser	Tyr	Val	Arg	Pro	Cys	Thr	Leu	Val	Arg	Ile	Cys	Asp	Glu	Cys	
	35					40				45						
aac	tat	gga	tct	tac	cag	ggg	cgc	tgt	gtg	atc	tgt	gga	gga	cct	ggg	250
Asn	Tyr	Gly	Ser	Tyr	Gln	Gly	Arg	Cys	Val	Ile	Cys	Gly	Gly	Pro	Gly	
	50				55					60				65		
gtc	tct	gat	gcc	tat	tat	tgt	aag	gag	tgc	acc	atc	cag	gag	aag	gac	298
Val	Ser	Asp	Ala	Tyr	Tyr	Cys	Lys	Glu	Cys	Thr	Ile	Gln	Glu	Lys	Asp	
				70				75						80		
aga	gat	ggc	tgc	cca	aag	att	gtc	aat	ctg	ggg	agc	tct	aag	aca	gac	346
Arg	Asp	Gly	Cys	Pro	Lys	Ile	Val	Asn	Leu	Gly	Ser	Ser	Lys	Thr	Asp	
			85					90					95			
ctc	ttc	tat	gaa													358
Leu	Phe	Tyr	Glu													
			100													

<210> 1173  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> 164..490

<400> 1173

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gggccg	aaac	aaaaat	gaag	ttttct	acca	atgtcc	agac	caa	atg	gct	cga	aat	175			
												Met				
												Ala				
												Arg				
												Asn				
												1				
cca	gct	gct	att	gac	atg	ttt	att	ata	ggg	gct	act	ttt	act	gac	tg	223
Pro	Ala	Ala	Ile	Asp	Met	Phe	Ile	Ile	Gly	Ala	Thr	Phe	Thr	Asp	Trp	
	5					10				15				20		
ttt	acc	tct	tat	gtc	aaa	aat	gtt	gta	tca	ggg	ggc	ttc	ccc	atc	atc	271
Phe	Thr	Ser	Tyr	Val	Lys	Asn	Val	Val	Ser	Gly	Gly	Phe	Pro	Ile	Ile	
				25				30				35				
aga	gac	caa	att	ttc	aga	tat	gtt	cac	gat	cca	gaa	tgt	gta	gca	aca	319
Arg	Asp	Gln	Ile	Phe	Arg	Tyr	Val	His	Asp	Pro	Glu	Cys	Val	Ala	Thr	

004220" 666E560

	40		45		50	
act ggg gat att act gtg tca gtt tcc aca tcg ttt ctg cca gaa ctt						367
Thr Gly Asp Ile Thr Val Ser Val Ser Thr Ser Phe Leu Pro Glu Leu						
	55		60		65	
agc tct gta cat cca ccc cac tat ttc ttc aca tac cga atc agg att						415
Ser Ser Val His Pro Pro His Tyr Phe Phe Thr Tyr Arg Ile Arg Ile						
	70		75		80	
gaa atg tca aaa gat gca ctt cct gag aag gcc tgt cag ttg gac agt						463
Glu Met Ser Lys Asp Ala Leu Pro Glu Lys Ala Cys Gln Leu Asp Ser						
	85		90		95	100
cgc tat tgg aga ata aca aat gct aag g						491
Arg Tyr Trp Arg Ile Thr Asn Ala Lys						
	105					

<210> 1174  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> 203..355

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ctgagaaacg ggtgacaatg aagaacaaga aaaattactg aagaaaagct gtacgttata	120
tgttgaaat ctttcttttt acacaactga agaacaaatc tatgaactct tcagcaaaaag	180
tggtgacata aagaaaatca tt atg ggt ctg gat aaa atg aag aaa aca gca	232
Met Gly Leu Asp Lys Met Lys Lys Thr Ala	
	1 5 10
tgt gga ttc tgt ttt gtg gaa tat tac tca cgc gca gat gcg gaa aac	280
Cys Gly Phe Cys Phe Val Glu Tyr Tyr Ser Arg Ala Asp Ala Glu Asn	
	15 20 25
gcc atg cgg tac ata aat ggg acg cgt ctg gat gac cga atc att cgc	328
Ala Met Arg Tyr Ile Asn Gly Thr Arg Leu Asp Asp Arg Ile Ile Arg	
	30 35 40
aca gac tgg gac gca ggc ttt aag gag	355
Thr Asp Trp Asp Ala Gly Phe Lys Glu	
	45 50

<210> 1175  
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 <212> DNA  
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 <222> 84..518

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cgcgtccctt tgggtttagc acg atg agc tca atc ggc act ggg tat gac ctg	113



	Met	Ser	Ser	Ile	Gly	Thr	Gly	Tyr	Asp	Leu	
	1				5					10	
tca gcc tct aca ttc tct cct gac gga aga gtt ttt caa gtt gaa tat											161
Ser Ala Ser Thr Phe Ser Pro Asp Gly Arg Val Phe Gln Val Glu Tyr											
	15				20				25		
gct atg aag gct gtg gaa aat agt agt aca gct att gga atc aga tgc											209
Ala Met Lys Ala Val Glu Asn Ser Ser Thr Ala Ile Gly Ile Arg Cys											
	30				35				40		
aaa gat ggt gtt gtc ttt ggg gta gaa aaa tta gtc ctt tct aaa ctt											257
Lys Asp Gly Val Val Phe Gly Val Glu Lys Leu Val Leu Ser Lys Leu											
	45				50				55		
tat gaa gaa ggt tcc aac aaa aga ctt ttt aat gtt gat cgg cat gtt											305
Tyr Glu Glu Gly Ser Asn Lys Arg Leu Phe Asn Val Asp Arg His Val											
	60				65				70		
gga atg gca gta gca ggt ttg ttg gca gat gct cgt tct tta gca gac											353
Gly Met Ala Val Ala Gly Leu Leu Ala Asp Ala Arg Ser Leu Ala Asp											
	75				80				85		90
ata gca aga gaa gaa gct tcc aac ttc aga tct aac ttt ggc tac aac											401
Ile Ala Arg Glu Glu Ala Ser Asn Phe Arg Ser Asn Phe Gly Tyr Asn											
	95				100				105		
att cca cta aaa cat ctt gca gac aga gtg gcc atg tat gtg cat gca											449
Ile Pro Leu Lys His Leu Ala Asp Arg Val Ala Met Tyr Val His Ala											
	110				115				120		
tat aca ctc tac agt gct gtt aga cct ttt ggc tgc agt ttc atg tta											497
Tyr Thr Leu Tyr Ser Ala Val Arg Pro Phe Gly Cys Ser Phe Met Leu											
	125				130				135		
ggg tct tac agt gtg aat gac gg											520
Gly Ser Tyr Ser Val Asn Asp											
	140				145						

<210> 1176  
 <211> 438  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 69..437

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ccagcacc atg ccc atg acw ctg ggg tac tgg aac atc cgc ggg ctg gcc	110
Met Pro Met Thr Leu Gly Tyr Trp Asn Ile Arg Gly Leu Ala	
1 5 10	
cat tcc atc cgc ctg ctc ctg gaa tac aca gac tca agc tac gag gaa	158
His Ser Ile Arg Leu Leu Leu Glu Tyr Thr Asp Ser Ser Tyr Glu Glu	
15 20 25 30	
aag aag tac acg atg ggg gac gct cct gat tat gac aga agc cag tgg	206
Lys Lys Tyr Thr Met Gly Asp Ala Pro Asp Tyr Asp Arg Ser Gln Trp	
35 40 45	
ctg aat gaa aaa ttc aag ctg ggc ctg gac ttt ccc aat ctg ccc tac	254
Leu Asn Glu Lys Phe Lys Leu Gly Leu Asp Phe Pro Asn Leu Pro Tyr	
50 55 60	

ttg att gat ggg act cac aag atc acc cag agc aac gcc atc ctg cgg	302
Leu Ile Asp Gly Thr His Lys Ile Thr Gln Ser Asn Ala Ile Leu Arg	
65 70 75	
tac att gcc cgc aag cac aac ctg tgc ggg gaa tca gaa aag gag cag	350
Tyr Ile Ala Arg Lys His Asn Leu Cys Gly Glu Ser Glu Lys Glu Gln	
80 85 90	
att cgc gaa gac att ttg gag aac cag ttt atg gac agc cgt atg cag	398
Ile Arg Glu Asp Ile Leu Glu Asn Gln Phe Met Asp Ser Arg Met Gln	
95 100 105 110	
ctg gcc aaa ctc tgc tat gac cca gat ttt gta agt ccc c	438
Leu Ala Lys Leu Cys Tyr Asp Pro Asp Phe Val Ser Pro	
115 120	

<210> 1177  
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Met Ser Cys Glu Ser Ser Met Val Leu Gly Tyr Trp	
1 5 10	
gat att cgt ggg ctg gcg cac gcc atc cgc ctg ctc ctg gag ttc acg	157
Asp Ile Arg Gly Leu Ala His Ala Ile Arg Leu Leu Leu Glu Phe Thr	
15 20 25	
gat acc tct tat gag gag aaa cgg tac acg tgc ggg gaa gct cct gac	205
Asp Thr Ser Tyr Glu Glu Lys Arg Tyr Thr Cys Gly Glu Ala Pro Asp	
30 35 40	
tat gat cga agc caa tgg ctg gat gtg aaa ttc aag cta gac ctg gac	253
Tyr Asp Arg Ser Gln Trp Leu Asp Val Lys Phe Lys Leu Asp Leu Asp	
45 50 55 60	
ttt cct aat ctg ccc tac ctc ctg gat ggg aag aac aag atc acc cag	301
Phe Pro Asn Leu Pro Tyr Leu Leu Asp Gly Lys Asn Lys Ile Thr Gln	
65 70 75	
agc aat gcc atc ttg cgc tac atc gct cgc aag cac aac atg tgt ggt	349
Ser Asn Ala Ile Leu Arg Tyr Ile Ala Arg Lys His Asn Met Cys Gly	
80 85 90	
gag act gaa gaa gaa aag att cga gtg gac atc ata gag aac caa gta	397
Glu Thr Glu Glu Glu Lys Ile Arg Val Asp Ile Ile Glu Asn Gln Val	
95 100 105	
atg gat ttc cgc aca caa ctg ata agg ctc tgt tac agc tct gac	442
Met Asp Phe Arg Thr Gln Leu Ile Arg Leu Cys Tyr Ser Ser Asp	
110 115 120	

<210> 1178  
 <211> 373  
 <212> DNA  
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<220>  
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 <222> 137..373

<400> 1178

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tcagcaktc actctgctga agggctgaga ggcgcacccg ggcggccagc tgggctcgga	120
gcggaacggg gtcagg atg gac gag gac gtg cta acc acc ctg aag atc ctc	172
Met Asp Glu Asp Val Leu Thr Thr Leu Lys Ile Leu	
1 5 10	
atc atc ggc gag agt ggg gtg ggc aag tcc agc ctg ctc ttg agg ttc	220
Ile Ile Gly Glu Ser Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe	
15 20 25	
aca gat gat acg ttt gat cca gaa ctt gca gca aca ata ggt gtt gac	268
Thr Asp Asp Thr Phe Asp Pro Glu Leu Ala Ala Thr Ile Gly Val Asp	
30 35 40	
ttt aag gtg aaa aca att tca gtg gat gga aat aag gct aaa ctt gca	316
Phe Lys Val Lys Thr Ile Ser Val Asp Gly Asn Lys Ala Lys Leu Ala	
45 50 55 60	
ata tgg gat act gct ggt caa gag agg ttt aga aca tta act ccc agc	364
Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Leu Thr Pro Ser	
65 70 75	
tat tat aga	373
Tyr Tyr Arg	

<210> 1179  
 <211> 277  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 85..276

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ggctcggmrt gcagcggkgt tagg atg gac gag gac gtg ttg cac cct gaa	111
Met Asp Glu Asp Val Leu His Pro Glu	
1 5	
gag cct cat cat cgc ctg ctc ttg agg ttc aca gat gat acc ttt gat	159
Glu Pro His His Arg Leu Leu Leu Arg Phe Thr Asp Asp Thr Phe Asp	
10 15 20 25	
cca gaa ctt gca gca aca ata ggt gag cct gtg ttt aaa aat tca ata	207
Pro Glu Leu Ala Ala Thr Ile Gly Glu Pro Val Phe Lys Asn Ser Ile	
30 35 40	
gaa atg tct aat att ttc ttg cct ttg ggc ttt ttt tat cta aat cct	255
Glu Met Ser Asn Ile Phe Leu Pro Leu Gly Phe Phe Tyr Leu Asn Pro	
45 50 55	
tct acc ttc ctc tta cca cgc c	277
Ser Thr Phe Leu Leu Pro Arg	
60	

<210> 1180  
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 <212> DNA  
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<220>  
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<400> 1180

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                               Met Ala Ile Pro Gly Ile Pro Tyr Glu Arg
                               1           5           10
cgg ctt ctc atc atg gcg gac cct aga gat aag gcg ctt cag gac tac      101
Arg Leu Leu Ile Met Ala Asp Pro Arg Asp Lys Ala Leu Gln Asp Tyr
              15           20           25
cgc aag aag ttg ctt gaa cac aag gag atc gac ggc cgt ctt aag gag      149
Arg Lys Lys Leu Leu Glu His Lys Glu Ile Asp Gly Arg Leu Lys Glu
              30           35           40
tta agg gaa caa tta aaa gaa ctt acc aag cag tat gaa aag tct gaa      197
Leu Arg Glu Gln Leu Lys Glu Leu Thr Lys Gln Tyr Glu Lys Ser Glu
              45           50           55
aat gat ctg aag gcc cta cag agt gtt ggg cag atc gtg ggt gaa gtg      245
Asn Asp Leu Lys Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val
              60           65           70
ctt aaa cag tta act gaa gaa aaa ttc att gtt aaa gct acc aat gga      293
Leu Lys Gln Leu Thr Glu Glu Lys Phe Ile Val Lys Ala Thr Asn Gly
              75           80           85           90
cca aga tat gtt gtg ggt tgt cgt cga cag ctt gac aaa agt aag ctg      341
Pro Arg Tyr Val Val Gly Cys Arg Arg Gln Leu Asp Lys Ser Lys Leu
              95           100           105
aag cca gga aca aga gtt gct ttg gat atg act aca cta act atc atg      389
Lys Pro Gly Thr Arg Val Ala Leu Asp Met Thr Thr Leu Thr Ile Met
              110           115           120
aga tat ttg ccg aga gag gtg gat cca ctg gtt tat aac atg tct cat      437
Arg Tyr Leu Pro Arg Glu Val Asp Pro Leu Val Tyr Asn Met Ser His
              125           130           135
gag gac cct ggg aat gtt tct tat tct gag att gga ggg cta tca gaa      485
Glu Asp Pro Gly Asn Val Ser Tyr Ser Glu Ile Gly Gly Leu Ser Glu
              140           145           150
cag atc cgg gaa tta aga gag gtg ata gaa tta cct c
Gln Ile Arg Glu Leu Arg Glu Val Ile Glu Leu Pro      522
155           160           165

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<220>  
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gaggatagag	cacatgtgag	attttacttt	ctactccagt	aaaaattctg	aagaattgca	180
ttggagactg	ttatattcaa	cacatacgtg	gattctgtgt	tatgatttac	atttttcttt	240
atttcagcac	tttcttatgc	aaggagctaa	acagtgatta	aaggagcagg	atgaaaag	298
atg gca cag tca	gtg ctg gta	ccg tca gga	cct gac agc	ttc cgc ttc		346
Met Ala Gln Ser	Val Leu Val	Pro Ser Gly	Pro Asp Ser	Phe Arg Phe		
1	5	10	15			
ttt acc agg gaa	tcc ctt gct	gct att gaa	caa cgc att	gca gaa gag		394
Phe Thr Arg Glu	Ser Leu Ala	Ala Ile Glu	Gln Arg Ile	Ala Glu Glu		
	20	25	30			
aaa gct aag aga	ccc aaa cag	gaa cgc aag	gat gag gat	gat gaa aat		442
Lys Ala Lys Arg	Pro Lys Gln	Glu Arg Lys	Asp Glu Asp	Asp Glu Asn		
	35	40	45			
ggc cca aag cca	a					455
Gly Pro Lys Pro						
50						

&lt;210&gt; 1182

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 75..455

&lt;400&gt; 1182

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	Met Ala Asp	Leu Glu	Glu Gln	Leu Ser	Asp Glu	Glu	
	1	5	10				
aag gtg cgt ata	gca gca aaa	ttc atc	att cat	gcc cct	cct gga	gaa	158
Lys Val Arg Ile	Ala Ala Lys	Phe Ile	Ile His	Ala Pro	Pro Gly	Glu	
	15	20	25				
ttt aat gag gtt	tty aat gat	gtt cgg	tta ctg	ctt aat	aat gac	aat	206
Phe Asn Glu Val	Phe Asn Asp	Val Arg	Leu Leu	Leu Asn	Asn Asp	Asn	
	30	35	40				
ctt ctc agg gaa	gga gca gcc	cat gca	ttt gca	cag tat	aac ttg	gac	254
Leu Leu Arg Glu	Gly Ala Ala	His Ala	Phe Ala	Gln Tyr	Asn Leu	Asp	
	45	50	55	60			
cag ttt act cca	gta aaa att	gaa ggt	tat gaa	gat cag	gta ttg	ata	302
Gln Phe Thr Pro	Val Lys Ile	Glu Gly	Tyr Glu	Asp Gln	Val Leu	Ile	
	65	70	75				
aca gaa cat ggc	gac ttg	gga aat	gga aag	ttt ttg	gat cca	aag aac	350
Thr Glu His Gly	Asp Leu Gly	Asn Gly	Lys Phe	Leu Asp	Pro Lys	Asn	
	80	85	90				
aga atc tgt ttt	aaa ttt gat	cac tta	agg aag	gag gca	act gat	cca	398
Arg Ile Cys Phe	Lys Phe Asp	His Leu	Arg Lys	Glu Ala	Thr Asp	Pro	
	95	100	105				

aga ccc tgt gaa gta gaa aat gca gtt gaa tca tgg aga act tca gta 446  
 Arg Pro Cys Glu Val Glu Asn Ala Val Glu Ser Trp Arg Thr Ser Val  
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 gaa act gct c 456  
 Glu Thr Ala  
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<210> 1183  
 <211> 305  
 <212> DNA  
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<220>  
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 <222> 73..303

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 aaacacttta ag atg aga aaa att gat ctc tgt ctg agc tct gaa ggg tcc 111  
 Met Arg Lys Ile Asp Leu Cys Leu Ser Ser Glu Gly Ser  
 1 5 10  
 gaa gtg att tta gct aca tca agt gat gaa aaa cac cca cct gaa aat 159  
 Glu Val Ile Leu Ala Thr Ser Ser Asp Glu Lys His Pro Pro Glu Asn  
 15 20 25  
 atc att gat ggg aat cca gaa acg ttt tgg acc acc aca gga atg ttt 207  
 Ile Ile Asp Gly Asn Pro Glu Thr Phe Trp Thr Thr Thr Gly Met Phe  
 30 35 40 45  
 ccc cag gaa ttc att att tgt ttc cac aaa cat gta agg att gaa agg 255  
 Pro Gln Glu Phe Ile Ile Cys Phe His Lys His Val Arg Ile Glu Arg  
 50 55 60  
 ctt gta atc caa agt tac ttt gta cag acc ttg aag att gaa aaa agc 303  
 Leu Val Ile Gln Ser Tyr Phe Val Gln Thr Leu Lys Ile Glu Lys Ser  
 65 70 75  
 ac 305

<210> 1184  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> 234..443

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 tgaaatccca ggccgtgagg agttagcgag cctgctcac actcggcgct ctggttttcg 180  
 gtgggtgtgc cctgcacctg cctcttcccc cattctcatt aataaaggta tcc atg 236  
 Met  
 1  
 gag aas act gaa aac tca gtg gat tca aaa tcc att aaa aat ttg gaa 284

Glu Xaa Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu Glu	
5 10 15	
cca aag atc ata cat gga agc gaa tca atg gac tct gga ata tcc ctg	332
Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser Leu	
20 25 30	
gac aac agt tat aaa atg gat tat cct gag atg ggt tta tgt ata ata	380
Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile Ile	
35 40 45	
att aat aat aag aat ttt cat aaa agc act gga atg aca tct cgg tct	428
Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg Ser	
50 55 60 65	
ggt aca gat gtc gat	443
Gly Thr Asp Val Asp	
70	

<210> 1185  
 <211> 268  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 71..268

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aagagttgta gccgaggtgg cggcgcgggg cggggcgggc ggagagagaa gaaggaggtg	60
gttgtgcagg atg gcg acg gcg gcc tac gag cag ctg aag ctg cat atc	109
Met Ala Thr Ala Ala Tyr Glu Gln Leu Lys Leu His Ile	
1 5 10	
aca cct gaa aaa ttt tat gtg gaa gct tgt gat gat gga gca gat gac	157
Thr Pro Glu Lys Phe Tyr Val Glu Ala Cys Asp Asp Gly Ala Asp Asp	
15 20 25	
gta ctt acc att gac cgt gtg tcc aca gag gtt acc ctt gca gtc aag	205
Val Leu Thr Ile Asp Arg Val Ser Thr Glu Val Thr Leu Ala Val Lys	
30 35 40 45	
aaa gat gtt cct cct tca gct gtc aca aga cca ata ttt ggt ata ctg	253
Lys Asp Val Pro Pro Ser Ala Val Thr Arg Pro Ile Phe Gly Ile Leu	
50 55 60	
ggc aca atc cat ctg	268
Gly Thr Ile His Leu	
65	

<210> 1186  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 77..340

<400> 1186

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aagctcggttc ttccgccagc ttccctcctc ttccctttctc cgccatcggtg gtgtgtttctt    60
gactccgctg ctccgcc atg tct tct cac aag act ttc agg att aag cga ttc    112
      Met Ser Ser His Lys Thr Phe Arg Ile Lys Arg Phe
            1             5             10
ctg gcc aag aaa caa aag caa aat cgt ccc att ccc cag tgg att cgg    160
Leu Ala Lys Lys Gln Lys Gln Asn Arg Pro Ile Pro Gln Trp Ile Arg
            15             20             25
atg aaa act gga aat aaa atc ags tmc aca gaa aag ttc tcc aag tcc    208
Met Lys Thr Gly Asn Lys Ile Xaa Xaa Thr Glu Lys Phe Ser Lys Ser
            30             35             40
cca ctc gac cca gga agt cct gct gtc ttc acc tgt cac cag cta ctg    256
Pro Leu Asp Pro Gly Ser Pro Ala Val Phe Thr Cys His Gln Leu Leu
            45             50             55             60
ggg agg ctg agg cag gag aat cgc ttg aac cca gga ggt gga ggt tgc    304
Gly Arg Leu Arg Gln Glu Asn Arg Leu Asn Pro Gly Gly Gly Gly Cys
            65             70             75
tgg gag cca agc caa gat cac gcc act aca ctc cag    340
Trp Glu Pro Ser Gln Asp His Ala Thr Leu Gln
            80             85

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<210> 1187  
 <211> 238  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 28..237

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      Met Tyr Thr Gly His Glu Asn Lys Asp
            1             5
tgg ttt agc aga cat tgg ttt act ctg cag cct gtg ttt tct gtt tcc    102
Trp Phe Ser Arg His Trp Phe Thr Leu Gln Pro Val Phe Ser Val Ser
            10             15             20             25
ccc ttt ccc acc tcc ttc ccc cca ccc aat cct ttt ttt ttt ctt ttt    150
Pro Phe Pro Thr Ser Phe Pro Pro Pro Asn Pro Phe Phe Phe Leu Phe
            30             35             40
tgc ttt yct ttt ctt ttt ttt wag ttt tta ttt act tta cct agt atg    198
Cys Phe Xaa Phe Leu Phe Phe Xaa Phe Leu Phe Thr Leu Pro Ser Met
            45             50             55
cct ttt ttw agt tgc ttc tca agt cag aaa act ttt cag g    238
Pro Phe Xaa Ser Cys Phe Ser Ser Gln Lys Thr Phe Gln
            60             65             70

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<210> 1188  
 <211> 620  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS



<222> 260..619

<400> 1188

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ggacggagta atctgtttac attctgttct tctcgatgca ctcacaagcg ggtaactagg 120  
tgacaagaaa acaaagatct tattcaaaag aggtcttaca gcaacccaac gtctcatctt 180  
cccatagtaa agatgacggc gccttgaggt aagctacagg caacaccact tccgcgtttc 240  
tcttgcgccc tgggtccaag atg gcg gat gaa gcc acg cga cgt gtt gtg tct 292

Met Ala Asp Glu Ala Thr Arg Arg Val Val Ser

1

5

10

gag atc ccg gtg ctg aag act aac gcc gga ccc cga gat cgt gag ttg 340  
Glu Ile Pro Val Leu Lys Thr Asn Ala Gly Pro Arg Asp Arg Glu Leu

15

20

25

tgg gtg cag cga ctg aag gag gaa tat cag tcc ctt atc cgg tat gtg 388  
Trp Val Gln Arg Leu Lys Glu Tyr Gln Ser Leu Ile Arg Tyr Val

30

35

40

gag aac aac aag aat gct gac aac gat tgg ttc cga ctg gag tcc aac 436  
Glu Asn Asn Lys Asn Ala Asp Asn Asp Trp Phe Arg Leu Glu Ser Asn

45

50

55

aag gaa gga act cgg tgg ttt gga aaa tgc tgg tat atc cat gac ctc 484  
Lys Glu Gly Thr Arg Trp Phe Gly Lys Cys Trp Tyr Ile His Asp Leu

ctg aaa tat gag ttt gac atc gag ttt gac att cct atc aca tat cct 532  
Leu Lys Tyr Glu Phe Asp Ile Glu Phe Asp Ile Pro Ile Thr Tyr Pro

80

85

90

act act gcc cca gaa att gca gtt cct gag ctg gat gga aag acw gca 580  
Thr Thr Ala Pro Glu Ile Ala Val Pro Glu Leu Asp Gly Lys Thr Ala

95

100

105

aag atg tac agg ggt ggc aaa ata tgc ctg acg gat cat t 620  
Lys Met Tyr Arg Gly Gly Lys Ile Cys Leu Thr Asp His

110

115

120

<210> 1189

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 211..570

<400> 1189

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ctgcatctag aggaggact atatataagc aaaggaaaag ttcttcgaag aggaaacacg 120  
aatcgctcgt tttaggaata aagatgacgg cgccttgagg taagctacag gcaacaccac 180  
ttccgcgttt ctcttgcgcc ctgggtccaag atg gcg gat gaa gcc acg cga cgt 234

Met Ala Asp Glu Ala Thr Arg Arg

1

5

gtt gtg tct gag atc ccg gtg ctg aag act aac gcc gga ccc cga gat 282  
Val Val Ser Glu Ile Pro Val Leu Lys Thr Asn Ala Gly Pro Arg Asp

10

15

20

cgt gag ttg tgg gtg cag cga ctg aag gag gaa tat cag tcc ctt atc 330

Arg	Glu	Leu	Trp	Val	Gln	Arg	Leu	Lys	Glu	Glu	Tyr	Gln	Ser	Leu	Ile		
25					30					35					40		
cgg	tat	gtg	gag	aac	aac	aag	aat	gct	gac	aac	gat	tgg	ttc	cga	ctg	378	
Arg	Tyr	Val	Glu	Asn	Asn	Lys	Asn	Ala	Asp	Asn	Asp	Trp	Phe	Arg	Leu		
				45					50					55			
gag	tcc	aac	aag	gaa	gga	act	cgg	tgg	ttt	gga	aaa	tgc	tgg	tat	atc	426	
Glu	Ser	Asn	Lys	Glu	Gly	Thr	Arg	Trp	Phe	Gly	Lys	Cys	Trp	Tyr	Ile		
				60				65					70				
cat	gac	ctc	ctg	aaa	tat	gag	ttt	gac	atc	gag	ttt	gac	att	cct	atc	474	
His	Asp	Leu	Leu	Lys	Tyr	Glu	Phe	Asp	Ile	Glu	Phe	Asp	Ile	Pro	Ile		
				75				80					85				
aca	tat	cct	act	act	gcc	cca	gaa	att	gca	gtt	cct	gag	ctg	gat	gga	522	
Thr	Tyr	Pro	Thr	Thr	Ala	Pro	Glu	Ile	Ala	Val	Pro	Glu	Leu	Asp	Gly		
				90				95				100					
aag	acw	gca	aag	atg	tac	agg	ggt	ggc	aaa	ata	tgc	ctg	acg	gat	cat	t	571
Lys	Thr	Ala	Lys	Met	Tyr	Arg	Gly	Gly	Lys	Ile	Cys	Leu	Thr	Asp	His		
105						110				115					120		

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 <212> DNA  
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<220>  
 <221> CDS  
 <222> 292..573

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tgccaggggg	agggcccccag	agaaaaccag	aaaagagggt	gagagactga	ggmagataaa	120											
gcgtcccagg	gcctcctaca	ccagcgccctg	agcaggaagc	gggaggggcc	atgactacga	180											
ggccctggga	ggtcacttta	gggagggctg	tcctraaacc	wgragcytgg	agcagaaagt	240											
gaaaccctgg	tgctccagac	aaagatctta	gtcgggacta	gccggccaag	g atg aag	297											
					Met Lys												
					1												
cct cac ttc aga aac aca gtg gag cga atg tat cga gac aca ttc tcc	345																
Pro His Phe Arg Asn Thr Val Glu Arg Met Tyr Arg Asp Thr Phe Ser																	
	5				10				15								
tac aac ttt tat aat aga ccc atc ctt tct cgt cgg aat acc gtc tgg	393																
Tyr Asn Phe Tyr Asn Arg Pro Ile Leu Ser Arg Arg Asn Thr Val Trp																	
	20				25				30								
ctg tgc tac gaa gtg aaa aca aag ggt ccc tca agg ccc cgt ttg gac	441																
Leu Cys Tyr Glu Val Lys Thr Lys Gly Pro Ser Arg Pro Arg Leu Asp																	
	35				40				45					50			
gca aag atc ttt cga ggc cag gtg tat tcc cag cct gag cac cac gca	489																
Ala Lys Ile Phe Arg Gly Gln Val Tyr Ser Gln Pro Glu His His Ala																	
				55				60					65				
gaa atg tgc ttc ctc tct tgg ttc tgt ggc aac cag ctg cct gct tac	537																
Glu Met Cys Phe Leu Ser Trp Phe Cys Gly Asn Gln Leu Pro Ala Tyr																	
				70				75					80				
aag tgt ttc cag atc acc tgg ttt gta tcc tgg acc cc	575																
Lys Cys Phe Gln Ile Thr Trp Phe Val Ser Trp Thr																	
				85				90									

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2025-01-01

act gtt tcg aat gaa g  
 Thr Val Ser Asn Glu  
 220

693

<210> 1192  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 84..428

<400> 1192  
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 cggaacccag aggacgcgac acc atg act tat gct tat ctc ttc aag tat atc 113  
 Met Thr Tyr Ala Tyr Leu Phe Lys Tyr Ile  
 1 5 10  
 atc atc gga gac aca ggt gtg ggg aag tca tgt ctc ctc ctg cag ttt 161  
 Ile Ile Gly Asp Thr Gly Val Gly Lys Ser Cys Leu Leu Leu Gln Phe  
 15 20 25  
 aca gat aag cgg ttc cag cct gtc cac gac ctc aca ata ggt gtg gag 209  
 Thr Asp Lys Arg Phe Gln Pro Val His Asp Leu Thr Ile Gly Val Glu  
 30 35 40  
 ttt gga gct cgt atg gtc aac att gat gga aaa caa atc aaa ctg caa 257  
 Phe Gly Ala Arg Met Val Asn Ile Asp Gly Lys Gln Ile Lys Leu Gln  
 45 50 55  
 atc tgg gat acg gct ggg caa gaa tcc ttc cgt tct atc acc nrt ncc 305  
 Ile Trp Asp Thr Ala Gly Gln Glu Ser Phe Arg Ser Ile Thr Xaa Xaa  
 60 65 70  
 tac tac agg gga gca gct gga gca ctg ctg gtg tac gac att aca agg 353  
 Tyr Tyr Arg Gly Ala Ala Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg  
 75 80 85 90  
 cgt kra acc ttc wnc cas ctg acc tca tgg tta gag gat gcc cgg cag 401  
 Arg Xaa Thr Phe Xaa Xaa Leu Thr Ser Trp Leu Glu Asp Ala Arg Gln  
 95 100 105  
 cac tct agt tcc aac atg gtt atc atg c 429  
 His Ser Ser Ser Asn Met Val Ile Met  
 110 115

<210> 1193  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 149..325

<400> 1193  
 tatggaaacc atccctagtc aaggacactt taaatatata gtctaaatac cggttaaggta 60  
 ggcccactag ctgtgttcac attttccctt ggccacctta ccagggrctt taataacttg 120

ggaaagtgaa aacaacaagc taaccac atg ttc acc ata gaa aac aat ttt 172  
Met Phe Thr Ile Glu Asn Asn Phe  
1 5  
gtc ttg aaa aac aag gac tct ttt tcc cgt gtg gga cca gtt cct act 220  
Val Leu Lys Asn Lys Asp Ser Phe Ser Arg Val Gly Pro Val Pro Thr  
10 15 20  
tat gtt tta cca gcc aat tgg act gga acc tat aca gtt gtt tat tta 268  
Tyr Val Leu Pro Ala Asn Trp Thr Gly Thr Tyr Thr Val Val Tyr Leu  
25 30 35 40  
gcc ccc gaa att aat ata gct ccc aac aac caa tcc ntc att ata ctt 316  
Ala Pro Glu Ile Asn Ile Ala Pro Asn Asn Gln Ser Xaa Ile Ile Leu  
45 50 55  
tta act gca 325  
Leu Thr Ala

<210> 1194  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 153..446

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ctaggcggct ccctgggctc caggctgttg cggggtgtag gtgggagtca cggacgggtc 120  
ggggcccgag gtgtccgcga aggtggcgca gc atg gcg gca ggg gag agc atg 173  
Met Ala Ala Gly Glu Ser Met  
1 5  
gct cag cgg atg gtc tgg gtg gac ctg gag atg aca gga ttg gac att 221  
Ala Gln Arg Met Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp Ile  
10 15 20  
gag aag gac cag att att gag atg gcc tgt ctg ata act gac tct gat 269  
Glu Lys Asp Gln Ile Ile Glu Met Ala Cys Leu Ile Thr Asp Ser Asp  
25 30 35  
ctc aac att ttg gct gaa ggt cct aac ctg att ata aaa caa cca gat 317  
Leu Asn Ile Leu Ala Glu Gly Pro Asn Leu Ile Lys Gln Pro Asp  
40 45 50 55  
gag ttg ctg gac agc atg tca gat tgg tgt aag gag cat cac ggg aag 365  
Glu Leu Leu Asp Ser Met Ser Asp Trp Cys Lys Glu His His Gly Lys  
60 65 70  
tct ggc ctt acc aag gca gtg aag gag agt aca att aca ttg cag cag 413  
Ser Gly Leu Thr Lys Ala Val Lys Glu Ser Thr Ile Thr Leu Gln Gln  
75 80 85  
gca gag tat gaa ttt ctg tcc ttt gta cga cag ca 448  
Ala Glu Tyr Glu Phe Leu Ser Phe Val Arg Gln  
90 95

<210> 1195  
<211> 459  
<212> DNA  
<213> Homo sapiens

<220>  
 <221> CDS  
 <222> 80..457

<400> 1195

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aaaacaaccg actcctttcc aggtgaaggg tgacttggct gaagaaacac ttaaattctg      60
gaaatagcga ctcaagtatc atg gcc agc agc ctt aat gaa gat cca gaa gga      112
              Met Ala Ser Ser Leu Asn Glu Asp Pro Glu Gly
                1             5             10
agc aga atc act tat gtg aaa gga gac ctt ttt gca tgc ccg aaa aca      160
Ser Arg Ile Thr Tyr Val Lys Gly Asp Leu Phe Ala Cys Pro Lys Thr
              15             20             25
gac tct tta gcc cac tgt atc agt gag gat tgt cgc atg ggc gct ggg      208
Asp Ser Leu Ala His Cys Ile Ser Glu Asp Cys Arg Met Gly Ala Gly
              30             35             40
ata gct gtc ctc ttt aag aag aaa ttt gga ggg gtg caa gaa ctt tta      256
Ile Ala Val Leu Phe Lys Lys Lys Phe Gly Gly Val Gln Glu Leu Leu
              45             50             55
aat caa caa aag aaa tct gga gaa gtg gct gtt ctg aag aga gat ggg      304
Asn Gln Gln Lys Lys Ser Gly Glu Val Ala Val Leu Lys Arg Asp Gly
              60             65             70             75
cga tat atn nat tac ttg att aca aag aaa agg gct tcg cac aag cca      352
Arg Tyr Xaa Xaa Tyr Leu Ile Thr Lys Lys Arg Ala Ser His Lys Pro
              80             85             90
act tat gaa aac tta cag aag agt tta gag gca atg aag tct cat tgt      400
Thr Tyr Glu Asn Leu Gln Lys Ser Leu Glu Ala Met Lys Ser His Cys
              95             100             105
ctg aag aat gga gtc act gac ctc tcc atg ccc agg att gga tgt ggt      448
Leu Lys Asn Gly Val Thr Asp Leu Ser Met Pro Arg Ile Gly Cys Gly
              110             115             120
ctt gat cgt ct
Leu Asp Arg
              125

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<210> 1196  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 78..308

<400> 1196

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gcaaacmytt cccgtcaatt ggcagaaaac aaccttgagg aaccttgacg agtgtccgga      60
gtttagaaaa cttaggg atg gag ccc ccc aag atg aac cca gtg gtg gag      110
              Met Glu Pro Pro Lys Met Asn Pro Val Val Glu
                1             5             10
cca ctg tcc tgg atg ctg ggc acc tgg ctg tcg gac cca cct gga gcc      158
Pro Leu Ser Trp Met Leu Gly Thr Trp Leu Ser Asp Pro Pro Gly Ala
              15             20             25

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ggg acc tac ccc aca ctg cag ccc ttc cag tac ctg gag gag gtt cac	206
Gly Thr Tyr Pro Thr Leu Gln Pro Phe Gln Tyr Leu Glu Glu Val His	
30 35 40	
atc tcc cac gtg ggc cag ccc atg ctg aac ttc tgc ttc aac tcc ttc	254
Ile Ser His Val Gly Gln Pro Met Leu Asn Phe Ser Phe Asn Ser Phe	
45 50 55	
cac ccg gac acg cgc aas cga tgc aca gag agt gtg gct tca ytc gcc	302
His Pro Asp Thr Arg Xaa Arg Cys Thr Glu Ser Val Ala Ser Xaa Ala	
60 65 70 75	
tca agc cc	310
Ser Ser	

<210> 1197  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 193..462

<400> 1197	
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gggagtggag tggagcggct gtggttgccg actcttttct cttccccacg gtccagtcag	120
cggtttaatt aggccatcgg cctcgagcc gagacttgct tcttatttag ttctggggag	180
cgctcgtcgc ac atg agt gat gtg gag gaa aac aac ttc gag ggc aga gag	231
Met Ser Asp Val Glu Glu Asn Asn Phe Glu Gly Arg Glu	
1 5 10	
tct cgc tct cag tca aaa tct cca acg gga act cct gct cgt gta aaa	279
Ser Arg Ser Gln Ser Lys Ser Pro Thr Gly Thr Pro Ala Arg Val Lys	
15 20 25	
tgc gag agc agg tca gga tct cgt agt cca tca agg gtt tcc aaa cac	327
Ser Glu Ser Arg Ser Gly Ser Arg Ser Pro Ser Arg Val Ser Lys His	
30 35 40 45	
tct gaa tcc cat tct cga tca aga tca aat cca ggt cga ggt caa gga	375
Ser Glu Ser His Ser Arg Ser Arg Ser Asn Pro Gly Arg Gly Gln Gly	
50 55 60	
gac att ctg ata gac gtt aca ctg gat cca gat ccc act ctg act ctg	423
Asp Ile Leu Ile Asp Val Thr Leu Asp Pro Asp Pro Thr Leu Thr Leu	
65 70 75	
ata gga gac gat ctg gaa gta gat cat ata cac cag aat a	463
Ile Gly Asp Asp Leu Glu Val Asp His Ile His Gln Asn	
80 85 90	

<210> 1198  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 3..446

&lt;400&gt; 1198

ta atg cgc ccg ccg tgt cca tgg aga gaa gct gag gcg gcc gac ctt	47
Met Arg Pro Pro Cys Pro Trp Arg Glu Ala Glu Ala Ala Asp Leu	
1 5 10 15	
cgg ccc gag gca ccg ggg cgc cgg gac gsm aag atg tgc gct tcc tta	95
Arg Pro Glu Ala Pro Gly Arg Arg Asp Xaa Lys Met Ser Ala Ser Leu	
20 25 30	
gtc cgg gca act gtc cgg gct gtg agc aag agg aag ctg cag ccc acc	143
Val Arg Ala Thr Val Arg Ala Val Ser Lys Arg Lys Leu Gln Pro Thr	
35 40 45	
cgg gca gcc ctc acc ctg aca cct tca gca gta aac aag ata aaa caa	191
Arg Ala Ala Leu Thr Leu Thr Pro Ser Ala Val Asn Lys Ile Lys Gln	
50 55 60	
ctt ctt aaa gat aag cct gag cat gta ggt gta aaa gtt ggt gtc cga	239
Leu Leu Lys Asp Lys Pro Glu His Val Gly Val Lys Val Gly Val Arg	
65 70 75	
acc agg ggc tgt aat ggc ctt tct tat act cta gaa tat aca aag aca	287
Thr Arg Gly Cys Asn Gly Leu Ser Tyr Thr Leu Glu Tyr Thr Lys Thr	
80 85 90 95	
aaa gga gat tct gat gaa gaa gtt att caa gat gga gtc aga gta ttc	335
Lys Gly Asp Ser Asp Glu Glu Val Ile Gln Asp Gly Val Arg Val Phe	
100 105 110	
atc gaa aag aaa gca cag cta aca ctt tta gga aca gaa atg gac tat	383
Ile Glu Lys Lys Ala Gln Leu Thr Leu Leu Gly Thr Glu Met Asp Tyr	
115 120 125	
gtt gaa gac aaa tta tcc agt gag ttt gtg ttc aat aac cca rac atc	431
Val Glu Asp Lys Leu Ser Ser Glu Phe Val Phe Asn Asn Pro Xaa Ile	
130 135 140	
aaa ggg act tgt ggc t	447
Lys Gly Thr Cys Gly	
145	

&lt;210&gt; 1199

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 33..404

&lt;400&gt; 1199

gcgcacgcgc gctccctct cagcagcca ac atg gct cca gtg gag cac gtt	53
Met Ala Pro Val Glu His Val	
1 5	
gtg gcg gat gct ggg gct ttc ctg cgg cat gcg gct ctg cag gac atc	101
Val Ala Asp Ala Gly Ala Phe Leu Arg His Ala Ala Leu Gln Asp Ile	
10 15 20	
ggg aag aac att tac acc atc cgg gag gtg gtc act gag att cgg gac	149
Gly Lys Asn Ile Tyr Thr Ile Arg Glu Val Val Thr Glu Ile Arg Asp	
25 30 35	
aag gcc aca cgc agg cgg ctc gct gtc ctg ccc tac gag ctg cgg ttc	197



Lys	Ala	Thr	Arg	Arg	Arg	Leu	Ala	Val	Leu	Pro	Tyr	Glu	Leu	Arg	Phe		
40					45					50					55		
aag	gag	ccc	tta	ccg	gaa	tac	gtg	cgg	ctg	gtg	act	gag	ttt	tca	aag		245
Lys	Glu	Pro	Leu	Pro	Glu	Tyr	Val	Arg	Leu	Val	Thr	Glu	Phe	Ser	Lys		
				60					65					70			
aaa	aca	gga	gac	tac	ccc	agc	ctc	tct	gcc	acg	gac	atc	caa	gtg	ctt		293
Lys	Thr	Gly	Asp	Tyr	Pro	Ser	Leu	Ser	Ala	Thr	Asp	Ile	Gln	Val	Leu		
			75					80					85				
gca	ctc	aca	tac	cag	ttg	gaa	gca	gag	ttt	gtt	ggg	gtg	tct	cac	cta		341
Ala	Leu	Thr	Tyr	Gln	Leu	Glu	Ala	Glu	Phe	Val	Gly	Val	Ser	His	Leu		
		90					95					100					
aaa	caa	gaa	cca	cag	aag	ggt	aag	gtg	agc	tca	tcg	att	cag	cac	cca		389
Lys	Gln	Glu	Pro	Gln	Lys	Val	Lys	Val	Ser	Ser	Ser	Ile	Gln	His	Pro		
	105					110					115						
gaa	aca	cct	ctg	cac	a												405
Glu	Thr	Pro	Leu	His													
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<220>  
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 <222> 94..429

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				Met	Ser	Val	Pro	Gly	Pro	Ser							
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tct	ccg	gac	ggg	gcc	ctg	aca	cgg	cca	ccc	tac	tgc	ctg	gag	gcc	ggg		162
Ser	Pro	Asp	Gly	Ala	Leu	Thr	Arg	Pro	Pro	Tyr	Cys	Leu	Glu	Ala	Gly		
		10					15					20					
gag	ccg	acg	cct	ggt	tta	agt	gac	act	tct	cca	gat	gaa	ggg	tta	ata		210
Glu	Pro	Thr	Pro	Gly	Leu	Ser	Asp	Thr	Ser	Pro	Asp	Glu	Gly	Leu	Ile		
	25					30					35						
gag	gac	ttg	act	ata	gaa	gac	aaa	gca	gtg	gag	caa	ctg	gca	gaa	gga		258
Glu	Asp	Leu	Thr	Ile	Glu	Asp	Lys	Ala	Val	Glu	Gln	Leu	Ala	Glu	Gly		
40				45					50						55		
ttg	ctt	tct	cat	tat	ttg	cca	gat	ctg	cag	aga	tca	aaa	caa	gcc	ctc		306
Leu	Leu	Ser	His	Tyr	Leu	Pro	Asp	Leu	Gln	Arg	Ser	Lys	Gln	Ala	Leu		
			60					65					70				
cag	gaa	ctc	aca	cag	aac	caa	ggt	gta	ttg	tta	gac	aca	ctg	gaa	caa		354
Gln	Glu	Leu	Thr	Gln	Asn	Gln	Val	Val	Leu	Leu	Asp	Thr	Leu	Glu	Gln		
		75					80					85					
gag	att	tca	aaa	ttt	aaa	gaa	tgt	cat	tct	atg	ttg	gat	att	aat	gct		402
Glu	Ile	Ser	Lys	Phe	Lys	Glu	Cys	His	Ser	Met	Leu	Asp	Ile	Asn	Ala		
	90						95					100					
ttg	ttt	gct	gag	gct	aaa	cac	tat	cat	g								430
Leu	Phe	Ala	Glu	Ala	Lys	His	Tyr	His									
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<220>  
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 Pro Glu Val Val Glu Glu Leu Thr Arg Lys Thr Tyr Phe Thr Glu Lys  
 10 15 20 25  
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 Glu Val Gln Gln Trp Tyr Lys Gly Phe Ile Lys Asp Cys Pro Ser Gly  
 30 35 40  
 cag ctg gat gcg gca ggc ttc cag aag atc tac aag caa ttc ttc ccg 198  
 Gln Leu Asp Ala Ala Gly Phe Gln Lys Ile Tyr Lys Gln Phe Phe Pro  
 45 50 55  
 ttc gga gac ccc acc aag ttt gcc aca ttt gtt ttc aac gtc ttt gat 246  
 Phe Gly Asp Pro Thr Lys Phe Ala Thr Phe Val Phe Asn Val Phe Asp  
 60 65 70  
 gaa aac aag gac ggg cga att gag ttc tcc gag ttc atc cag gcg ctg 294  
 Glu Asn Lys Asp Gly Arg Ile Glu Phe Ser Glu Phe Ile Gln Ala Leu  
 75 80 85  
 tcg gtg acc tca cgg gga acc tgg atg aga agc tac ggt ggg cct tca 342  
 Ser Val Thr Ser Arg Gly Thr Trp Met Arg Ser Tyr Gly Gly Pro Ser  
 90 95 100 105  
 agc tct acg act tgg aca atg atg gct aca tca cca gga atg aga tgc 390  
 Ser Ser Thr Thr Trp Thr Met Met Ala Thr Ser Pro Gly Met Arg Cys  
 110 115 120  
 tgg aca ttg tgg a 403  
 Trp Thr Leu Trp  
 125

<210> 1202  
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 <212> DNA  
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<220>  
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 <222> 88..459

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 cgagtatcgc cgggatttcg aatcgcg atg atc atc ccc tct cta gag gag ctg 114  
 Met Ile Ile Pro Ser Leu Glu Glu Leu

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gac tcc ctc aag tac agt gac ctg cag aac tta gcc aag agt ctg ggt			162
Asp Ser Leu Lys Tyr Ser Asp Leu Gln Asn Leu Ala Lys Ser Leu Gly			
10 15 20 25			
ctc cgg gcc aac ctg agg gca acc aag ttg tta aaa gcc ttg aaa ggc			210
Leu Arg Ala Asn Leu Arg Ala Thr Lys Leu Leu Lys Ala Leu Lys Gly			
30 35 40			
tac att aaa cat gag gca aga aaa gga aat gag aat cag gat gaa agt			258
Tyr Ile Lys His Glu Ala Arg Lys Gly Asn Glu Asn Gln Asp Glu Ser			
45 50 55			
caa act tct gca tcc tct tgt gat gag act gag ata cag atc agc aac			306
Gln Thr Ser Ala Ser Ser Cys Asp Glu Thr Glu Ile Gln Ile Ser Asn			
60 65 70			
cag gaa gaa gct gag aga cag cca ctt ggc cat gtc acc aaa aca agg			354
Gln Glu Glu Ala Glu Arg Gln Pro Leu Gly His Val Thr Lys Thr Arg			
75 80 85			
aga agg tgc aag act gtc cgt gtg gac cct gac tca cag aat cat gaa			402
Arg Arg Cys Lys Thr Val Arg Val Asp Pro Asp Ser Gln Asn His Glu			
90 95 100 105			
aag cag gaa agn cag gat ctc tnn agc tac tgc aaa agt tcc ttc tcc			450
Lys Gln Glu Xaa Gln Asp Leu Xaa Ser Tyr Cys Lys Ser Ser Phe Ser			
110 115 120			
acc aga cga gc			461
Thr Arg Arg			

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 <212> DNA  
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<220>  
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gagagtgttg tctaaaacaa gttccggaag ggaggctgcc cttcgcggtc cgagaaccac	120
cggcctcccc agtttgaggg ctgttaccct gtgcgcgctt cgacgttgct gctgttggt	180
ctcctcgccc ctcgctccctt gggaaccgcc tgggaactcc gcc atg tca tcc act	235
Met Ser Ser Thr	
1	
tcg ccc aan ctc cag aaa gcg ata gat ctg gct agc aaa gca gcg caa	283
Ser Pro Xaa Leu Gln Lys Ala Ile Asp Leu Ala Ser Lys Ala Ala Gln	
5 10 15 20	
gaa gac aag gct ggg aac tac gaa gaa gcc ctt cag ctc tat cag cat	331
Glu Asp Lys Ala Gly Asn Tyr Glu Glu Ala Leu Gln Leu Tyr Gln His	
25 30 35	
gct rtg cag tat ttt ctt cat gtc gtt aaa tat gaa gca cag ggt gat	379
Ala Xaa Gln Tyr Phe Leu His Val Val Lys Tyr Glu Ala Gln Gly Asp	
40 45 50	
aaa gcc aag caa agt atc agg g	401
Lys Ala Lys Gln Ser Ile Arg	
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 <212> DNA  
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<220>  
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 <222> 60..428

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 atg aag ttt cgg gcc aag atc gtg gac ggg gcc tgt ctg aac cac ttc 107  
 Met Lys Phe Arg Ala Lys Ile Val Asp Gly Ala Cys Leu Asn His Phe  
 1 5 10 15  
 aca cga atc agt aac atg ata gcc aag ctt gcc aaa acc tgc acc ctc 155  
 Thr Arg Ile Ser Asn Met Ile Ala Lys Leu Ala Lys Thr Cys Thr Leu  
 20 25 30  
 cgc atc agc cct gat aag ctt aac ttc atc ctt tgt gac aag ctg gct 203  
 Arg Ile Ser Pro Asp Lys Leu Asn Phe Ile Leu Cys Asp Lys Leu Ala  
 35 40 45  
 aat gga gga gtg agc atg tgg tgt gag ctg gaa cag gag aac ttc ttc 251  
 Asn Gly Gly Val Ser Met Trp Cys Glu Leu Glu Gln Glu Asn Phe Phe  
 50 55 60  
 aac gaa ttt caa atg gag ggt gtc tct gca gaa aac aat gag att tat 299  
 Asn Glu Phe Gln Met Glu Gly Val Ser Ala Glu Asn Asn Glu Ile Tyr  
 65 70 75 80  
 tta gag cta aca tcg gaa aac tta tct cga gcc ttg aag act gcc cag 347  
 Leu Glu Leu Thr Ser Glu Asn Leu Ser Arg Ala Leu Lys Thr Ala Gln  
 85 90 95  
 aat gcc agg gct ttg aaa atc aaa ctg act aat aaa cac ttt ccc tgc 395  
 Asn Ala Arg Ala Leu Lys Ile Lys Leu Thr Asn Lys His Phe Pro Cys  
 100 105 110  
 ctc acg gtc tcc gtg gag ctg tta tct atg tca ag 430  
 Leu Thr Val Ser Val Glu Leu Leu Ser Met Ser  
 115 120

<210> 1205  
 <211> 387  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 35..385

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 Met Ser Lys Leu Trp Arg Arg  
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 Gly Ser Thr Ser Gly Ala Met Glu Ala Pro Glu Pro Gly Glu Ala Leu

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gag ttg agc ctg gcg ggt gcc cat ggc cat gga gtg cac aag aaa aaa			151
Glu Leu Ser Leu Ala Gly Ala His Gly His Gly Val His Lys Lys Lys			
25	30	35	
cac aag aag cac aag aag aaa cac aag aag aaa cac cat cag gaa gaa			199
His Lys Lys His Lys Lys Lys His Lys Lys Lys His His Gln Glu Glu			
40	45	50	55
gac gcc ggg ccc acg cag ccg tcc cct gcc aag cct cag ctc aaa ctc			247
Asp Ala Gly Pro Thr Gln Pro Ser Pro Ala Lys Pro Gln Leu Lys Leu			
60	65	70	
aaa atc aag ctt ggg gga caa gtc ctg ggg acc aag agt gtt cct acc			295
Lys Ile Lys Leu Gly Gly Gln Val Leu Gly Thr Lys Ser Val Pro Thr			
75	80	85	
ttc act gtg atc cca gag ggg cct cgc tca ccc tct ccc ctt atg gtt			343
Phe Thr Val Ile Pro Glu Gly Pro Arg Ser Pro Ser Pro Leu Met Val			
90	95	100	
gtg gat aat gaa gag gaa cct atg gaa gga gtc ccc ctt gag ca			387
Val Asp Asn Glu Glu Glu Pro Met Glu Gly Val Pro Leu Glu			
105	110	115	

<210> 1206  
 <211> 431  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 220..429

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 tgcggagaga gttcttact accacaacca aggagggata tgataggcgg ccagtggata 180  
 taactccttt agaacaaagg aaattaactt ttgataccc atg cat tgg ttc agg 234  
 Met His Trp Phe Arg  
 1 5  
 act tgg aaa ctc atg gaa ata aca gta caa cag cta atg gct cat ttg 282  
 Thr Trp Lys Leu Met Glu Ile Thr Val Gln Gln Leu Met Ala His Leu  
 10 15 20  
 gat gct atc agg aaa gac atg gtc atc cta gag aaa agt gaa ttt gca 330  
 Asp Ala Ile Arg Lys Asp Met Val Ile Leu Glu Lys Ser Glu Phe Ala  
 25 30 35  
 aat ctg aga gca gag aat gag aaa atg aaa att gaa tta gac caa gtt 378  
 Asn Leu Arg Ala Glu Asn Glu Lys Met Lys Ile Glu Leu Asp Gln Val  
 40 45 50  
 aag caa caa cta atg cat gaa acc agt yga atc aga gca gat aat aaa 426  
 Lys Gln Gln Leu Met His Glu Thr Ser Xaa Ile Arg Ala Asp Asn Lys  
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 ctg ga 431  
 Leu  
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<210> 1207

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<211> 855  
 <212> DNA  
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<220>  
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 tgcggagagg tgaggcaagg cgtcgtgtca tagatgcctg agtgctctct agggagacga 180  
 tgcccgtggg gtcgcgcctg ctcgagcgaa cgggaagaga aggtgccacg ccctcctccc 240  
 ggattcacgc cttgtgctgg gcgacgcgcg tgccctgtgc cccgacttgc ccagctcgcc 300  
 ccaaggggcg aggactgagg aaagcactgc ctttctgttc tttaaagcgaa cctttgaagg 360  
 cctgggcttc gcgcccggct tctttctcag ccgttggttc cgttttttgg tgacaagagg 420  
 ctagtaatct cgtcaggagc caacgtaaga gttcttctact accacaacca aggagggmta 480  
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 atcagcggtta actgctttat caaatgtcag gctggmtact atctataaag ag atg gtc 658  
 Met Val  
 1  
 act caa gct caa cag gra ata aca gta caa cag cta atg gct cat ttg 706  
 Thr Gln Ala Gln Gln Xaa Ile Thr Val Gln Gln Leu Met Ala His Leu  
 5 10 15  
 gat gct atc agg aaa gac atg gtc atc cta gag aaa agt gaa ttt gca 754  
 Asp Ala Ile Arg Lys Asp Met Val Ile Leu Glu Lys Ser Glu Phe Ala  
 20 25 30  
 aat ctg aga gca gag aat gag aaa atg aaa att gaa tta gac caa gtt 802  
 Asn Leu Arg Ala Glu Asn Glu Lys Met Lys Ile Glu Leu Asp Gln Val  
 35 40 45 50  
 aag caa caa cta atg cat gaa acc agt yga atc aga gca gat aat aaa 850  
 Lys Gln Gln Leu Met His Glu Thr Ser Xaa Ile Arg Ala Asp Asn Lys  
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 Leu

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 <211> 439  
 <212> DNA  
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<220>  
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 <222> 106..438

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 Met Glu Val Ser  
 1  
 cca ttg cag cct gta aat gaa aat atg caa gtc aac aaa ata aag aaa 165

Pro	Leu	Gln	Pro	Val	Asn	Glu	Asn	Met	Gln	Val	Asn	Lys	Ile	Lys	Lys		
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Asn	Glu	Asp	Ala	Lys	Lys	Arg	Leu	Ser	Val	Glu	Arg	Ile	Tyr	Gln	Lys		
				25					30					35			
aaa	aca	caa	ttg	gaa	cat	att	ttg	ctc	cgc	cca	gac	acc	tac	att	ggg		261
Lys	Thr	Gln	Leu	Glu	His	Ile	Leu	Leu	Arg	Pro	Asp	Thr	Tyr	Ile	Gly		
			40				45						50				
tct	gtg	gaa	tta	gtg	acc	cag	caa	atg	tgg	ggt	tac	gat	gaa	gat	ggt		309
Ser	Val	Glu	Leu	Val	Thr	Gln	Gln	Met	Trp	Val	Tyr	Asp	Glu	Asp	Val		
		55					60					65					
ggc	att	aac	tat	agg	gaa	gtc	act	ttt	ggt	cct	ggg	ttg	tac	aaa	atc		357
Gly	Ile	Asn	Tyr	Arg	Glu	Val	Thr	Phe	Val	Pro	Gly	Leu	Tyr	Lys	Ile		
	70					75				80							
ttt	gat	gag	att	cta	ggt	aat	gct	gcg	gac	aac	aaa	caa	agg	gac	cca		405
Phe	Asp	Glu	Ile	Leu	Val	Asn	Ala	Ala	Asp	Asn	Lys	Gln	Arg	Asp	Pro		
	85				90					95				100			
aaa	atg	tct	tgt	att	aga	gtc	aca	att	gat	ccg	g						439
Lys	Met	Ser	Cys	Ile	Arg	Val	Thr	Ile	Asp	Pro							
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<220>  
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			Met	Glu	Ile	Lys	Asp	Gln	Gly								
			1				5										
gcc	caa	atg	gag	ccg	ctg	ctg	cct	acg	aga	aat	gat	gaa	gaa	gca	ggt		162
Ala	Gln	Met	Glu	Pro	Leu	Leu	Pro	Thr	Arg	Asn	Asp	Glu	Glu	Ala	Val		
		10					15					20					
gtg	gat	aga	ggg	gga	act	cgt	tct	att	ctc	aaa	aca	cac	ttt	gag	aaa		210
Val	Asp	Arg	Gly	Gly	Thr	Arg	Ser	Ile	Leu	Lys	Thr	His	Phe	Glu	Lys		
		25				30				35							
gaa	gat	tta	gaa	ggg	cat	cga	aca	cta	ttt	att	gga	gta	cat	gtg	ccc		258
Glu	Asp	Leu	Glu	Gly	His	Arg	Thr	Leu	Phe	Ile	Gly	Val	His	Val	Pro		
	40				45				50					55			
tyg	gga	gga	aga	aaa	agc	cat	cga	cgt	ca								287
Xaa	Gly	Gly	Arg	Lys	Ser	His	Arg	Arg									
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 <212> DNA  
 <213> Homo sapiens

<220>  
<221> CDS  
<222> 253..405

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 gtatgttagc agaagagggg cagtcagctc tggttccatg cctgacatgt atcaaagatc 180  
 tgggacctct tcccagtggg ggcactaggg ttgcttggtt aaaggggtgct tgaacaacta 240  
 accagcaaag ag atg tct gat gcc aaa tgg gca aga tca aat act gga atg 291  
 Met Ser Asp Ala Lys Trp Ala Arg Ser Asn Thr Gly Met  
 1 5 10  
 cta aaa cac agc tgg aat cta aga agg gaa gag ggc ttc tct gac cat 339  
 Leu Lys His Ser Trp Asn Leu Arg Arg Glu Glu Gly Phe Ser Asp His  
 15 20 25  
 ttt cat acc agc aac aat tta ggc aga att atr aac atc tat tta tct 387  
 Phe His Thr Ser Asn Asn Leu Gly Arg Ile Xaa Asn Ile Tyr Leu Ser  
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 agt gac aat aca aac cga a 406  
 Ser Asp Asn Thr Asn Arg  
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<210> 1211  
<211> 346  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> 150..344

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 aactggcctt gttgaccggg agaaacgag atg ggg gtg aag ctg gag ata ttt 173  
 Met Gly Val Lys Leu Glu Ile Phe  
 1 5  
 cgg atg ata atc tac ctc act ttc cct gtg gct atg ttc tgg gtt tcc 221  
 Arg Met Ile Ile Tyr Leu Thr Phe Pro Val Ala Met Phe Trp Val Ser  
 10 15 20  
 aat cag gcc gag tgg ttt gag gac gat gtc ata cag cgc aag agg gag 269  
 Asn Gln Ala Glu Trp Phe Glu Asp Asp Val Ile Gln Arg Lys Arg Glu  
 25 30 35 40  
 ctg tgg cca cct gag aag gta agt gat ctc ttc ttc ctg cca gag gga 317  
 Leu Trp Pro Pro Glu Lys Val Ser Asp Leu Phe Phe Leu Pro Glu Gly  
 45 50 55  
 tgg agg agg ctg gat tct tgt atc cgg ga 346  
 Trp Arg Arg Leu Asp Ser Cys Ile Arg  
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<210> 1212  
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<212> DNA  
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<220>  
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 <222> 134..514

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 ggcctagcga gtt atg gcg acg aag gcc gtg tgc gtg ctg aag ggc gac 169  
                   Met Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp  
                   1                  5                  10  
 ggc cca gtg cag ggc atc atc aat ttc gag cag aag gaa agt aat gga 217  
 Gly Pro Val Gln Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly  
                   15                  20                  25  
 cca gtg aag gtg tgg gga agc att aaa gga ctg act gaa ggc ctg cat 265  
 Pro Val Lys Val Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His  
                   30                  35                  40  
 gga ttc cat gtt cat gag ttt gga gat aat aca gca ggc tgt acc agt 313  
 Gly Phe His Val His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser  
                   45                  50                  55                  60  
 gca ggt cct cac ttt aat cct cta tcc aga aaa cac ggt ggg cca aag 361  
 Ala Gly Pro His Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys  
                   65                  70                  75  
 gat gaa gag agg cat gtt gga gac ttg ggc aat gtg act gct gac aaa 409  
 Asp Glu Glu Arg His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys  
                   80                  85                  90  
 gat ggt gtg gcc gat gtg tct att gaa gat tct gtg atc tca ctc tca 457  
 Asp Gly Val Ala Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser  
                   95                  100                  105  
 gga gac cat tgc atc att ggc cgc aca ctg gtg gtc cat gaa aaa gca 505  
 Gly Asp His Cys Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala  
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 Asp Asp Leu  
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<210> 1213  
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 <212> DNA  
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<220>  
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 cgtagtctcc tgcagcgtct ggggtttccg ttgcagtcct cggaaccagg acctcggcgt 120  
 ggcctagcga gtt atg gcg acg aag gcc gtg tgc gtg ctg aag ggc gac 169  
                   Met Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp

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ggc cca gtg cag ggc atc atc aat ttc gag cag aag gaa agt aat gga						217
Gly Pro Val Gln Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly						
	15		20		25	
cca gtg aag gtg tgg gga agc ata ggg ggg tgc cgt tca ctt ctg gtt						265
Pro Val Lys Val Trp Gly Ser Ile Gly Gly Ser Arg Ser Leu Leu Val						
	30		35		40	
ccg gag ctg att gga cag cca gtc cag tcc ttc ata gag ccc gtc gcc						313
Pro Glu Leu Ile Gly Gln Pro Val Gln Ser Phe Ile Glu Pro Val Ala						
45		50		55	60	
gct ggt ggc gca ggt ggc ctg aat gta ctc cat ttt ttc cac atc acc						361
Ala Gly Gly Ala Gly Gly Leu Asn Val Leu His Phe Phe His Ile Thr						
	65		70		75	
atc gac att cgg aat gtc tgt gtg ttc ctg gcc cca ctc ttc tcc tcc						409
Ile Asp Ile Arg Asn Val Cys Val Phe Leu Ala Pro Leu Phe Ser Ser						
	80		85		90	
ttc acc acc atc gtc ac						426
Phe Thr Thr Ile Val						
	95					

<210> 1214  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 98..304

<400> 1214	
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tgtcctctgtc gccttcgcct cctaatecct agccact atg cgt gag tgc atc tcc	115
Met Arg Glu Cys Ile Ser	
	1
atc cac gtt ggc cgg gct ggt gtc cgg att ggc aat gcc tgc tgg gag	163
Ile His Val Gly Arg Ala Gly Val Arg Ile Gly Asn Ala Cys Trp Glu	
	10
ctc tac tgc ctg gcc atc cgt tgt cct tct ggc ttc aaa att tct gct	211
Leu Tyr Cys Leu Ala Ile Arg Cys Pro Ser Gly Phe Lys Ile Ser Ala	
	25
att att act gtt ttt cct cct ttt gat ctt cct ttt ggg cgc gtt gtt	259
Ile Ile Thr Val Phe Pro Pro Phe Asp Leu Pro Phe Gly Arg Val Val	
	40
ctc gtc gcg ggc gcc ctt gct gcc gcc gat gat gac atc cgc cgc	304
Leu Val Ala Gly Ala Leu Ala Ala Ala Asp Asp Asp Ile Arg Arg	
	55
	60
	65

<210> 1215  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 65..304

<400> 1215

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cacc atg cgt gaa tgc atc tca gtc cac gtg ggg cag gca ggt gtc cag      109
      Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln
        1           5           10           15
atg ggc aat gcc tgc tgg gag ctc tat tgc ttg gaa cat ggg att cag      157
Met Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln
           20           25           30
cct gat ggg cag atg ccc agt gac aag acc att ggt gga ggg gac gac      205
Pro Asp Gly Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp
           35           40           45
tcc ttc acc acc ttc ttc tgt gaa act ggt gct gga aaa cac gta ccc      253
Ser Phe Thr Thr Phe Phe Cys Glu Thr Gly Ala Gly Lys His Val Pro
           50           55           60
cgg gca gtt ttt gtg gat ctg gag cct acg gtc att gat gag atc cga      301
Arg Ala Val Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Ile Arg
           65           70           75
aat
Asn
80

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<210> 1216  
<211> 324  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 82..324

<400> 1216

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gctgaagcag cggagttcgc c atg cgc gag tgt atc tct atc cac gtg ggg      111
      Met Arg Glu Cys Ile Ser Ile His Val Gly
        1           5           10
cag gcg ggt gtc cag atc ggc aat gcc tgc tgg gaa ctg tac tgc ctt      159
Gln Ala Gly Val Gln Ile Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu
           15           20           25
gaa cat gna att cag ccc gat ggc caa atg cca agt gat aaa acc att      207
Glu His Xaa Ile Gln Pro Asp Gly Gln Met Pro Ser Asp Lys Thr Ile
           30           35           40
ggg ggc ggg gac gac tcc ttc aac acg ttc ttc agt gag act gga gct      255
Gly Gly Gly Asp Asp Ser Phe Asn Thr Phe Phe Ser Glu Thr Gly Ala
           45           50           55
ggc aag cac gtg ccc aga gca gtg ttt gtg gac ctg gag ccc act ktg      303
Gly Lys His Val Pro Arg Ala Val Phe Val Asp Leu Glu Pro Thr Xaa
           60           65           70
gtc gat gaa gtg cgc aca ggg
Val Asp Glu Val Arg Thr Gly

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75

80

<210> 1217  
 <211> 414  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 126..413

<400> 1217  
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 tccgctccga gcccgctcgg actccccga tcccagcttt ctctcctttg aaaacactaa 120  
 gaata atg tca ctg cat cag ttt tta cta gag cca atc acc tgt cat gcc 170  
 Met Ser Leu His Gln Phe Leu Leu Glu Pro Ile Thr Cys His Ala  
 1 5 10 15  
 tgg aac agg gat cgt act cag att gcc ctc agt ccc aat aat cac gaa 218  
 Trp Asn Arg Asp Arg Thr Gln Ile Ala Leu Ser Pro Asn Asn His Glu  
 20 25 30  
 gtg cac atc tat aag aag aac ggg agc cag tgg gtg aaa gct cat gaa 266  
 Val His Ile Tyr Lys Lys Asn Gly Ser Gln Trp Val Lys Ala His Glu  
 35 40 45  
 ctc aag gag cac aac gga cac atc aca ggt att gac tgg gct ccc aag 314  
 Leu Lys Glu His Asn Gly His Ile Thr Gly Ile Asp Trp Ala Pro Lys  
 50 55 60  
 agc gac cgc att gtc act tgt ggg gca gan cgc aat gcc tat gtc tgg 362  
 Ser Asp Arg Ile Val Thr Cys Gly Ala Xaa Arg Asn Ala Tyr Val Trp  
 65 70 75  
 agt cag aaa gat ggt gtt tgg aag cca acc ctg gtg atc ctg aga att 410  
 Ser Gln Lys Asp Gly Val Trp Lys Pro Thr Leu Val Ile Leu Arg Ile  
 80 85 90 95  
 aat c 414  
 Asn

<210> 1218  
 <211> 255  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 96..254

<400> 1218  
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 tgctgggcgc gctgcgggag ctgggcttcc cgtac atg acg ccg gtg cag tcc 113  
 Met Thr Pro Val Gln Ser  
 1 5  
 gca acc atc cct ctg ttc atg cga aac aaa gat gtc gct gca gaa gcg 161  
 Ala Thr Ile Pro Leu Phe Met Arg Asn Lys Asp Val Ala Ala Glu Ala  
 10 15 20

gtc	aca	ggt	agt	ggc	aaa	aca	ctc	gct	ttt	gtc	atc	ccc	atc	ctg	gaa	209
Val	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Ala	Phe	Val	Ile	Pro	Ile	Leu	Glu	
	25						30				35					
att	ctt	ctg	aga	aga	gaa	gag	aag	tta	aaa	aag	art	cag	ggt	gga	g	255
Ile	Leu	Leu	Arg	Arg	Glu	Glu	Lys	Leu	Lys	Lys	Xaa	Gln	Val	Gly		
	40					45					50					

<210> 1219  
 <211> 561  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 142..561

<400> 1219																	
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cwrtcttatt	tggcagctgc	tgccacccc	acagcttttg	atatctagga	ggcactcttc											120	
tctcccaaac	tacctgtcac	c	atg	gcc	cac	cga	ttt	cca	gcc	ctc	acc	cag				171	
			Met	Ala	His	Arg	Phe	Pro	Ala	Leu	Thr	Gln					
			1				5					10					
gag	cag	aag	aag	gag	ctc	tca	gaa	att	gcc	cag	agc	att	ggt	gcc	aat	219	
Glu	Gln	Lys	Lys	Glu	Leu	Ser	Glu	Ile	Ala	Gln	Ser	Ile	Val	Ala	Asn		
			15				20						25				
gga	aag	ggg	atc	ctg	gct	gca	gat	gaa	tct	gta	ggg	acc	atg	ggg	aac	267	
Gly	Lys	Gly	Ile	Leu	Ala	Ala	Asp	Glu	Ser	Val	Gly	Thr	Met	Gly	Asn		
			30				35					40					
cgc	ctg	cag	agg	atc	aag	gtg	gaa	aac	act	gaa	gag	aac	cgc	cgg	cag	315	
Arg	Leu	Gln	Arg	Ile	Lys	Val	Glu	Asn	Thr	Glu	Glu	Asn	Arg	Arg	Gln		
			45				50					55					
ttc	cga	gaa	atc	ctc	ttc	tct	gtg	gac	agt	tcc	atc	aac	cag	agc	atc	363	
Phe	Arg	Glu	Ile	Leu	Phe	Ser	Val	Asp	Ser	Ser	Ile	Asn	Gln	Ser	Ile		
			60				65				70						
ggg	ggt	gtg	atc	ctt	ttc	cac	gag	acc	ctc	tac	cag	aag	gac	agc	cag	411	
Gly	Gly	Val	Ile	Leu	Phe	His	Glu	Thr	Leu	Tyr	Gln	Lys	Asp	Ser	Gln		
			75			80				85				90			
gga	aag	ctg	ttc	aga	aac	atc	ctc	aag	gaa	aag	ggg	atc	gtg	rtg	ggr	459	
Gly	Lys	Leu	Phe	Arg	Asn	Ile	Leu	Lys	Glu	Lys	Gly	Ile	Val	Xaa	Gly		
			95						100				105				
atc	aag	tta	gac	caa	gga	ggt	gct	cct	ctt	gca	ggm	aca	aac	aaa	gaa	507	
Ile	Lys	Leu	Asp	Gln	Gly	Gly	Ala	Pro	Leu	Ala	Gly	Thr	Asn	Lys	Glu		
			110				115						120				
acc	acc	att	caa	ggg	ctt	gat	ggc	ctc	tca	gag	cgc	tgt	gct	cag	tac	555	
Thr	Thr	Ile	Gln	Gly	Leu	Asp	Gly	Leu	Ser	Glu	Arg	Cys	Ala	Gln	Tyr		
			125				130					135					
aag	aaa															561	
Lys	Lys																
			140														

<210> 1220  
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 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 159..494

<400> 1220

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tagtagtttc caggcgctgc cgggcggctg gcactaagcg gtcctgaggc tgtggctacg 120  
gctgctccgg agctggtggc gccgcgatag gagagccg atg gcc aag tgg ggt gag 176  
Met Ala Lys Trp Gly Glu  
1 5  
gga gac cca cgc tgg atc gtg gag gag cgg gcg gac gcc acc aac gtc 224  
Gly Asp Pro Arg Trp Ile Val Glu Glu Arg Ala Asp Ala Thr Asn Val  
10 15 20  
aac aac tgg cac tgg acg gag aga gat gct tca aat tgg tcc acg gat 272  
Asn Asn Trp His Trp Thr Glu Arg Asp Ala Ser Asn Trp Ser Thr Asp  
25 30 35  
aag ctg aaa aca ctg ttc ytg gca gtg cag gtt caa aat gaa gaa ggc 320  
Lys Leu Lys Thr Leu Phe Leu Ala Val Gln Val Gln Asn Glu Glu Gly  
40 45 50  
aak tgt gag gtg acg gaa gtg agt aag ctt gat gga gag gca tcc att 368  
Xaa Cys Glu Val Thr Glu Val Ser Lys Leu Asp Gly Glu Ala Ser Ile  
55 60 65 70  
aac aat cgc aaa ggg aaa ctt atc ttc ttt tat gaa tgg agc gtc aaa 416  
Asn Asn Arg Lys Gly Lys Leu Ile Phe Phe Tyr Glu Trp Ser Val Lys  
75 80 85  
cta aac tgg aca ggt act tct aag tca gga gta car tac aaa gga cat 464  
Leu Asn Trp Thr Gly Thr Ser Lys Ser Gly Val Gln Tyr Lys Gly His  
90 95 100  
gtg gag atc cca att tgt ctg atg aaa cag cg 496  
Val Glu Ile Pro Ile Cys Leu Met Lys Gln  
105 110

<210> 1221

<211> 406

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 159..404

<400> 1221

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tagtagtttc caggcgctgc cgggcggctg gcactaagcg gtcctgaggc tgtggctacg 120  
gctgctccgg agctggtggc gccgcgatag gagagccg atg gcc aag tgg ggt gag 176  
Met Ala Lys Trp Gly Glu  
1 5  
gga gac cca cgc tgg atc gtg gag gag cgg gcg gac gcc acc aac gtc 224  
Gly Asp Pro Arg Trp Ile Val Glu Glu Arg Ala Asp Ala Thr Asn Val  
10 15 20

aac aac tgg cac tgg acg gag aga gat gct tca aat tgg tcc acg gat	272
Asn Asn Trp His Trp Thr Glu Arg Asp Ala Ser Asn Trp Ser Thr Asp	
25 30 35	
aag ctg aaa aca ctg ttc ttg gca gtg cag gtt caa aat gaa gaa ggc	320
Lys Leu Lys Thr Leu Phe Leu Ala Val Gln Val Gln Asn Glu Glu Gly	
40 45 50	
atc cca aag tgc tgg gat tac agg cag gaa cca cgg ccc ctg gcc ctc	368
Ile Pro Lys Cys Trp Asp Tyr Arg Gln Glu Pro Arg Pro Leu Ala Leu	
55 60 65 70	
atc ata gtc tta agt gtc gtt gtt gcc ttc aaa aac ct	406
Ile Ile Val Leu Ser Val Val Val Ala Phe Lys Asn	
75 80	

<210> 1222  
 <211> 1776  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 1388..1774

<400> 1222

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ccgacctcca gcagcagtcg gcttctctac gcagaaccg ggagtaggag actcagaatc	120
gaatctcttc tccctccctt tcttgttttc ggctttgtga gaaaccttac catcaaacac	180
gatggccagc aacgttacca acaagacaga tcctcgctcc atgaactccc gtgtattcat	240
tgggaatctc aacactcttg tggtaagaa atctgatgtg gaggcaatct tttcgaagta	300
tggcaaaatt gtgggctgct ctgttcataa gggctttgcc ttcgttcagt atgttaatga	360
gagaaatgcc cgggctgctg tgaagagacg aagactgagc ggttggtggc gcgttgccga	420
cctccagcag cagtcggctt ctctacgcag aaccggggag taggagactc agaatcgaat	480
ctcttctccc tcccttctt gtgagatttt tttgatcttc agctacattt tcggctttgt	540
gagaaacctt accatcaaac acgatggcca gcaacgttac caacaagaca gatcctcgct	600
ccatgaactc ccgtgtattc attgggaatc tcaacactct tgtggtcaag aaatctgatg	660
tggaggcaat cttttcgaag tatggcaaaa ttgtgggctg ctctgttcat aagggtttg	720
cttcgttcag tatgttaag agagaaatgc cnnggctgct gtagmagaga sgaagactga	780
gcggttggtg ccgcgttgcc gacctccagc agcagtcggc ttctctacgc agaaccggg	840
agtaggagac tcagaatcga atctcttctc cctcccttctc ttgttttcgg ctttgtgaga	900
aaccttacca tcaaacacga tggccagcaa cgttaccaac aagacagatc ctcgctccat	960
gaactcccggt gtattcattg ggaatctcaa cactcttggt gtcaagaaat ctgatgtgga	1020
ggcaatcttt tcgaagtatg gcaaaattgt gggctgctct gttcataagg gctttgcctt	1080
cgttcagtat gttaatgaga gaaatgcccg ggctgctgta gcaggagagg atggcagaat	1140
gattgctggc caggtttnyg atattaacct ggctgcagas caaaagtga ccgaggaaaa	1200
gcaggtgtga racgaagwct gagcgggttg ggccgcgttg ccgacctcca gcagcagtcg	1260
gcttctctac gcagaaccg ggagtaggag actcagaatc gaatctcttc tccctccctt	1320
tcttgtgaga ttttttgat cttcagctac attttcggct ttgtgagaaa cttaccatc	1380
aaacacg atg gcc agc aac gtt acc aac aag aca gat cct cgc tcc atg	1429
Met Ala Ser Asn Val Thr Asn Lys Thr Asp Pro Arg Ser Met	
1 5 10	
aac tcc cgt gta ttc att ggg aat ctc aac act ctt gtg gtc aag aaa	1477
Asn Ser Arg Val Phe Ile Gly Asn Leu Asn Thr Leu Val Val Lys Lys	
15 20 25 30	
tct gat gtg gag gca atc ttt tcg aag tat ggc aaa att gtg ggc tgc	1525

Ser	Asp	Val	Glu	Ala	Ile	Phe	Ser	Lys	Tyr	Gly	Lys	Ile	Val	Gly	Cys	
				35					40					45		
tct	ggt	cat	aag	ggc	ttt	gcc	ttc	ggt	cag	tat	gtk	aat	gag	aga	aat	1573
Ser	Val	His	Lys	Gly	Phe	Ala	Phe	Val	Gln	Tyr	Val	Asn	Glu	Arg	Asn	
			50					55					60			
gcc	cgg	gct	gct	gta	gca	gga	gag	gat	ggc	aga	atg	att	gct	ggc	cag	1621
Ala	Arg	Ala	Ala	Val	Ala	Gly	Glu	Asp	Gly	Arg	Met	Ile	Ala	Gly	Gln	
			65				70					75				
ggt	tta	gat	att	aac	ctg	gct	gca	gag	cca	aaa	gtg	aac	cga	gga	aaa	1669
Val	Leu	Asp	Ile	Asn	Leu	Ala	Ala	Glu	Pro	Lys	Val	Asn	Arg	Gly	Lys	
			80				85				90					
gca	ggt	gtg	aaa	cga	tct	gca	gcg	gag	atg	tac	ggg	tca	gta	aca	gaa	1717
Ala	Gly	Val	Lys	Arg	Ser	Ala	Ala	Glu	Met	Tyr	Gly	Ser	Val	Thr	Glu	
			95			100				105					110	
cac	cct	tct	ccg	tcc	cct	cta	ctc	agc	tcc	tct	ttt	gac	ttg	gac	tat	1765
His	Pro	Ser	Pro	Ser	Pro	Leu	Leu	Ser	Ser	Ser	Phe	Asp	Leu	Asp	Tyr	
				115					120					125		
gac	ttt	caa	cg													1776
Asp	Phe	Gln														

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 <212> DNA  
 <213> Homo sapiens

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 <222> 706..1092

<400> 1223																
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tcccccttct	ggttacaaaa	cacttgaaat	atataagtta	gtggaacttt	gcttgagtga											180
gatttttttg	atcttcagct	acattttcgg	ctttgtgaga	aaccttacca	tcaaacacga											240
tggcnagcaa	cgttaccaac	aagacagatc	ctcgtcccat	gaactcccg	gtattcattg											300
ggaatctcaa	cactcttggt	gtcaagaaat	ctgatgtgga	ggcaatcttt	tccaagtatg											360
gcaaaattgt	gggctgctct	gttcataagg	gctttgcttc	gttcagtatg	ttaatgagag											420
aaatgccggg	ctgctgtagc	aggagaggat	ggcagaatga	ttgctggcca	ggtttnygat											480
attaacctgg	ctgcagasca	aaagtgaacc	gaggaaaagc	aggtgtgara	cgaagwctga											540
gcggttggtg	ccgcgttgcc	gacctccagc	agcagtcggc	ttctctacgc	agaacccggg											600
agtaggagac	tcagaatcga	atctcttctc	cctccccttc	ttgtgagatt	tttttgatct											660
tcagctacat	tttcggcttt	gtgagaaacc	ttaccatcaa	acacg atg	gcc agc aac											717
				Met	Ala	Ser	Asn									
				1												
ggt acc aac aag aca gat cct cgc tcc atg aac tcc cgt gta ttc att																765
Val Thr Asn Lys Thr Asp Pro Arg Ser Met Asn Ser Arg Val Phe Ile																
5				10				15					20			
ggg aat ctc aac act ctt gtg gtc aag aaa tct gat gtg gag gca atc																813
Gly Asn Leu Asn Thr Leu Val Val Lys Lys Ser Asp Val Glu Ala Ile																
			25				30					35				
ttt tcg aag tat ggc aaa att gtg ggc tgc tct gtt cat aag ggc ttt																861
Phe Ser Lys Tyr Gly Lys Ile Val Gly Cys Ser Val His Lys Gly Phe																
			40				45					50				



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gcc ttc gtt cag tat gtk aat gag aga aat gcc cgg gct gct gta gca      909
Ala Phe Val Gln Tyr Val Asn Glu Arg Asn Ala Arg Ala Ala Val Ala
      55                      60                      65
gga gag gat ggc aga atg att gct ggc cag gtt tta gat att aac ctg      957
Gly Glu Asp Gly Arg Met Ile Ala Gly Gln Val Leu Asp Ile Asn Leu
      70                      75                      80
gct gca gag cca aaa gtg aac cga gga aaa gca ggt gtg aaa cga tct      1005
Ala Ala Glu Pro Lys Val Asn Arg Gly Lys Ala Gly Val Lys Arg Ser
      85                      90                      95                      100
gca gcg gag atg tac ggg tca gta aca gaa cac cct tct ccg tcc cct      1053
Ala Ala Glu Met Tyr Gly Ser Val Thr Glu His Pro Ser Pro Ser Pro
      105                      110                      115
cta ctc agc tcc tct ttt gac ttg gac tat gac ttt caa cg      1094
Leu Leu Ser Ser Ser Phe Asp Leu Asp Tyr Asp Phe Gln
      120                      125

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<220>  
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gcagcttg atg ggc gac aac cct ttt caa cca aaa agt aat tca aaa atg      170
      Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met
      1                      5                      10
gca gaa ctg ttt atg gaa tgt gaa gaa gag gag ctg gaa cca tgg cag      218
Ala Glu Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu Pro Trp Gln
      15                      20                      25                      30
aag aaa gta aaa gaa gtt gag gat gac gat gat gat gag cca atc ttt      266
Lys Lys Val Lys Glu Val Glu Asp Asp Asp Asp Asp Glu Pro Ile Phe
      35                      40                      45
gtt ggc gag ata tca agt tca aaa cca gca att tca aat att ttg aac      314
Val Gly Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn
      50                      55                      60
aga gtt aac ccc agc tca tat tca agg gga cta aag aat ggt gca ctc      362
Arg Val Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu
      65                      70                      75
agt cga ggt att act gct gca ttc aag cct aca agt caa cac tac acg      410
Ser Arg Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr
      80                      85                      90

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 <211> 608  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 394..606

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acaccaggtg gtgaatagag cccctcctaa ggttgctcag gataaatcat ttattaaata 180  
ggtctgctta tcaggagggg cgtgaaggct cccaaaagga aatgctggca cctgggcca 240  
gaagccaggg cctctaaact ctgggggttga tttcttcagt gaagttgcac cctacaaagg 300  
gaatatggcc aaagcggcac tcaactgaag gctgatatca ggcgattaga cagccatgca 360  
ttctgcgttt gtctggaatt ggattgwaga gag atg gac tta tat gag gac tac 414  
Met Asp Leu Tyr Glu Asp Tyr

1 5  
cag tcc ccg ttt gat ttt gat gca gga gtg aac aaa agc tat ctc tac 462  
Gln Ser Pro Phe Asp Phe Asp Ala Gly Val Asn Lys Ser Tyr Leu Tyr  
10 15 20  
ttg tyt cct agt gga aat tca tct cca ccc gga tca cct act ctt cag 510  
Leu Xaa Pro Ser Gly Asn Ser Ser Pro Pro Gly Ser Pro Thr Leu Gln  
25 30 35  
aaa ttt ggt ctg ctg aga aca gac cca gtc cct gag gaa ggm gaa gat 558  
Lys Phe Gly Leu Leu Arg Thr Asp Pro Val Pro Glu Glu Gly Glu Asp  
40 45 50 55  
gtt gct gcc acg atc agt gcc aca gag acc ctc tcg gaa gag gag cag 606  
Val Ala Ala Thr Ile Ser Ala Thr Glu Thr Leu Ser Glu Glu Glu Gln  
60 65 70  
ga 608

<210> 1226  
<211> 282  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 118..282

<400> 1226  
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gggtccatca ctagcttcag ggtcacggca ctgtggctat gagaggagc ccctaaa 117  
atg act gct agc cat gca aca gga ggc agc cac ctg cgt aga cag gga 165  
Met Thr Ala Ser His Ala Thr Gly Gly Ser His Leu Arg Arg Gln Gly  
1 5 10 15  
tgg gtg cct ggt gaa acc cac ctt caa gcc aaa aac agc ctg aag gct 213  
Trp Val Pro Gly Glu Thr His Leu Gln Ala Lys Asn Ser Leu Lys Ala  
20 25 30  
gaa aga ctg gac cgc tgg tgc cgg atg aaa ccg aga cgc aga gtg aga 261  
Glu Arg Leu Asp Arg Trp Cys Arg Met Lys Pro Arg Arg Arg Val Arg  
35 40 45  
act tct gtt cct gtt tgc ccg 282  
Thr Ser Val Pro Val Cys Pro  
50 55

<210> 1227  
 <211> 460  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 206..460

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 tccctcartg gtagggagac agccaggagc gggtttcttg gaactgtggg atgtgccctt 180  
 gggggccccg gaaaacagaa ggaag atg ctc cag acc agt aac tac agc ctg 232  
 Met Leu Gln Thr Ser Asn Tyr Ser Leu  
 1 5  
 gtg ctc tct ctg cag ttc ctg ctg tcc tat gac ctc ttt gtc aat 280  
 Val Leu Ser Leu Gln Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn  
 10 15 20 25  
 tcc ttc tca gaa ctg ctc caa aag act cct gtc atc cag ctt gtg ctc 328  
 Ser Phe Ser Glu Leu Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu  
 30 35 40  
 ttc atc atc cag gat att gca gtc ctc ttc aac atc atc atc att ttc 376  
 Phe Ile Ile Gln Asp Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe  
 45 50 55  
 ctc atg ttc ttc aac acc ttc gtc ttc cag nct ggc ctg gtc aac ctc 424  
 Leu Met Phe Phe Asn Thr Phe Val Phe Gln Xaa Gly Leu Val Asn Leu  
 60 65 70  
 cta ttc cat aag ttc aaa ggg acc atc atc ctg aca 460  
 Leu Phe His Lys Phe Lys Gly Thr Ile Ile Leu Thr  
 75 80 85

<210> 1228  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 42..461

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 Met Ala Ala Pro Ala  
 1 5  
 gtg tcc ggg ctc tcc cgg cag gtg cga tgc ttc agt acc tct gtg gtc 104  
 Val Ser Gly Leu Ser Arg Gln Val Arg Cys Phe Ser Thr Ser Val Val  
 10 15 20  
 aga cca ttt gcc aag ctt gtg agg cct cct gtt cag gta tac ggt att 152  
 Arg Pro Phe Ala Lys Leu Val Arg Pro Pro Val Gln Val Tyr Gly Ile  
 25 30 35  
 gaa ggt cgc tat gcc aca gct ctt tat tct gct gca tca aaa cag aat 200

Glu Gly Arg Tyr Ala Thr Ala Leu Tyr Ser Ala Ala Ser Lys Gln Asn	
40 45 50	
aag ctg gag caa gta gaa aag gag ttg ttg aga gta gca caa atc ctg	248
Lys Leu Glu Gln Val Glu Lys Glu Leu Leu Arg Val Ala Gln Ile Leu	
55 60 65	
aag gaa ccc aaa gtg gct gct tct gtt ttg aat ccc tat gtg aag cgt	296
Lys Glu Pro Lys Val Ala Ala Ser Val Leu Asn Pro Tyr Val Lys Arg	
70 75 80 85	
tcc att aaa gtg aaa agc cta aat gac atc aca gca aaa gag agg ttc	344
Ser Ile Lys Val Lys Ser Leu Asn Asp Ile Thr Ala Lys Glu Arg Phe	
90 95 100	
tct ccc ctc act acc aay ctg atc aat ttg ctt gct gaa aat ggt cga	392
Ser Pro Leu Thr Thr Asn Leu Ile Asn Leu Leu Ala Glu Asn Gly Arg	
105 110 115	
tta agc aat acc caa gga gtc gtt tct gcc ttt tct acc atg atg agt	440
Leu Ser Asn Thr Gln Gly Val Val Ser Ala Phe Ser Thr Met Met Ser	
120 125 130	
gtc cat cgc gga gag gta cct tg	463
Val His Arg Gly Glu Val Pro	
135 140	

<210> 1229  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 128..355

<400> 1229	
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cccgcaggag cgtagagagc gcgggactag agtgcagagc tccgggacgt ggatcggagc	120
cggcgcg atg ggc gga gag cag gag gag gag cgg ttc gac ggc atg ttg	169
Met Gly Gly Glu Gln Glu Glu Glu Arg Phe Asp Gly Met Leu	
1 5 10	
ctg gcc atg gct cag cag cac gag ggc ggc gtg cag gag ctt gtg aac	217
Leu Ala Met Ala Gln Gln His Glu Gly Gly Val Gln Glu Leu Val Asn	
15 20 25 30	
acc ttc ttc agc ttc ctt cga cgc aaa aca gac ttt ttc att gga gga	265
Thr Phe Phe Ser Phe Leu Arg Arg Lys Thr Asp Phe Phe Ile Gly Gly	
35 40 45	
gaa gaa ggg atg gca gag aag ctt atc aca cag act ttc agc cac cac	313
Glu Glu Gly Met Ala Glu Lys Leu Ile Thr Gln Thr Phe Ser His His	
50 55 60	
aat cag ctg gca cag aag acc cgg cgg gag aag aga gcc cgg	355
Asn Gln Leu Ala Gln Lys Thr Arg Arg Glu Lys Arg Ala Arg	
65 70 75	

<210> 1230  
 <211> 329  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 128..328

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 cccgcagayg cgtagagagc gcgggactag agtgcagagc tccgggacgt ggatcggagc 120  
 cggcgcg atg ggc gga gag cag gag gag gag cgg ttc gac ggc atg ttg 169  
 Met Gly Gly Glu Gln Glu Glu Glu Arg Phe Asp Gly Met Leu  
 1 5 10  
 ctg gcc atg gct cag cag cac gag ggc ggc gtg cag gag ctt gtg aac 217  
 Leu Ala Met Ala Gln Gln His Glu Gly Gly Val Gln Glu Leu Val Asn  
 15 20 25 30  
 acc ttc ttc agc ttc ctt cga cgc aaa aca gac ttt ttc att gga gga 265  
 Thr Phe Phe Ser Phe Leu Arg Arg Lys Thr Asp Phe Phe Ile Gly Gly  
 35 40 45  
 gaa gaa ggg atg gca gag aag att ggc agg aga gag aat gag tnc cag 313  
 Glu Glu Gly Met Ala Glu Lys Ile Gly Arg Arg Glu Asn Glu Xaa Gln  
 50 55 60  
 cag aag aaa tgc cag a 329  
 Gln Lys Lys Cys Gln  
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<210> 1231  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 330..566

<400> 1231  
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 tgcgcgccatc ttggttccgc gttccctgca caaaatgccc ggcgaacaca gaaaccgtcc 120  
 ctgctacaga gcaggagttg ccgcagcccc aggctgagac agggctctgga acagaatctg 180  
 acagtgatga atcagtacca gagcttgaag aacaggattc caccaggca accacacaac 240  
 aagcccagct ggcggcagca gctgaaatyg atgaagaacc agtcagtata gcaaaacaga 300  
 gtcggagtgaa aaagaaggca cggaaggct atg tcc aaa ctg ggt ctt cgg cag 353  
 Met Ser Lys Leu Gly Leu Arg Gln  
 1 5  
 gtt aca gga gtt act aga gtc act atc cgg aaa tct aag aat atc ctc 401  
 Val Thr Gly Val Thr Arg Val Thr Ile Arg Lys Ser Lys Asn Ile Leu  
 10 15 20  
 ttt gtc atc aca aaa cca gat gtc tac aag agc cct gct tca gat act 449  
 Phe Val Ile Thr Lys Pro Asp Val Tyr Lys Ser Pro Ala Ser Asp Thr  
 25 30 35 40  
 tac awn gtt ttt ggg gaa gcn aag atc gaa gat tta tcc cag caa gca 497  
 Tyr Xaa Val Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser Gln Gln Ala  
 45 50 55  
 caa cta gca gct gct gag aaa ttc aaa gtt caa ggt gaa gct gtc tca 545

Gln Leu Ala Ala Ala Glu Lys Phe Lys Val Gln Gly Glu Ala Val Ser  
60 65 70

aac att caa gaa aac aca cag  
Asn Ile Gln Glu Asn Thr Gln  
75

566

<210> 1232  
<211> 309  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 91..309

<400> 1232

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ttcaaaacag catcgcccat aacaacagaa atg gcc agt cag tcc caa ggt atc 114  
Met Ala Ser Gln Ser Gln Gly Ile

1 5  
cag cag ctt ctg caa gct gag aag cgg gca gct gag aag gtg gca gat 162  
Gln Gln Leu Leu Gln Ala Glu Lys Arg Ala Ala Glu Lys Val Ala Asp  
10 15 20

gcc aga aag agg aag gcc cgg cga ctg aag cag gca aag gag gag gca 210  
Ala Arg Lys Arg Lys Ala Arg Arg Leu Lys Gln Ala Lys Glu Glu Ala  
25 30 35 40

cag atg gag gtg gag caa tac cgc aga gag cga gag cac gaa ttc cag 258  
Gln Met Glu Val Glu Gln Tyr Arg Arg Glu Arg Glu His Glu Phe Gln  
45 50 55

agc aag cag cag gcg gcc atg ggc tcc cag ggg aac ctg tct gct gag 306  
Ser Lys Gln Gln Ala Ala Met Gly Ser Gln Gly Asn Leu Ser Ala Glu  
60 65 70

gtg 309  
Val

<210> 1233  
<211> 630  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 233..628

<400> 1233

cttcgccgct cgggccgccc gggggaaaac atggcgtctg ccctggagca gtctgtgaac 60  
agtgtccgac agctctcagc tcaagggcaa atgacacagc ttgtgtgaact gatcaacaag 120  
agtgggggaac tccttgcgaa gaaactwatc ccatctggac actgtgctcg gggctctgga 180  
tgtacaagaa cactccttgg gcgtccttgc tgttttgttt gtgaagtttt ct atg ccc 238  
Met Pro

1  
agt gtt cct gac ttc gaa acg cta ttc tca cag gtt cag ctc ttc atc 286

Ser	Val	Pro	Asp	Phe	Glu	Thr	Leu	Phe	Ser	Gln	Val	Gln	Leu	Phe	Ile	
	5						10				15					
agc	act	tgt	aat	ggg	gag	cac	att	cga	tat	gca	aca	gac	act	ttt	gct	334
Ser	Thr	Cys	Asn	Gly	Glu	His	Ile	Arg	Tyr	Ala	Thr	Asp	Thr	Phe	Ala	
	20						25				30					
ggg	ctt	tgc	cat	cag	cta	aca	aat	gca	ctt	gtg	gaa	aga	aaa	cag	ccc	382
Gly	Leu	Cys	His	Gln	Leu	Thr	Asn	Ala	Leu	Val	Glu	Arg	Lys	Gln	Pro	
	35					40				45				50		
ctg	cga	gga	att	ggc	atc	ctt	aag	caa	gcc	ata	gac	aag	atg	cag	atg	430
Leu	Arg	Gly	Ile	Gly	Ile	Leu	Lys	Gln	Ala	Ile	Asp	Lys	Met	Gln	Met	
				55					60					65		
aat	aca	aac	cag	ctg	acc	tca	ata	cat	gct	gat	ctc	tgc	cag	ctt	tgt	478
Asn	Thr	Asn	Gln	Leu	Thr	Ser	Ile	His	Ala	Asp	Leu	Cys	Gln	Leu	Cys	
			70					75					80			
ttg	cta	gca	aaa	tgc	ttt	aag	cct	gcc	ctt	cca	tat	ctt	gac	gtg	gat	526
Leu	Leu	Ala	Lys	Cys	Phe	Lys	Pro	Ala	Leu	Pro	Tyr	Leu	Asp	Val	Asp	
		85					90					95				
atg	atg	gat	atc	tgt	aaa	gag	aat	gga	gcc	tat	gat	gca	aaa	cac	ttt	574
Met	Met	Asp	Ile	Cys	Lys	Glu	Asn	Gly	Ala	Tyr	Asp	Ala	Lys	His	Phe	
		100				105					110					
tta	tgt	tac	tat	tat	tat	ggn	ngg	atg	atc	tat	act	ggg	ctg	aag	aac	622
Leu	Cys	Tyr	Tyr	Tyr	Tyr	Gly	Xaa	Met	Ile	Tyr	Thr	Gly	Leu	Lys	Asn	
		115				120				125					130	
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Phe	Glu															
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<212> DNA																
<213> Homo sapiens																
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<221> CDS																
<222> 281..538																
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ttcacatcgg	aaacaaaaca	gcggctgggc	tggaaggaaac	ctgagctacg	agccgcggcg											120
gcagcggggc	ggcggggaag	cgtataccta	atctgggagc	ctgcaagtga	caacagcctt											180
tgcggtcctt	agacagcttg	gcctggagga	gaacacatga	aagaaagaac	ctcaagaggc											240
tttgttttct	gtgaaacagt	atttctatac	agttgctcca	atg aca gag	tta cct											295
				Met Thr Glu Leu Pro												
				1	5											
gca ccg ttg tcc tac ttc cag aat gca cag atg tct gag gac aac cac																343
Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met Ser Glu Asp Asn His																
			10					15					20			
ctg agc aat act gta cgt agc cag aat gac aat aga gaa cgg cag gag																391
Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn Arg Glu Arg Gln Glu																
			25					30					35			
cac aac gac aga cgg agc ctt ggc cac cct gag cca tta tct aat gga																439
His Asn Asp Arg Arg Ser Leu Gly His Pro Glu Pro Leu Ser Asn Gly																
			40					45					50			
cga ccc cag ggt aac tcc cgg cag gtg gtg gag caa gat gag gaa gaa																487

Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu Gln Asp Glu Glu Glu  
 55 60 65  
 gat gag gag ctg rca ttg aaa tat ggc gcc aag cat gtg atc atg ctc 535  
 Asp Glu Glu Leu Xaa Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu  
 70 75 80 85  
 ttt gt 540  
 Phe

<210> 1235  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 75..380

<400> 1235  
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 ttttctaagc cata atg gca ggt gaa gaa att aat gaa gac tat cca gta 110  
 Met Ala Gly Glu Glu Ile Asn Glu Asp Tyr Pro Val  
 1 5 10  
 gaa att cac gag tat ttg tca gcg ttt gag aat tcc att ggt gct gtg 158  
 Glu Ile His Glu Tyr Leu Ser Ala Phe Glu Asn Ser Ile Gly Ala Val  
 15 20 25  
 gat gag atg ctg aag acc atg atg tct gtt tct aga aat gag ttg ttg 206  
 Asp Glu Met Leu Lys Thr Met Met Ser Val Ser Arg Asn Glu Leu Leu  
 30 35 40  
 cag aag ttg gat cca ctt gaa caa gca aaa gtg gat ttg gtt tct gca 254  
 Gln Lys Leu Asp Pro Leu Glu Gln Ala Lys Val Asp Leu Val Ser Ala  
 45 50 55 60  
 tac aca tta aat tca atg ttt tgg gtt tat ttg gca acc caa gga gtt 302  
 Tyr Thr Leu Asn Ser Met Phe Trp Val Tyr Leu Ala Thr Gln Gly Val  
 65 70 75  
 aat cct aag gaa cat cca gta aaa cag gaa ttg gaa aga atc aga gta 350  
 Asn Pro Lys Glu His Pro Val Lys Gln Glu Leu Glu Arg Ile Arg Val  
 80 85 90  
 tat atg aac aga gtc aag gaa ata aca gac 380  
 Tyr Met Asn Arg Val Lys Glu Ile Thr Asp  
 95 100

<210> 1236  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 117..347

<400> 1236  
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accgctctcc tggaagcaca gaacggactt ttcgtgtccc gctgtaagga aacaag atg 119  
Met  
1  
gtc ctt aaa acc gaa gag gag gac gtt ccc agt gac ckg aca gca gag 167  
Val Leu Lys Thr Glu Glu Glu Asp Val Pro Ser Asp Xaa Thr Ala Glu  
5 10 15  
gag cgt caa gaa ctg gag aac atc cga cgg aga aaa cag gag ctg ctg 215  
Glu Arg Gln Glu Leu Glu Asn Ile Arg Arg Arg Lys Gln Glu Leu Leu  
20 25 30  
gct gac att cag agg ctg aag gat gag ata gca gaa gta gct aat gaa 263  
Ala Asp Ile Gln Arg Leu Lys Asp Glu Ile Ala Glu Val Ala Asn Glu  
35 40 45  
att gaa aac ctg gga tcc aca gag gaa agg aaa aac atg cag agg aac 311  
Ile Glu Asn Leu Gly Ser Thr Glu Glu Arg Lys Asn Met Gln Arg Asn  
50 55 60 65  
aaa cag gta gcc atg ggc agg aaa aaa ttt aat atg ga 349  
Lys Gln Val Ala Met Gly Arg Lys Lys Phe Asn Met  
70 75

<210> 1237  
<211> 532  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 325..531

<400> 1237  
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ctgcaacacc ttacagatgt ggaagatgtg aaatttgtca tcaattatga ctaccctaac 120  
tctcagagg attatattca tcgaattgga agaactgtct gcagtaccaa aacaggcaca 180  
gcatacactt tctttacacc taataacata aagcaagtga gcgaccttat ctctgtgctt 240  
cgtgaagcta atcaagcaat taatcccaag ttgcttcagt tggtcgaaga cagaggttca 300  
ggtcgttcca ggggtagakg aggc atg aag gat gac cgt cgg grc asa tac 351  
Met Lys Asp Asp Arg Arg Xaa Xaa Tyr  
1 5  
tct gcg ggc aaa agg ggt gga ttt aat acc ttt aga gac rgg gaa aat 399  
Ser Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Xaa Glu Asn  
10 15 20 25  
tat grc rga ggt tac tct agc ctg ctt aaa aga gat ttt ggg gca aaa 447  
Tyr Xaa Xaa Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala Lys  
30 35 40  
act cag aat ggt gtt tac agt gct gca aat tas acc aaa tkg gaa gst 495  
Thr Gln Asn Gly Val Tyr Ser Ala Ala Asn Xaa Thr Lys Xaa Glu Xaa  
45 50 55  
ttk gga gta awt ttg tgw ctg ctg gta tac aga cca g 532  
Xaa Gly Val Xaa Leu Xaa Leu Leu Val Tyr Arg Pro  
60 65

<210> 1238  
<211> 396  
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 165..395

<400> 1238

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atcttgcccg aagcygggcg gaggagagct caagctaagg gtgatcagcc catgacctaa 120  
acctccagac aaaataaaac agggaaaatt tgctagaatc aaga atg atg gat cca 176  
Met Met Asp Pro  
1  
trt tca gtt gga gtc cag ctt cgt act aca aat gag tgc cat aaa acc 224  
Xaa Ser Val Gly Val Gln Leu Arg Thr Thr Asn Glu Cys His Lys Thr  
5 10 15 20  
tac tat act cgt cac aca ggt ttt aag act ttg caa gaa ttg tca tca 272  
Tyr Tyr Thr Arg His Thr Gly Phe Lys Thr Leu Gln Glu Leu Ser Ser  
25 30 35  
aat gat atg ctt tta ctt caa ctt aga act gga atg asa ctt tct ggg 320  
Asn Asp Met Leu Leu Leu Gln Leu Arg Thr Gly Met Xaa Leu Ser Gly  
40 45 50  
aac aat aca att tgc ttt cat cat gta aaa att tac att grc aga ttt 368  
Asn Asn Thr Ile Cys Phe His His Val Lys Ile Tyr Ile Xaa Arg Phe  
55 60 65  
gag gat tta cag aag tca tgt tgt gac c 396  
Glu Asp Leu Gln Lys Ser Cys Cys Asp  
70 75

<210> 1239

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 79..318

<400> 1239

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gggaagggtca gcgccgta atg gcg ttc ttg gcg tcg gga ccc tac ctg acc 111  
Met Ala Phe Leu Ala Ser Gly Pro Tyr Leu Thr  
1 5 10  
cat cag caa aag gtg ttg cgg ctt tat aag cgg gcg cta cgc cac ctc 159  
His Gln Gln Lys Val Leu Arg Leu Tyr Lys Arg Ala Leu Arg His Leu  
15 20 25  
gag tcg tgg tgc gtc cag aga gac aaa tac cga tac ttt gct tgt ttg 207  
Glu Ser Trp Cys Val Gln Arg Asp Lys Tyr Arg Tyr Phe Ala Cys Leu  
30 35 40  
atg aga ggc cca atc aag aac ctt aaa gag caa ctt tct atg aaa aga 255  
Met Arg Gly Pro Ile Lys Asn Leu Lys Glu Gln Leu Ser Met Lys Arg  
45 50 55  
tct cag tgg gaa atg gaa aaa cat aat ctg gaa agc aca atg aaa aca 303

Ser Gln Trp Glu Met Glu Lys His Asn Leu Glu Ser Thr Met Lys Thr  
 60 65 70 75  
 tac gta agc nrr ctg aa 320  
 Tyr Val Ser Xaa Leu  
 80

<210> 1240  
 <211> 583  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 260..583

<400> 1240  
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 aggagctcaa aaggagaaga aaacagtagg aggcagggga agcagcctct gtctccatct 120  
 ctgccctttg aaacaaaagg gtatttcttt tctctcttca gcccacaacc cagtggaggc 180  
 ccggttsgg asnttgttca cttccctctg cttccctctt agaagcccc tttgcatcc 240  
 ctgcaccttg tttcgggtg atg ccc gag agg gag ctg tgg cca gcg ggg act 292  
 Met Pro Glu Arg Glu Leu Trp Pro Ala Gly Thr  
 1 5 10  
 ggc tca gaa ccc gtg acc cgt gtc ggc agc tgt gac agc atg atg agc 340  
 Gly Ser Glu Pro Val Thr Arg Val Gly Ser Cys Asp Ser Met Met Ser  
 15 20 25  
 agc acc tcc acc cgc tct gga tct agt gat agc agc tac gac ttc ctg 388  
 Ser Thr Ser Thr Arg Ser Gly Ser Ser Asp Ser Ser Tyr Asp Phe Leu  
 30 35 40  
 tcc act gra gag aas gag tgt ctg ctc ttc ctg gas gag acc att cgc 436  
 Ser Thr Xaa Glu Xaa Glu Cys Leu Leu Phe Leu Xaa Glu Thr Ile Arg  
 45 50 55  
 tca ctg gac acg gag gct gac agc gga ctg tcc act gac gag tct gag 484  
 Ser Leu Asp Thr Glu Ala Asp Ser Gly Leu Ser Thr Asp Glu Ser Glu  
 60 65 70 75  
 cca gcc aca act ccc aga ggt ttc cga gca ctg ccc atn acc caa scc 532  
 Pro Ala Thr Thr Pro Arg Gly Phe Arg Ala Leu Pro Xaa Thr Gln Xaa  
 80 85 90  
 act ccc cgg gga ggt cca gag gag acc atc act cag caa gga cga acg 580  
 Thr Pro Arg Gly Gly Pro Glu Glu Thr Ile Thr Gln Gln Gly Arg Thr  
 95 100 105  
 cca 583  
 Pro

<210> 1241  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 69..476

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 gcgtngcg atg ttg tcc tct aca gcc atg tat tgc gct cct ggc aga gac 110  
 Met Leu Ser Ser Thr Ala Met Tyr Ser Ala Pro Gly Arg Asp  
 1 5 10  
 ttg ggg atg gaa ccg cac aga gcc gcg ggc cct ttg cag ctg cga ttt 158  
 Leu Gly Met Glu Pro His Arg Ala Ala Gly Pro Leu Gln Leu Arg Phe  
 15 20 25 30  
 tcg ccc tac gtt ttc aac gga ggt act ata ctg gca att gct gga gaa 206  
 Ser Pro Tyr Val Phe Asn Gly Gly Thr Ile Leu Ala Ile Ala Gly Glu  
 35 40 45  
 gat ttt gca att gtt gct tct gat act cga ttg agt gaa ggg ttt tca 254  
 Asp Phe Ala Ile Val Ala Ser Asp Thr Arg Leu Ser Glu Gly Phe Ser  
 50 55 60  
 att cat acg cgg gat agc ccc aaa tgt tac aaa tta aca gac aaa aca 302  
 Ile His Thr Arg Asp Ser Pro Lys Cys Tyr Lys Leu Thr Asp Lys Thr  
 65 70 75  
 gtc att gga tgc agc ggt ttt cat gga gac tgt ctt acg ctg aca aag 350  
 Val Ile Gly Cys Ser Gly Phe His Gly Asp Cys Leu Thr Leu Thr Lys  
 80 85 90  
 att att gaa gca aga cta aag atg tat aag cat tcc aat aat aag gcc 398  
 Ile Ile Glu Ala Arg Leu Lys Met Tyr Lys His Ser Asn Asn Lys Ala  
 95 100 105 110  
 atg act acg ggg gca att gct gca atg ctg tct aca atc ctg tat tca 446  
 Met Thr Thr Gly Ala Ile Ala Ala Met Leu Ser Thr Ile Leu Tyr Ser  
 115 120 125  
 agg cgc ttc ttt cca tac tat gtt tac aac a 477  
 Arg Arg Phe Phe Pro Tyr Tyr Val Tyr Asn  
 130 135

<210> 1242  
 <211> 547  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 279..545

<400> 1242  
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 tgggaaatgg cggastatct ggcctccatc ttcggcacs rsaaakacar agtcaactgt 120  
 tcatytwatt tcaaaattgg agcatgtcgt catggagaca ggtgctctcg gttgcacaat 180  
 aaaccgacgt ttagccagac cattgccctc ttgaacattt accgtaaccc tcaaaactct 240  
 tcccagctcg ctgacggywg cgcggcgrcg rgtgggaa atg gcg gag tat ctg gcc 296  
 Met Ala Glu Tyr Leu Ala  
 1 5  
 tcc atc ttc ggc acc gag aaa gac aaa gtc aac tgt tca ttt tat ttc 344  
 Ser Ile Phe Gly Thr Glu Lys Asp Lys Val Asn Cys Ser Phe Tyr Phe  
 10 15 20  
 aaa att gga gca tgt cgt cat gga gac agg tgc tct cgg ttg cac aat 392  
 Lys Ile Gly Ala Cys Arg His Gly Asp Arg Cys Ser Arg Leu His Asn

25	30	35	
aaa ccg acg ttt agc cag acc atc ttg att caa aac atc tat cgt aat			440
Lys Pro Thr Phe Ser Gln Thr Ile Leu Ile Gln Asn Ile Tyr Arg Asn			
40	45	50	
ccc caa aac agt gca cag acg gct gac ggc tca cac tgt gcc gtg agc			488
Pro Gln Asn Ser Ala Gln Thr Ala Asp Gly Ser His Cys Ala Val Ser			
55	60	65	70
gat gtg gag atg cag gaa cac tat gat gag ttt ttt gag gag gtt ttt			536
Asp Val Glu Met Gln Glu His Tyr Asp Glu Phe Phe Glu Glu Val Phe			
	75	80	85
aca gaa atg aa			547
Thr Glu Met			

<210> 1243  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 170..358

<400> 1243	
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ttgtgatgtg gttattcatg atccttccat attgcttttg aatgacatat ttatctargc	120
aactgttgta agttaaagct aaaactgact gttctttgat caattttga atg ttt agg	178
	Met Phe Arg
	1
ata cag cag tta aaa cag tta ctg gag gat tct acc tca ggt gaa gat	226
Ile Gln Gln Leu Lys Gln Leu Leu Glu Asp Ser Thr Ser Gly Glu Asp	
5	10
agg agc agc tcc agt tcc tct gaa ggt aaa gag aaa cac aag aaa aag	274
Arg Ser Ser Ser Ser Ser Ser Glu Gly Lys Glu Lys His Lys Lys Lys	
20	25
aag aag aaa gaa aag cat aag aaa agg aag aaa gaa aag aaa aag aag	322
Lys Lys Lys Glu Lys His Lys Lys Arg Lys Lys Glu Lys Lys Lys Lys	
	40
aaa aaa cgg aag cac aaa tct tcc aag tca aat gag	358
Lys Lys Arg Lys His Lys Ser Ser Lys Ser Asn Glu	
	55
	60

<210> 1244  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 149..373

<400> 1244	
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ccttcctgct ggctgctctg tgaccgcttc cgggctctgc cctcttgccc gaagtgcccg 120
ctgccggggcg cgggcctcag acaatata atg gtg ggt gaa gag aag atg tct 172
                               Met Val Gly Glu Glu Lys Met Ser
                               1           5
cta aga aac cgg ctg tca aag tcc agg gaa aat cct gag gaa gat gaa 220
Leu Arg Asn Arg Leu Ser Lys Ser Arg Glu Asn Pro Glu Glu Asp Glu
10           15           20
gac cag aga aac cct gca aag gag tcc cta gag aca cct agt aat ggt 268
Asp Gln Arg Asn Pro Ala Lys Glu Ser Leu Glu Thr Pro Ser Asn Gly
25           30           35           40
cga att gac ata aaa cag ttg ata gca aag aag ata aag ttg aca gca 316
Arg Ile Asp Ile Lys Gln Leu Ile Ala Lys Lys Ile Lys Leu Thr Ala
45           50           55
gag gca gag gaa ttg aag cca ttt ttt atg aag gaa gtt gnc agt cac 364
Glu Ala Glu Glu Leu Lys Pro Phe Phe Met Lys Glu Val Xaa Ser His
60           65           70
ttt gat gat tt 375
Phe Asp Asp
75

<210> 1245
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 134..409

<400> 1245
aatcatgcag gaaactagat actgagaaaa cagttgtagc tcagcgtggc tacaagtaac 60
tgtggtgtgg aagcagagta gagagaaaac ttgttctca ttagagagag agccacactt 120
ctcactgctc aca atg aga ggc caa aga tta ccc ttg gac atc cag att 169
                               Met Arg Gly Gln Arg Leu Pro Leu Asp Ile Gln Ile
                               1           5           10
ttc tat tgt gcc aga cct gac gaa gag cct ttt gtg aag atc atc act 217
Phe Tyr Cys Ala Arg Pro Asp Glu Glu Pro Phe Val Lys Ile Ile Thr
15           20           25
gtt gaa gag gca aag cgc agg aag agc aca tgc agc tac tat gaa gac 265
Val Glu Glu Ala Lys Arg Arg Lys Ser Thr Cys Ser Tyr Tyr Glu Asp
30           35           40
gag gac gaa gag gtg ctg cct gtc cta cgg ccc cac agc gcg ctc ctg 313
Glu Asp Glu Glu Val Leu Pro Val Leu Arg Pro His Ser Ala Leu Leu
45           50           55           60
gag aat atg cac atc gag cag ctg gcc cga cgc ctt cct gca agg gtg 361
Glu Asn Met His Ile Glu Gln Leu Ala Arg Arg Leu Pro Ala Arg Val
65           70           75
caa ggg tat cca tgg aga ctg gcc tat agc acg tta gag cac ggg aca 409
Gln Gly Tyr Pro Trp Arg Leu Ala Tyr Ser Thr Leu Glu His Gly Thr
80           85           90
gc 411

<210> 1246

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<211> 445  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 94..444

<400> 1246  
 ctctctccgcc gccggctccc ggggtgtgggtg gtcgtctccag ctctctgctc tcccagcgca 60  
 gsnccgccgcc cggccccctcc agcttccccgg acc atg gcc aac ctg gag cgc acc 114  
 Met Ala Asn Leu Glu Arg Thr  
 1 5  
 ttc atc gcc atc aag ccg gac ggc gtg cag cgc ggc ctg gtg ggc gag 162  
 Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Val Gly Glu  
 10 15 20  
 atc atc aag cgc ttc gag cag aag gga ttc cgc ctg gtg gcc atg aag 210  
 Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg Leu Val Ala Met Lys  
 25 30 35  
 ttc ctg cgg gcc tct gaa gaa cac ctg aag cag cac tac att gac ctg 258  
 Phe Leu Arg Ala Ser Glu Glu His Leu Lys Gln His Tyr Ile Asp Leu  
 40 45 50 55  
 aaa gac cga cca ttc ttc cct ggg ctg gtg aag tac atg aac tca ggc 306  
 Lys Asp Arg Pro Phe Phe Pro Gly Leu Val Lys Tyr Met Asn Ser Gly  
 60 65 70  
 ccg gtt gtg gcc atg gtc cgg gag ggg ctg aac gtg gtg aag aca ggc 354  
 Pro Val Val Ala Met Val Arg Glu Gly Leu Asn Val Val Lys Thr Gly  
 75 80 85  
 cga gtg atg ctt ggg gag acc aat cca gca gat tca aag cca ggc acc 402  
 Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp Ser Lys Pro Gly Thr  
 90 95 100  
 att cgt ggg gac ttc tgc att cag gtt ggc agg aac atc att c 445  
 Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg Asn Ile Ile  
 105 110 115

<210> 1247  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 98..346

<400> 1247  
 gtcgacggct ggagagaagc cgggagcgcag cccaggcggc agtcttgatt cccttttggc 60  
 cagcagtttt taggtctgtc agtactgcac tgcaaga atg gca gat ttt ggg atc 115  
 Met Ala Asp Phe Gly Ile  
 1 5  
 tct gct ggc cag ttt gtg gca gtg gtc tgg gat aag tca tcc cca gtg 163  
 Ser Ala Gly Gln Phe Val Ala Val Trp Asp Lys Ser Ser Pro Val  
 10 15 20

gag gct ctg aaa ggt ctg gtg gat aag ctt caa gcg tta acc ggc aat	211
Glu Ala Leu Lys Gly Leu Val Asp Lys Leu Gln Ala Leu Thr Gly Asn	
25 30 35	
gag ggc cgc gtg tct gtg gaa aac atc aag cag ctg ttg caa tgt tta	259
Glu Gly Arg Val Ser Val Glu Asn Ile Lys Gln Leu Leu Gln Cys Leu	
40 45 50	
gtc cca gga agc acc act ctg cac agt gct gag att ttg gct gaa atc	307
Val Pro Gly Ser Thr Thr Leu His Ser Ala Glu Ile Leu Ala Glu Ile	
55 60 65 70	
gcc cgg atc ctt cgg cct ggt gga tgt ctt ttt ctg aag ga	348
Ala Arg Ile Leu Arg Pro Gly Gly Cys Leu Phe Leu Lys	
75 80	

<210> 1248  
 <211> 338  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 184..336

<400> 1248	
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ttgagaggat cggggtgggg agaccaaaca agagagacat ttctggctct gaaggcgaac	120
gcttcgctgg ccatttagga gctctgctca aagccagacg tatectagaa ggaaaacatc	180
acc atg gct aca gaa att ggt tct cct cct cgt ttt ttc cat atg cca	228
Met Ala Thr Glu Ile Gly Ser Pro Pro Arg Phe Phe His Met Pro	
1 5 10 15	
agg ttc cag cac cag gca cct cga cag ctg ttt tat aag cga cct gat	276
Arg Phe Gln His Gln Ala Pro Arg Gln Leu Phe Tyr Lys Arg Pro Asp	
20 25 30	
ttt gca caa cag caa gca atg caa cag ctt act ttt gat gga aaa cga	324
Phe Ala Gln Gln Gln Ala Met Gln Gln Leu Thr Phe Asp Gly Lys Arg	
35 40 45	
atg aga aaa gct gt	338
Met Arg Lys Ala	
50	

<210> 1249  
 <211> 484  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 176..484

<400> 1249	
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tctctcggtta gtccacggtc tggctctcag ctacccgcct tcgtctccga gtttgcgact	120
cgcggaccgg cgtcccgcc gcgaagaggc tggactcgga ttcggtgcct gagca atg	178



Met  
1

gct gcc atc cgg aag aaa ctg gtg att gtt ggt gat gga gcc tgt gga	226
Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala Cys Gly	
5 10 15	
aag aca tgc ttg ctc ata gtc ttc agc aag gac cag ttc cca gag gtg	274
Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu Val	
20 25 30	
tat gtg ccc aca gtg ttt gag aac tat gtg gca gat atc gag gtg gat	322
Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu Val Asp	
35 40 45	
gga aag cag gta gag ttg gct ttg tgg gac aca gct ggg cag gaa gat	370
Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp	
50 55 60 65	
tat gat cgc ctg agg ccc ctc tcc tac cca gat acc gat gtt ata ctg	418
Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val Ile Leu	
70 75 80	
atg tgt ttt tcc atc gac agc cct gat ant tta gaa aac atc cca gaa	466
Met Cys Phe Ser Ile Asp Ser Pro Asp Xaa Leu Glu Asn Ile Pro Glu	
85 90 95	
aag tgg acc cag aag tca	484
Lys Trp Thr Gln Lys Ser	
100	

<210> 1250  
 <211> 468  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 159..467

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 gacccttggc tcttattgtt cttgctggtg tggatgttc acggctgaaa agatggcag 120  
 aaggggaaag gaggaagtga gaagaaagaa acagggaa atg aca gag tgt tgc tca 176  
 Met Thr Glu Cys Cys Ser  
 1 5  
 gtt acc cag gct gga gtg caa tgg cat gat ctt ggc tca ctg cag cct 224  
 Val Thr Gln Ala Gly Val Gln Trp His Asp Leu Gly Ser Leu Gln Pro  
 10 15 20  
 cca cct cct ggg ttc aag cgg ttc tcg tgc ctc agt ctc cca agt agc 272  
 Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser Leu Pro Ser Ser  
 25 30 35  
 tgg gat tac agg ctg gag tgc gat ggc atg atc ttg gct cac ggc aaa 320  
 Trp Asp Tyr Arg Leu Glu Cys Asp Gly Met Ile Leu Ala His Gly Lys  
 40 45 50  
 ctc cgc ctc cct ggt tca agt gat tct cct gcc tca gcc tcc cga gta 368  
 Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg Val  
 55 60 65 70  
 gcc ggg att aca ggc atg tgc cas cat gcc ccg ttg gcc agg ctg gtc 416  
 Ala Gly Ile Thr Gly Met Cys Xaa His Ala Pro Leu Ala Arg Leu Val

	75		80		85	
tcg ars acc tta cct cag gtg atc tcc cac ctt tgg gat tac aga cct						464
Ser Xaa Thr Leu Pro Gln Val Ile Ser His Leu Trp Asp Tyr Arg Pro						
	90		95		100	
gca t						468
Ala						

<210> 1251  
 <211> 494  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 100..492

<400> 1251  
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 taatccggca gtgaccgtgt gtcagaacaa tcttgaatc atg aag cta cta acc 114  
 Met Lys Leu Leu Thr  
 1 5  
 aga gcc ggc tct ttc tcg aga ttt tat tcc ctc aaa gtt gcc ccc aaa 162  
 Arg Ala Gly Ser Phe Ser Arg Phe Tyr Ser Leu Lys Val Ala Pro Lys  
 10 15 20  
 gtt aaa gcc aca gct gcg cct gca gga gca ccg cca caa cct cag gac 210  
 Val Lys Ala Thr Ala Ala Pro Ala Gly Ala Pro Pro Gln Pro Gln Asp  
 25 30 35  
 ctt gag ttt acc aag tta cca aat ggc ttg gtg att gct tct ttg gaa 258  
 Leu Glu Phe Thr Lys Leu Pro Asn Gly Leu Val Ile Ala Ser Leu Glu  
 40 45 50  
 aac tat tct cct gta tca aga att ggt ttg ttc att aaa gca ggc agt 306  
 Asn Tyr Ser Pro Val Ser Arg Ile Gly Leu Phe Ile Lys Ala Gly Ser  
 55 60 65  
 aga tat gag gac ttc agc aat tta gga acc acc cat ttg ctg cgt ctt 354  
 Arg Tyr Glu Asp Phe Ser Asn Leu Gly Thr Thr His Leu Leu Arg Leu  
 70 75 80 85  
 aca tcc agt ctg acg aca aaa gga gct tca tct ttc aag ata acc cgt 402  
 Thr Ser Ser Leu Thr Thr Lys Gly Ala Ser Ser Phe Lys Ile Thr Arg  
 90 95 100  
 gga att gaa gca gtt ggt ggc aaa tta agt gtg acc gca aca agg gaa 450  
 Gly Ile Glu Ala Val Gly Gly Lys Leu Ser Val Thr Ala Thr Arg Glu  
 105 110 115  
 aac atg gct tat act gtg gaa tgc ctg cgg ggt gat gtt gat at 494  
 Asn Met Ala Tyr Thr Val Glu Cys Leu Arg Gly Asp Val Asp  
 120 125 130

<210> 1252  
 <211> 308  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 141..308

<400> 1252

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gcggagggtc ggcgtaggta ctttgaactc aagtaaacia aagggaagat tttctcgttg      120
atactggaga ctgcacaaca atg ggg cca cga aag aaa agt gtg aaa aca tgt      173
                Met Gly Pro Arg Lys Lys Ser Val Lys Thr Cys
                  1             5             10
atc atg aat aat gaa att cca gaa gaa atg aca gca gat gaa aca aag      221
Ile Met Asn Asn Glu Ile Pro Glu Glu Met Thr Ala Asp Glu Thr Lys
                15             20             25
gac tat atg aat caa ctt tca cat gaa gta ctt tgc cat att ttt aga      269
Asp Tyr Met Asn Gln Leu Ser His Glu Val Leu Cys His Ile Phe Arg
                30             35             40
tac ctc cct ctg cag gat atc atg tgt atg ttc ttt ccc      308
Tyr Leu Pro Leu Gln Asp Ile Met Cys Met Phe Pro
                45             50             55
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<210> 1253

<211> 338

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 183..338

<400> 1253

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gacagacacc atattgccgg ccaagcttaa aacatgtatg aatgtgacct ctgggtctaga      60
aaactgacct cataccagtt cagtttttta gcagataatc cttttagat gatgatgggt      120
tcaacacaat agtaaagggt tagcctttta aagactccca ggtatgtatt acaggttgat      180
ct atg aca gaa gta atg aaa gtt aga aaa aga tgg ctg gga ata gtg      227
    Met Thr Glu Val Met Lys Val Arg Lys Arg Trp Leu Gly Ile Val
      1             5             10             15
gct cat gcc tat aat ttc agc act ttg gga ggn cgg kkc agg agg atc      275
Ala His Ala Tyr Asn Phe Ser Thr Leu Gly Gly Arg Xaa Arg Arg Ile
                20             25             30
tct tgg ggc cag gag ttt gag acc agc ctg ggc aac aca gac act ttc      323
Ser Trp Gly Gln Glu Phe Glu Thr Ser Leu Gly Asn Thr Asp Thr Phe
                35             40             45
tct aca aaa aaa aaa
Ser Thr Lys Lys Lys      338
                50
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<210> 1254

<211> 748

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 138..746

&lt;400&gt; 1254

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gagttcggca tgcaagagcg gaagaaaagc ggctggtacc ccggaagcag tcgctgcaac      60
ttccgggagg tgcttgtgtg cctggtgctg gagctacggg gccagggat tgtgtttaa      120
gtagtgcttc taccaac atg tcc cgt ggt tcc agc gcc ggt ttt gac cgc      170
      Met Ser Arg Gly Ser Ser Ala Gly Phe Asp Arg
      1           5           10
cac att acc att ttt tca ccc gag ggt cgg ctc tac caa gta gaa tat      218
His Ile Thr Ile Phe Ser Pro Glu Gly Arg Leu Tyr Gln Val Glu Tyr
      15           20           25
gct ttt aag gct att aac cag ggt ggc ctt aca tca gta gct gtc aga      266
Ala Phe Lys Ala Ile Asn Gln Gly Gly Leu Thr Ser Val Ala Val Arg
      30           35           40
ggg aaa gac tgt gca gta att gtc aca cag aag aaa gta cct gac aaa      314
Gly Lys Asp Cys Ala Val Ile Val Thr Gln Lys Lys Val Pro Asp Lys
      45           50           55
tta ttg gat tcc agc aca gtg act cac tta ttc aag ata act gaa aac      362
Leu Leu Asp Ser Ser Thr Val Thr His Leu Phe Lys Ile Thr Glu Asn
      60           65           70           75
att ggt tgt gtg atg acc gga atg aca gct gac agc aga tcc cag gta      410
Ile Gly Cys Val Met Thr Gly Met Thr Ala Asp Ser Arg Ser Gln Val
      80           85           90
cag agg gca cgc tat gag gca gct aac tgg aaa tac aag tat ggc tat      458
Gln Arg Ala Arg Tyr Glu Ala Ala Asn Trp Lys Tyr Lys Tyr Gly Tyr
      95           100           105
gag att cct gtg gac atg ctg tgk raa aga att gcc gat att tct cag      506
Glu Ile Pro Val Asp Met Leu Xaa Xaa Arg Ile Ala Asp Ile Ser Gln
      110           115           120
gtc tac aca cag aat gct gaa atg agg cct ctt ggt tgt tgt atg att      554
Val Tyr Thr Gln Asn Ala Glu Met Arg Pro Leu Gly Cys Cys Met Ile
      125           130           135
tta att ggt ata gat gaa gag caa ggc cct cag gta tat aag tgt gat      602
Leu Ile Gly Ile Asp Glu Glu Gln Gly Pro Gln Val Tyr Lys Cys Asp
      140           145           150           155
cct gca ggt tac tac tgt ggg ttt aaa gcc act gca gcg gga gtt aaa      650
Pro Ala Gly Tyr Tyr Cys Gly Phe Lys Ala Thr Ala Ala Gly Val Lys
      160           165           170
caa act gag tca acc agc ttc ctt gaa aaa naa gtg aag aag aaa ttt      698
Gln Thr Glu Ser Thr Ser Phe Leu Glu Lys Xaa Val Lys Lys Lys Phe
      175           180           185
gat tgg aca ttt gag cag aca gtg gaa act gca att aca tgc ctg tct      746
Asp Trp Thr Phe Glu Gln Thr Val Glu Thr Ala Ile Thr Cys Leu Ser
      190           195           200
ac

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748

&lt;210&gt; 1255

&lt;211&gt; 626

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 73..624

&lt;400&gt; 1255

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agggtagtgt cctargettg gagaatggga tggagcctcc acctcatgaa gtagcttcct      60
ttggaggtgg ct atg gca ggt ctt cgg aga gaa tat gct ttt aag gct att      111
      Met Ala Gly Leu Arg Arg Glu Tyr Ala Phe Lys Ala Ile
            1             5             10
aac cag ggt ggc ctt aca tca gta gct gtc aga ggg aaa gac tgt gca      159
Asn Gln Gly Gly Leu Thr Ser Val Ala Val Arg Gly Lys Asp Cys Ala
      15             20             25
gta att gtc aca cag aag aaa gta cct gac aaa tta ttg gat tcc agc      207
Val Ile Val Thr Gln Lys Lys Val Pro Asp Lys Leu Leu Asp Ser Ser
      30             35             40             45
aca gtg act cac tta ttc aag ata act gaa aac att ggt tgt gtg atg      255
Thr Val Thr His Leu Phe Lys Ile Thr Glu Asn Ile Gly Cys Val Met
            50             55             60
acc gga atg aca gct gac agc aga tcc cag gta cag agg gca cgc tat      303
Thr Gly Met Thr Ala Asp Ser Arg Ser Gln Val Gln Arg Ala Arg Tyr
            65             70             75
gag gca gct aac tgg aaa tac aag tat ggc tat gag att cct gtg gac      351
Glu Ala Ala Asn Trp Lys Tyr Lys Tyr Gly Tyr Glu Ile Pro Val Asp
            80             85             90
atg ctg tgt aaa aga att gcc gat att tct cag gtc tac aca cag aat      399
Met Leu Cys Lys Arg Ile Ala Asp Ile Ser Gln Val Tyr Thr Gln Asn
            95             100             105
gct gaa atg agg cct ctt ggt tgt tgt atg att ttn att ggt ata gat      447
Ala Glu Met Arg Pro Leu Gly Cys Cys Met Ile Xaa Ile Gly Ile Asp
            110             115             120             125
gaa gag caa ggc cct cag gta tat aag tgt gat cct gca ggt tac tac      495
Glu Glu Gln Gly Pro Gln Val Tyr Lys Cys Asp Pro Ala Gly Tyr Tyr
            130             135             140
tgt ggg ttt aaa gcc act gca gcg gga gtt aaa caa act gag tca acc      543
Cys Gly Phe Lys Ala Thr Ala Ala Gly Val Lys Gln Thr Glu Ser Thr
            145             150             155
agc ttc ctt gaa aaa naa gtg aag aag aaa ttt gat tgg aca ttt gag      591
Ser Phe Leu Glu Lys Xaa Val Lys Lys Lys Phe Asp Trp Thr Phe Glu
            160             165             170
cag aca gtg gaa act gca att aca tgc ctg tct ac      626
Gln Thr Val Glu Thr Ala Ile Thr Cys Leu Ser
            175             180

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&lt;210&gt; 1256

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 155..391

&lt;400&gt; 1256

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ctctctggga tgtgtagctt tggaaatctg tctttgttgc tctgggagag gggactcctg      60
gaatgtgtct gtgaataaag actagccgaa ggtgcgaagt gactagacgg gagcaaagga      120

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<220>  
 <221> CDS  
 <222> 83..454

<400> 1258

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agcggcagma gcggcgccgc ctcccagagt tcagacccag gaagcggccg ggagggcagg      60
agcgaatcgg gccgccgccg cc atg gag ctg aga gtc ggg aac agg tac cgg      112
                    Met Glu Leu Arg Val Gly Asn Arg Tyr Arg
                        1             5             10
ctg ggc cgg aag atc ggc agc ggc tcc ttc gga gac atc tat ctc ggt      160
Leu Gly Arg Lys Ile Gly Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly
                        15             20             25
acg gac att gct gca gga gaa gag gtt gcc atc aag ctt gaa tgt gtc      208
Thr Asp Ile Ala Ala Gly Glu Glu Val Ala Ile Lys Leu Glu Cys Val
                        30             35             40
aaa acc aaa cac cct cag ctc cac att gag agc aaa atc tac aag atg      256
Lys Thr Lys His Pro Gln Leu His Ile Glu Ser Lys Ile Tyr Lys Met
                        45             50             55
atg cag gga gga gtg ggc atc ccc acc atc aga tgg tgc ggg gca gag      304
Met Gln Gly Gly Val Gly Ile Pro Thr Ile Arg Trp Cys Gly Ala Glu
                        60             65             70
ggg gac tac aac gtc atg gtg atg gag ctg ctg ggg cca agc ctg gag      352
Gly Asp Tyr Asn Val Met Val Met Glu Leu Leu Gly Pro Ser Leu Glu
                        75             80             85
gac ctc ttc aac ttc tgc tcc agg aaa ttc agc ctc aaa acc gtc ctg      400
Asp Leu Phe Asn Phe Cys Ser Arg Lys Phe Ser Leu Lys Thr Val Leu
                        95             100             105
ntg ctt gct gac caa atg atc agt cgc atc gaa tac att cat tca aag      448
Xaa Leu Ala Asp Gln Met Ile Ser Arg Ile Glu Tyr Ile His Ser Lys
                        110             115             120
aac ttc
Asn Phe

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<210> 1259  
 <211> 260  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 34..258

<400> 1259

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acccccggcc ccgaagctcc gccacccgcc gcc atg agt agc ttt gga gct ggc      54
                    Met Ser Ser Phe Gly Ala Gly
                        1             5
aaa acc aaa gaa gtt atc ttc agt gtg gag gat ggc tcc gtg aaa atg      102
Lys Thr Lys Glu Val Ile Phe Ser Val Glu Asp Gly Ser Val Lys Met
                        10             15             20
ttc ctg agg ggc cgc cct gtg ccc atg atg atc cca gac gag ctg gca      150
Phe Leu Arg Gly Arg Pro Val Pro Met Met Ile Pro Asp Glu Leu Ala

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25	30	35	
ccc acc tac agc ctg gac aca cgc tcg gag ctg cct tct tgc cgg ctc			198
Pro Thr Tyr Ser Leu Asp Thr Arg Ser Glu Leu Pro Ser Cys Arg Leu			
40	45	50	55
aag ctg gag tgg gtc tat ggc tac cgt ggc cga gac tgc cgg gcc aac			246
Lys Leu Glu Trp Val Tyr Gly Tyr Arg Gly Arg Asp Cys Arg Ala Asn			
	60	65	70
ctt tat ttg ctg cc			260
Leu Tyr Leu Leu			
75			

<210> 1260  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 116..334

<400> 1260	
actcgttccc taacattaaa gagaaaatgc tgctatccgt gacttccagg cccgggattt	60
cgacttttgg ctacaataga aacaacaaga agccatatgt gcactggctc agcag atg	118
	Met
	1
gca cca cct agc cca agc aac agt aca cct aac agc agt agt gga agc	166
Ala Pro Pro Ser Pro Ser Asn Ser Thr Pro Asn Ser Ser Ser Gly Ser	
	5 10 15
aat gga aat gac cag ctg agc aaa acc aac cta tac atc cga gga ttg	214
Asn Gly Asn Asp Gln Leu Ser Lys Thr Asn Leu Tyr Ile Arg Gly Leu	
	20 25 30
caa cca ggc act act gac car gat ctt gtc aag ctg tgt cag cca tat	262
Gln Pro Gly Thr Thr Asp Gln Asp Leu Val Lys Leu Cys Gln Pro Tyr	
	35 40 45
ggc aag att gtt tcm act aag gcc rta ctg gmc aag acc aca rac ara	310
Gly Lys Ile Val Ser Thr Lys Ala Xaa Leu Xaa Lys Thr Thr Xaa Xaa	
	50 55 60 65
tgt raa ggc tat ggc ttt gta gat tt	336
Cys Xaa Gly Tyr Gly Phe Val Asp	
	70

<210> 1261  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 119..433

<400> 1261	
gcgcaggcgc ggacggcggtt gggttgaaga ccttcagcgt tgccctggcg gasagagaca	60



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ggccctcggg gtggagggtct ttggtttcat aagagcctga gagagatttt tctaagat      118
atg tgt aac aca cca acg tac tgt gac cta gga aag gct gyt aag gat      166
Met Cys Asn Thr Pro Thr Tyr Cys Asp Leu Gly Lys Ala Xaa Lys Asp
1          5          10          15
gtc ttc aac aaa gga tat ggc ttt ggc atg gtc aag ata gac ctg aaa      214
Val Phe Asn Lys Gly Tyr Gly Phe Gly Met Val Lys Ile Asp Leu Lys
20          25          30
acc aag tct tgt agt gga gtg atg gaa ttt tct act tct ggt cat gct      262
Thr Lys Ser Cys Ser Gly Val Met Glu Phe Ser Thr Ser Gly His Ala
35          40          45
tac act gat aca ggg aaa gca tca ggc aac cta gaa acc aaa tat aag      310
Tyr Thr Asp Thr Gly Lys Ala Ser Gly Asn Leu Glu Thr Lys Tyr Lys
50          55          60
gtc tgt aac tat gga ctt acc ttc acc cag aaa tgg aac aca gay aat      358
Val Cys Asn Tyr Gly Leu Thr Phe Thr Gln Lys Trp Asn Thr Asp Asn
65          70          75          80
act cta ggg aca gaa atc tct tgg gag aat aag ttg gct gaa ggg ttg      406
Thr Leu Gly Thr Glu Ile Ser Trp Glu Asn Lys Leu Ala Glu Gly Leu
85          90          95
aaa ctg act ctt gat acc ata ttt gta cc      435
Lys Leu Thr Leu Asp Thr Ile Phe Val
100          105

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<210> 1262  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 170..424

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<400> 1262
acaggtgggt gcagaagttt cgtggtgtcg ggcgcgcgtc tgcactgcag acgcagaggg      60
tttgggagcg agcagtttcc tgcccaggga tgggggtcct ggctgcactt cacgggggag      120
gccctttcgt ttcgctctgc gtgacaggtc tcgcttgatt gggtttctc atg ggt ntc      178
Met Gly Xaa
1
tgg cgt ttc tac ggc gcg gct ctc acg gac tca ggc cag gcc act cgc      226
Trp Arg Phe Tyr Gly Ala Ala Leu Thr Asp Ser Gly Gln Ala Thr Arg
5          10          15
agg att aat tgg aat tct tca aaa tgt cag gtg tgg tac cca cag ccc      274
Arg Ile Asn Trp Asn Ser Ser Lys Cys Gln Val Trp Tyr Pro Gln Pro
20          25          30          35
ctg aac agc ctg cag gtg aaa tgg aaa atc aaa caa aac cac cag atc      322
Leu Asn Ser Leu Gln Val Lys Trp Lys Ile Lys Gln Asn His Gln Ile
40          45          50
caa ggc ctg atg ctc ctc ctg aat aca gtt ctc att nkt tta cca gga      370
Gln Gly Leu Met Leu Leu Leu Asn Thr Val Leu Ile Xaa Leu Pro Gly
55          60          65
ccc cct gga aac agc tgt ccc tcc acc tac tgg cta cca gag ctt gct      418
Pro Pro Gly Asn Ser Cys Pro Ser Thr Tyr Trp Leu Pro Glu Leu Ala
70          75          80

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004220 66627560

atg gga  
Met Gly  
85 424

<210> 1263  
<211> 456  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 228..455

<400> 1263  
aaaagtagag gnaaaaccac cgaattgagc tctgtcagag gcgctttcgg cttccaaggg 60  
ggaagtgtcg ggctataatt aatgttttta ttaaatttgg agggaagttt ttgcagcctt 120  
tcgcctagcg tggccttcag gttgatagaa gtccagatcc tgaggaaatc tccagctaaa 180  
tgctcaaaat ataaaatact gagctgagat ttgcgaagag cagcagc atg gat gga 236  
Met Asp Gly  
1  
ttt tat gac cag caa gtg cct tac atg gtc acc aat agt cag cgt ggg 284  
Phe Tyr Asp Gln Gln Val Pro Tyr Met Val Thr Asn Ser Gln Arg Gly  
5 10 15  
aga aat tgt aac gag aaa cca aca aat gtc agg aaa aga aaa ttc att 332  
Arg Asn Cys Asn Glu Lys Pro Thr Asn Val Arg Lys Arg Lys Phe Ile  
20 25 30 35  
aac aga gat ctg gct cat gat tca gaa gaa ctc ttt caa gat cta agt 380  
Asn Arg Asp Leu Ala His Asp Ser Glu Glu Leu Phe Gln Asp Leu Ser  
40 45 50  
caa tta cag gaa aca tgg ctt gca gaa gst mag gya cct gac aat gat 428  
Gln Leu Gln Glu Thr Trp Leu Ala Glu Xaa Xaa Xaa Pro Asp Asn Asp  
55 60 65  
gag cag ttt gta cca gac tat cag gct g 456  
Glu Gln Phe Val Pro Asp Tyr Gln Ala  
70 75

<210> 1264  
<211> 349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 129..347

<400> 1264  
agaacacagt ggaagcatcc tccaagccag ccaacaaatt tccgttttct actgcccttt 60  
cgggccaggg gttattttat gagcatctcc gatgttgac acgtggcgtg tgaaccgaga 120  
gaaagaag atg gag aga tca ccc tcc aga cgt cgt cgc ctg gaa gag gcc 170  
Met Glu Arg Ser Pro Ser Arg Arg Arg Arg Leu Glu Glu Ala  
1 5 10  
cca ata cca aag gat gac ctg gac ttc cgc tta gca gcc ttg tac aac 218

Pro	Ile	Pro	Lys	Asp	Asp	Leu	Asp	Phe	Arg	Leu	Ala	Ala	Leu	Tyr	Asn	
15					20				25					30		
cac	cac	act	ggg	aca	ttc	aag	aac	aaa	agt	gag	ata	ctg	tta	aac	cag	266
His	His	Thr	Gly	Thr	Phe	Lys	Asn	Lys	Ser	Glu	Ile	Leu	Leu	Asn	Gln	
			35					40					45			
aaa	acc	acg	cag	gat	acc	tat	aga	acc	aag	atc	caa	ttc	cct	gga	gaa	314
Lys	Thr	Thr	Gln	Asp	Thr	Tyr	Arg	Thr	Lys	Ile	Gln	Phe	Pro	Gly	Glu	
			50					55					60			
ttt	tta	acc	cct	ccc	act	cca	ccc	atc	act	ttc	ct					349
Phe	Leu	Thr	Pro	Pro	Thr	Pro	Pro	Ile	Thr	Phe						
		65						70								

<210> 1265  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 141..320

<400> 1265															
agctagaagg	atgccatgaa	ggaaatgact	gctttgtaaa	gcgagggtaa	acttctgaaa		60								
tgctttgatt	aaaataagct	atattaaaga	ccccaaaacc	acttcctcgc	cagctttcct		120								
ctgaatgtct	ttcacatgaa	atg ggc	ctg agt	cac tct	aag act	cac ctt	agg 173								
		Met Gly	Leu Ser	His Ser	Lys Thr	His Leu	Arg								
		1		5		10									
gtg atc	aaa gta	gca cct	ttg caa	anc aaa	gag gta	gag act	ccc tcg 221								
Val Ile	Lys Val	Ala Pro	Leu Gln	Xaa Lys	Glu Val	Glu Thr	Pro Ser								
	15		20		25										
gct ggc	cgt gtg	gac ttt	gca ttc	aat cag	aat ttg	gaa gaa	aag act 269								
Ala Gly	Arg Val	Asp Phe	Ala Phe	Asn Gln	Asn Leu	Glu Glu	Lys Thr								
	30		35		40										
tca tat	tca ctg	gca aga	ctg cag	gac cag	aat aaa	gcc ttg	gaa ggg 317								
Ser Tyr	Ser Leu	Ala Arg	Leu Gln	Asp Gln	Asn Lys	Ala Leu	Glu Gly								
	45		50		55										
cag ct							322								
Gln															
60															

<210> 1266  
 <211> 238  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 10..237

<400> 1266															
attgtcact	atg tcc	tgc ctg	acc aaa	gag gac	acg ggc	tgg tac	tgg tgt	51							
	Met Ser	Cys Leu	Thr Lys	Glu Asp	Thr Gly	Trp Tyr	Trp Cys								

1	5	10	
ggc atc cag cgg gac ttt gcc agg gat gac atg gat ttt aca gag ctg			99
Gly Ile Gln Arg Asp Phe Ala Arg Asp Asp Met Asp Phe Thr Glu Leu			
15	20	25	30
att gta act gac gac aaa gga acc ctg gcc aat gac ttt tgg tct ggg			147
Ile Val Thr Asp Asp Lys Gly Thr Leu Ala Asn Asp Phe Trp Ser Gly			
35	40	45	
aaa gac cta tca ggc aac aaa acc aga agc tgc aag gct ccc aaa gtt			195
Lys Asp Leu Ser Gly Asn Lys Thr Arg Ser Cys Lys Ala Pro Lys Val			
50	55	60	
gtc cgc aar gct gam cgc tcc agg acg tcc att ctc atc att t			238
Val Arg Lys Ala Xaa Arg Ser Arg Thr Ser Ile Leu Ile Ile			
65	70	75	

<210> 1267  
 <211> 458  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 187..456

<400> 1267			
gaggtgtatt agattgctgt gtgttgagca caaggggaag aatgaacaca gctttttatt	60		
gaagttaaag gttacttttg agtttgtttg gaaatgtgta aggtcaaata ctatagtttt	120		
cagcatatgt agtacttcag aggaagaatt aaggggcatg ttggtgcatt taactacaaa	180		
accaga atg att gaa gat agt ggg aaa aga gga aat acc atg gca gaa	228		
Met Ile Glu Asp Ser Gly Lys Arg Gly Asn Thr Met Ala Glu			
1	5	10	
aga aga cag ctg ttt gca gag atg agg gct caa gat ctg gat cgc atc			276
Arg Arg Gln Leu Phe Ala Glu Met Arg Ala Gln Asp Leu Asp Arg Ile			
15	20	25	30
cga ctc tcc acc tac aga aca gca tgc aag ctt agg ttt gtt cag aag			324
Arg Leu Ser Thr Tyr Arg Thr Ala Cys Lys Leu Arg Phe Val Gln Lys			
35	40	45	
aaa tgc aat ttg cac ctg gtg gac ata tgg aat gtc ata gaa gca ttg			372
Lys Cys Asn Leu His Leu Val Asp Ile Trp Asn Val Ile Glu Ala Leu			
50	55	60	
cgg gaa aat gct ctg aac aac ctg gac cca aac act gaa ctc aac gtg			420
Arg Glu Asn Ala Leu Asn Asn Leu Asp Pro Asn Thr Glu Leu Asn Val			
65	70	75	
tcc cgc tta gar gct gtg ctc act att ttt tac ca			458
Ser Arg Leu Glu Ala Val Leu Ser Thr Ile Phe Tyr			
80	85	90	

<210> 1268  
 <211> 252  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 48..251

<400> 1268

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agtctggggtt gggcagaagg cagaaaacca gcagagtcac agaggag atg gcc aac      56
                                     Met Ala Asn
                                     1
tgc caa ata gcc atc ttg tac cag aga ttc cag aga gtg gtc ttt gga      104
Cys Gln Ile Ala Ile Leu Tyr Gln Arg Phe Gln Arg Val Val Phe Gly
   5             10             15
att tcc caa ctc ctt tgc ttc agt gcc ctg atc tct gaa cta aca aac      152
Ile Ser Gln Leu Leu Cys Phe Ser Ala Leu Ile Ser Glu Leu Thr Asn
  20             25             30             35
cag aaa gaa gtg gca gca tgg act tat cat tac agc aca aaa gca tac      200
Gln Lys Glu Val Ala Ala Trp Thr Tyr His Tyr Ser Thr Lys Ala Tyr
           40             45             50
tca tgg aat att tcc cgt aaa tac tgc cag aat cgc tac aca gac tta      248
Ser Trp Asn Ile Ser Arg Lys Tyr Cys Gln Asn Arg Tyr Thr Asp Leu
           55             60             65
gtg g
Val
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<210> 1269

<211> 540

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 367..540

<400> 1269

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cttttctttt gcgtctgcgg tgctcggagt gtggtacttc tcctagttgc agtcaggctt      60
catacgctrt tgtcctgccc gtaagttccc gttttgtgtg tggttagagc agccagcggg      120
taacagaawk grwttnngga agagggagtc accactggac ctccaaggaa gccacgtgca      180
gacatctaca accttcgata tcctgacgag tttattgttg gccaaaacca ggctttgatt      240
gaaccaggat gaatgcgggt gttggaagta gaatatatat atacatataa aattggttgg      300
gagccacgtg taccagtgtg tgttgatctt ggcttgattc agtctgcctt gtaacagaaa      360
ctggcg atg gaa tat gag agg agc cct ctg gaa aga aaa gga cag acc      408
      Met Glu Tyr Glu Arg Ser Pro Leu Glu Arg Lys Gly Gln Thr
           1             5             10
ctg tgc ttt cat gaa agt gaa gat ctg gct gaa cca gtt cca caa ggt      456
Leu Cys Phe His Glu Ser Glu Asp Leu Ala Glu Pro Val Pro Gln Gly
  15             20             25             30
tac tgt ata cat agc ctg agt tta aaa ggc tgt gcc act tca aga atg      504
Tyr Cys Ile His Ser Leu Ser Leu Lys Gly Cys Ala Thr Ser Arg Met
           35             40             45
tca ttg tta gac ttt gaa att tct aac tgc cta cct      540
Ser Leu Leu Asp Phe Glu Ile Ser Asn Cys Leu Pro
           50             55
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<210> 1270

<211> 516

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 343..516

<400> 1270  
cttttttttc gcgtctgcgg tgctcggagt gtggtacttc tctagttgc agtcaggctt 60  
catacgctat tgctctgccc gttagagcag ccagcgggta cagaatggat tttggaagag 120  
ggagtcacca ctggacctcc aaggaagcca cgtgcagaca tctacaacct tcgatctcct 180  
gacgagttta ttgttgGCCa aaaccaggct ttgattgaac caggatgaat gcgggtgttg 240  
gaagtagaat atatatatac atataaaatt ggttgggagc cacgtgtacc agtgtgtgtt 300  
gatcttggtc tgattcagtc tgccttgtaa cagaaactgg cg atg gaa tat gag 354  
Met Glu Tyr Glu  
1  
agg agc cct ctg gaa aga aaa gga cag acc ctg tgc ttt cat gaa agt 402  
Arg Ser Pro Leu Glu Arg Lys Gly Gln Thr Leu Cys Phe His Glu Ser  
5 10 15 20  
gaa gat ctg gct gaa cca gtt cca caa ggt tac tgt ata cat agc ctg 450  
Glu Asp Leu Ala Glu Pro Val Pro Gln Gly Tyr Cys Ile His Ser Leu  
25 30 35  
agt tta aaa ggc tgt gcc act tca aga atg tca ttg tta gac ttt gaa 498  
Ser Leu Lys Gly Cys Ala Thr Ser Arg Met Ser Leu Leu Asp Phe Glu  
40 45 50  
att tct aac tgc cta cct 516  
Ile Ser Asn Cys Leu Pro  
55

<210> 1271  
<211> 440  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 25..438

<400> 1271  
atcactcgcg gcattggagt caag atg gag gag tac gcg cga gag cct tgc 51  
Met Glu Glu Tyr Ala Arg Glu Pro Cys  
1 5  
cca tgg cga att gtg gat gac tgt ggt ggg gcc ttt acg atg ggt acc 99  
Pro Trp Arg Ile Val Asp Asp Cys Gly Gly Ala Phe Thr Met Gly Thr  
10 15 20 25  
att ggt ggt ggt atc ttt caa gca atc aaa ggt ttt cgc aat tct cca 147  
Ile Gly Gly Gly Ile Phe Gln Ala Ile Lys Gly Phe Arg Asn Ser Pro  
30 35 40  
gtg gga gta aac cac aga cta cga ggg agt ttg aca gct att aaa acc 195  
Val Gly Val Asn His Arg Leu Arg Gly Ser Leu Thr Ala Ile Lys Thr  
45 50 55  
agg gct cca cag tta gga ggt agc ttt gca gtt tgg gga ggg ctg ttt 243

Arg	Ala	Pro	Gln	Leu	Gly	Gly	Ser	Phe	Ala	Val	Trp	Gly	Gly	Leu	Phe	
	60						65					70				
tcc	atg	att	gac	tgt	agt	atg	gtt	caa	gtc	aga	gga	aag	gaa	gat	ccc	291
Ser	Met	Ile	Asp	Cys	Ser	Met	Val	Gln	Val	Arg	Gly	Lys	Glu	Asp	Pro	
	75					80					85					
tgg	aac	tcc	atc	aca	agt	ggg	gcc	tta	acg	gga	gcc	ata	ctg	gca	gca	339
Trp	Asn	Ser	Ile	Thr	Ser	Gly	Ala	Leu	Thr	Gly	Ala	Ile	Leu	Ala	Ala	
90					95				100					105		
aga	aat	gga	cca	gtg	gcc	atg	gtt	ggg	tca	gcc	gca	atg	ggg	ggc	att	387
Arg	Asn	Gly	Pro	Val	Ala	Met	Val	Gly	Ser	Ala	Ala	Met	Gly	Gly	Ile	
				110					115					120		
ctc	cta	gct	tta	att	gaa	gga	gct	ggg	atc	ttg	ttg	aca	aga	ttt	gcc	435
Leu	Leu	Ala	Leu	Ile	Glu	Gly	Ala	Gly	Ile	Leu	Leu	Thr	Arg	Phe	Ala	
			125					130					135			
tct	gc															440
Ser																

<210> 1272  
 <211> 290  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 30..290

<400> 1272																
gcgtgcgccg	gtgggggact	ctgggggaaa	atg	gct	gcg	tct	tcg	agt	ggg	gag						53
			Met	Ala	Ala	Ser	Ser	Ser	Gly	Glu						
			1				5									
aag	gag	aag	gag	cgg	ctg	gga	ggc	ggg	ttg	gga	gtg	gag	ggg	ggg	aac	101
Lys	Glu	Lys	Glu	Arg	Leu	Gly	Gly	Gly	Leu	Gly	Val	Ala	Gly	Gly	Asn	
10					15					20						
agc	aca	cga	gag	cgg	ctg	ctg	tct	gag	gac	ttg	gag	gtc	ctg			149
Ser	Thr	Arg	Glu	Arg	Leu	Leu	Ser	Ala	Leu	Glu	Asp	Leu	Glu	Val	Leu	
25				30					35				40			
tct	agg	gaa	ctt	ata	gaa	atg	ctg	gca	att	tca	aga	aac	caa	aag	ttg	197
Ser	Arg	Glu	Leu	Ile	Glu	Met	Leu	Ala	Ile	Ser	Arg	Asn	Gln	Lys	Leu	
				45				50					55			
tta	cag	gct	gga	gag	gaa	aac	cag	gtc	ctg	gag	ttg	tta	att	cac	cga	245
Leu	Gln	Ala	Gly	Glu	Glu	Asn	Gln	Val	Leu	Glu	Leu	Leu	Ile	His	Arg	
		60						65				70				
gat	ggg	gaa	ttt	caa	gaa	cta	atg	aaa	ttg	gca	ctt	aat	cag	gga		290
Asp	Gly	Glu	Phe	Gln	Glu	Leu	Met	Lys	Leu	Ala	Leu	Asn	Gln	Gly		
	75						80					85				

<210> 1273  
 <211> 374  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 58..372

<400> 1273

gaaamaccac gcaggggaag agaaagcagg agccgtccag cacggaggaa ggcgacc	57
atg gcc aag gag tgg ggc tac gcc agt cac aac ggt cct gac cac tgg	105
Met Ala Lys Glu Trp Gly Tyr Ala Ser His Asn Gly Pro Asp His Trp	
1 5 10 15	
cat gaa ctt ttc cca aat gcc aag ggg gaa aac cag tcg ccc gtt gag	153
His Glu Leu Phe Pro Asn Ala Lys Gly Glu Asn Gln Ser Pro Val Glu	
20 25 30	
ctg cat act aaa gac atc agg cat gac cct tct ctg cag cca tgg tct	201
Leu His Thr Lys Asp Ile Arg His Asp Pro Ser Leu Gln Pro Trp Ser	
35 40 45	
gtg tct tat gat ggt ggc tct gcc aag acc atc ctg aat aat ggg aag	249
Val Ser Tyr Asp Gly Gly Ser Ala Lys Thr Ile Leu Asn Asn Gly Lys	
50 55 60	
acc tgc cga gtt gta ttt gat gat act tat gat agg tca atg ctg aga	297
Thr Cys Arg Val Val Phe Asp Asp Thr Tyr Asp Arg Ser Met Leu Arg	
65 70 75 80	
ggg ggt cct ctc cct gga ccc tac cga ctt cgc cag ttt cat ctt cac	345
Gly Gly Pro Leu Pro Gly Pro Tyr Arg Leu Arg Gln Phe His Leu His	
85 90 95	
tgg ggc tct tcg gat gat cat ggc tct ga	374
Trp Gly Ser Ser Asp Asp His Gly Ser	
100 105	

<210> 1274

<211> 436

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 137..436

<400> 1274

atttccgggt cccggcgggg gcttttctct ctctctttca ctgcaaggcg gcggcaggag	60
aggttggtggt gctagtttct ctaagccatc cagtgccatc ctgctcgctg cagcgacaca	120
cgctctcgcc gccgcc atg act gag cag atg acc ctt cgt ggc acc ctc aag	172
Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys	
1 5 10	
ggc cac aac ggc tgg gta acc cag atc gct act acc ccg cag ttc ccg	220
Gly His Asn Gly Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro	
15 20 25	
gac atg atc ctc tcc gcc tct cga gat aag acc atc atc atg tgg aaa	268
Asp Met Ile Leu Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys	
30 35 40	
ctg acc agg gat gag acc aac tat gga att cca cag cgt gct ctg cgg	316
Leu Thr Arg Asp Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg	
45 50 55 60	
ggg cac tcc cac ttt gtt agt gat gtg gtt atc tcc tca gat ggc cag	364
Gly His Ser His Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln	



	65		70		75	
ttt gcc ctc tca ggc tcc tgg gat gga acc ctg cgc ctc tgg gat ctc						412
Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu						
	80		85		90	
aca acg caa gta rct gct cac tta						436
Thr Thr Gln Val Xaa Ala His Leu						
	95		100			

<210> 1275  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 12..416

<400> 1275	
aaatagtggg g atg tca tgc agg caa gat ggc gga agg gga gga cgt ggg	50
Met Ser Cys Arg Gln Asp Gly Gly Arg Gly Gly Arg Gly	
atg gtg gcg gac tgg ctg cag cag agc tac caa gca gtc aaa gag aag	98
Met Val Ala Asp Trp Leu Gln Gln Ser Tyr Gln Ala Val Lys Glu Lys	
tcc tct gaa gcc ttg gag ttt atg aag cgg gac ctg acg gag ttt acc	146
Ser Ser Glu Ala Leu Glu Phe Met Lys Arg Asp Leu Thr Glu Phe Thr	
cag gtg gtg cag cat gac acg gcc tgt acc atc gca gcc acg gcc agc	194
Gln Val Val Gln His Asp Thr Ala Cys Thr Ile Ala Ala Thr Ala Ser	
gtg gtc aag gag aag ctg gct acg gaa ggc tcc tca gga gca aca gag	242
Val Val Lys Glu Lys Leu Ala Thr Glu Gly Ser Ser Gly Ala Thr Glu	
aag atg aag aaa ggg tta tct gac ttc cta ggg gtg atc tca gac acc	290
Lys Met Lys Lys Gly Leu Ser Asp Phe Leu Gly Val Ile Ser Asp Thr	
ttt gcc cct tcg cca gac aaa acc atc gac tgc gat gtc atc acc ctg	338
Phe Ala Pro Ser Pro Asp Lys Thr Ile Asp Cys Asp Val Ile Thr Leu	
atg ggc aca ccg tct ggc aca gct gag cct atg atg gca cca agg ctc	386
Met Gly Thr Pro Ser Gly Thr Ala Glu Pro Met Met Ala Pro Arg Leu	
gcc tct ata gcc tgc agt cgg acc cag caa	416
Ala Ser Ile Ala Cys Ser Arg Thr Gln Gln	

<210> 1276  
 <211> 249  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 85..249

<400> 1276

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ctgaccacaa atgagccacc tgggggcttg ttgaaagcac ggaatcctgg cccaccact      60
gccttgccgc tgcccagcaa aacc atg tgg gcc cag cct ctc ctg tgg gca      111
               Met Trp Ala Gln Pro Leu Leu Trp Ala
                   1               5
cac cca cac act gtc cct ctc tct ccc ctt tct ttc ccc caa agg gcc      159
His Pro His Thr Val Pro Leu Ser Pro Leu Ser Phe Pro Gln Arg Ala
10               15               20               25
atg acc gtt ttc cat gca gcc ctg ccc ggc cct gcc atc ctg ctc cca      207
Met Thr Val Phe His Ala Ala Leu Pro Gly Pro Ala Ile Leu Leu Pro
               30               35               40
gcc cca cgc cga gag gac acc tgt ctg cct ccc tcc tgc cga      249
Ala Pro Arg Arg Glu Asp Thr Cys Leu Pro Pro Ser Cys Arg
               45               50               55
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<210> 1277

<211> 372

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 55..372

<400> 1277

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aagaggacag acgcctcgaa gaatccgcta tcggctgtct gcacaaccgg aatc atg      57
                                   Met
                                   1
tcg agt ttg gcg gtg aga gac ccg gca atg gat cga tca ctg cgt tcc      105
Ser Ser Leu Ala Val Arg Asp Pro Ala Met Asp Arg Ser Leu Arg Ser
5               10               15
gtg ttc gtg ggg aac att cca tat gag gca act gag gag cag tta aag      153
Val Phe Val Gly Asn Ile Pro Tyr Glu Ala Thr Glu Glu Gln Leu Lys
20               25               30
gac att ttc tcg gag gtt ggt tct gtt gtc agt ttc cgg ctg gta tac      201
Asp Ile Phe Ser Glu Val Gly Ser Val Val Ser Phe Arg Leu Val Tyr
35               40               45
gat aga gag acg gga aaa ccc aag ggc tat ggc ttc tgc gaa tac caa      249
Asp Arg Glu Thr Gly Lys Pro Lys Gly Tyr Gly Phe Cys Glu Tyr Gln
50               55               60               65
gac cag gag acc gcg ctt agt gcc atg cgg aac ctc aat ggg cgg gag      297
Asp Gln Glu Thr Ala Leu Ser Ala Met Arg Asn Leu Asn Gly Arg Glu
70               75               80
ttc agt ggg aga gcg ctt cgg gtg gac aat gct gcc agt gaa aag aat      345
Phe Ser Gly Arg Ala Leu Arg Val Asp Asn Ala Ala Ser Glu Lys Asn
85               90               95
aag gag gag tta aag agc ctt ggg cct      372
Lys Glu Glu Leu Lys Ser Leu Gly Pro
100               105
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<210> 1278  
 <211> 592  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 259..591

<400> 1278  
 aaaaagaagg tgggtgattgg ctggattctt gctcatggct cctggcagat ctgacaaatc 60  
 ctcttgcttt tgctctaata tctgtctgga tacttttagg aaaagaacct tggtattatg 120  
 tactaaagtg aataatttgt gctcttagag taggagttgg aactatagga cttgaaggca 180  
 agagcaggta tcttatcaag gatctactca ctcagtttcc ctaaagctct ctctccagat 240  
 cggattcaac cgcacatc atg aca gat gtt ccg gct aca ttt acc cag gct 291  
 Met Thr Asp Val Pro Ala Thr Phe Thr Gln Ala  
 1 5 10  
 gag tgt aat ggg gat aaa cca cct gaa aac ggt caa caa aca atc act 339  
 Glu Cys Asn Gly Asp Lys Pro Pro Glu Asn Gly Gln Gln Thr Ile Thr  
 15 20 25  
 aaa atc agt gag gaa ttg act gat gtg gac agc ccc ctg cca cac tac 387  
 Lys Ile Ser Glu Glu Leu Thr Asp Val Asp Ser Pro Leu Pro His Tyr  
 30 35 40  
 agg gta gaa ccc agt ctg gaa ggt gca ctc acc aaa gga agt cag gag 435  
 Arg Val Glu Pro Ser Leu Glu Gly Ala Leu Thr Lys Gly Ser Gln Glu  
 45 50 55  
 gaa aga aga aaa tta caa ggg aac atg ctg ctc aac tca tcc atg gag 483  
 Glu Arg Arg Lys Leu Gln Gly Asn Met Leu Leu Asn Ser Ser Met Glu  
 60 65 70 75  
 gac aaa atg cta aaa gaa aac cca gaa gag aaa ctc ttt att gtt cat 531  
 Asp Lys Met Leu Lys Glu Asn Pro Glu Glu Lys Leu Phe Ile Val His  
 80 85 90  
 aag gct atc aca gat ctt tct ctc caa gaa act agt gct gat gaa atg 579  
 Lys Ala Ile Thr Asp Leu Ser Leu Gln Glu Thr Ser Ala Asp Glu Met  
 95 100 105  
 aca ttc aga gaa g 592  
 Thr Phe Arg Glu  
 110

<210> 1279  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..409

<400> 1279  
 gtggcggtcc tctctcccaa ttcggaagct acagctacct ccggacgctc tcaag atg 58  
 Met  
 1

gcg acc tct ctg ggt tcc aac acc tac aac agg cag aac tgg gag gat	106
Ala Thr Ser Leu Gly Ser Asn Thr Tyr Asn Arg Gln Asn Trp Glu Asp	
5 10 15	
gcg gac ttc ccc att ctg tgc cag aca tgt ctt gga gaa aac cca tat	154
Ala Asp Phe Pro Ile Leu Cys Gln Thr Cys Leu Gly Glu Asn Pro Tyr	
20 25 30	
atc cga atg acc aaa gaa aag tat ggg aag gaa tgc aaa atc tgt gcc	202
Ile Arg Met Thr Lys Glu Lys Tyr Gly Lys Glu Cys Lys Ile Cys Ala	
35 40 45	
agg cca ttc aca gtg ttt cgc tgg tgc cct gga gtc cgc atg cgt ttc	250
Arg Pro Phe Thr Val Phe Arg Trp Cys Pro Gly Val Arg Met Arg Phe	
50 55 60 65	
aag aag act gaa gtg tgc caa acc tgc agt aaa ttg aag aat gtc tgt	298
Lys Lys Thr Glu Val Cys Gln Thr Cys Ser Lys Leu Lys Asn Val Cys	
70 75 80	
cag acc tgc ctc tta gac cta gag tat ggc ctg ccc atc cag gtt cgt	346
Gln Thr Cys Leu Leu Asp Leu Glu Tyr Gly Leu Pro Ile Gln Val Arg	
85 90 95	
gac gcagat tgt ctt tta aag atg aca tgc caa agt cag atg tca nca	394
Asp Ala Asp Cys Leu Leu Lys Met Thr Cys Gln Ser Gln Met Ser Xaa	
100 105 110	
aag agt act ata cac ag	411
Lys Ser Thr Ile His	
115	

<210> 1280  
 <211> 364  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 119..364

<400> 1280	
ggacgcgagg ggcggggcga gcgcgggaca aagggaagcg aancggagct gcgggcgctt	60
tttctgcccg cgggtgtctca gattcattct taaggaactg agaacttaat cttccaaa	118
atg tca aaa aga cca tct tat gcc cca cct ccc acc cca gct cct gca	166
Met Ser Lys Arg Pro Ser Tyr Ala Pro Pro Pro Thr Pro Ala Pro Ala	
1 5 10 15	
aca caa atg ccc agc aca cca ggg ttt gtg gga tac aat nca tac agt	214
Thr Gln Met Pro Ser Thr Pro Gly Phe Val Gly Tyr Asn Xaa Tyr Ser	
20 25 30	
cat ctc gcc tac aac aac tac agg ctg gga ggg aac ccg ggc acc aam	262
His Leu Ala Tyr Asn Asn Tyr Arg Leu Gly Gly Asn Pro Gly Thr Xaa	
35 40 45	
agc cgg gtc acg gta gga gaa tca act att aca gca tcc ggc aaa caa	310
Ser Arg Val Thr Val Gly Glu Ser Thr Ile Thr Ala Ser Gly Lys Gln	
50 55 60	
ctg gaa ttg acc aga aat gcc ttc aga att agg tct ttt tgr atc ata	358
Leu Glu Leu Thr Arg Asn Ala Phe Arg Ile Arg Ser Phe Xaa Ile Ile	
65 70 75 80	
agc aca	364

Ser Thr

<210> 1281  
<211> 370  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 119..370

<400> 1281  
ggacgcgagg ggcggggcga ggcgcgggaca aaggggaagcg aaccggagct gcggggcgctt 60  
tttctgcccc cggtgtctca gattcattct taaggaactg agaacttaat cttccaaa 118  
atg tca aaa aga cca tct tat gcc cca cct ccc acc cca gct cct gca 166  
Met Ser Lys Arg Pro Ser Tyr Ala Pro Pro Pro Thr Pro Ala Pro Ala  
1 5 10 15  
aca gca tcm wct ggt atc asg att cca aaa ccc cca aag cca cca gat 214  
Thr Ala Ser Xaa Gly Ile Xaa Ile Pro Lys Pro Pro Lys Pro Pro Asp  
20 25 30  
aag ccg ctg atg ccc tac atg agg tac agc aga aag gtc tgg gac caa 262  
Lys Pro Leu Met Pro Tyr Met Arg Tyr Ser Arg Lys Val Trp Asp Gln  
35 40 45  
gta aag gct tcc aac cct gac cta aag ttg tgg gag att ggc aag att 310  
Val Lys Ala Ser Asn Pro Asp Leu Lys Leu Trp Glu Ile Gly Lys Ile  
50 55 60  
att ggt ggc atg tgg cga gat ctc act gat gaa gaa aaa caa gaa tat 358  
Ile Gly Gly Met Trp Arg Asp Leu Thr Asp Glu Glu Lys Gln Glu Tyr  
65 70 75 80  
tta aac gaa tac 370  
Leu Asn Glu Tyr

<210> 1282  
<211> 475  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 119..475

<400> 1282  
ggacgcgagg ggcggggcga ggcgcgggaca aaggggaagcg aaccggagct gcggggcgctt 60  
tttctgcccc cggtgtctca gattcattct taaggaactg agaacttaat cttccaaa 118  
atg tca aaa aga cca tct tat gcc cca cct ccc acc cca gct cct gca 166  
Met Ser Lys Arg Pro Ser Tyr Ala Pro Pro Pro Thr Pro Ala Pro Ala  
1 5 10 15  
aca caa atg ccc agc aca cca ggg ttt gtg gga tac aat cca tac agt 214  
Thr Gln Met Pro Ser Thr Pro Gly Phe Val Gly Tyr Asn Pro Tyr Ser  
20 25 30  
cat ctc gcc tac aac aac tac agg ctg gga ggg aac ccg ggc acc aac 262  
His Leu Ala Tyr Asn Asn Tyr Arg Leu Gly Gly Asn Pro Gly Thr Asn

35	40	45	
agc cgg gtc acg gca tcc tct ggt atc acg att cca aaa ccc cca aag			310
Ser Arg Val Thr Ala Ser Ser Gly Ile Thr Ile Pro Lys Pro Pro Lys			
50	55	60	
cca cca gat aag ccg ctg atg ccc tac atg agg tac agc aga aag gtc			358
Pro Pro Asp Lys Pro Leu Met Pro Tyr Met Arg Tyr Ser Arg Lys Val			
65	70	75	80
tgg gac caa gta aan gct tcc aac cct gac cta aag ttg tgg gag att			406
Trp Asp Gln Val Xaa Ala Ser Asn Pro Asp Leu Lys Leu Trp Glu Ile			
	85	90	95
ggc aag att att ggt ggc atg tgg cga gat ctc act gat gaa gaa aaa			454
Gly Lys Ile Ile Gly Gly Met Trp Arg Asp Leu Thr Asp Glu Glu Lys			
	100	105	110
caa gaa tat tta aac gaa tac			475
Gln Glu Tyr Leu Asn Glu Tyr			
115			

<210> 1283  
 <211> 557  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 228..557

<400> 1283	
attttccaga tgatgaatct cgtcacgttg atcttggagg tggattgaaa cctcctggat	60
attatgtgca gaggtcatgt ggactgttca cagcaccatt tccacaggat agtgatgagc	120
ttgaaaggat cagcaaactg tttcatttcc ttggaatttt cttggccaaa tgcattcaag	180
acaatagact tgtggactta cctattttcta aacctttttt taaactt atg tgt atg	236
	Met Cys Met
	1
ggt gac att aaa agc aat atg rgt aam ctg att tat gag tca cga ggt	284
Gly Asp Ile Lys Ser Asn Met Xaa Xaa Leu Ile Tyr Glu Ser Arg Gly	
5	10
gat aga gac tta cac tgt act gaa agt cag tct gaa gct tct aca gaa	332
Asp Arg Asp Leu His Cys Thr Glu Ser Gln Ser Glu Ala Ser Thr Glu	
20	25
gaa ggt cat gat tca ctc tcg gta gga agc ttt gaa gag gat tca aaa	380
Glu Gly His Asp Ser Leu Ser Val Gly Ser Phe Glu Glu Asp Ser Lys	
	40
tca gaa ttt att ctt gat ccc cct aaa cca aaa ccc cca gct tgg ttt	428
Ser Glu Phe Ile Leu Asp Pro Pro Lys Pro Lys Pro Pro Ala Trp Phe	
	55
aat gga att ttg act tgg gaa gac ttt gaa tta gta aac cca cac aga	476
Asn Gly Ile Leu Thr Trp Glu Asp Phe Glu Leu Val Asn Pro His Arg	
	70
gcc aga ttt tta aaa gaa att aaa gac ctt gct atc aag agg cgc caa	524
Ala Arg Phe Leu Lys Glu Ile Lys Asp Leu Ala Ile Lys Arg Arg Gln	
	85
att tta agc aac aaa ggt ctt tct gaa gat gag	557
Ile Leu Ser Asn Lys Gly Leu Ser Glu Asp Glu	

100 105 110

<210> 1284  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 58..396

<400> 1284  
 cccattcttt ttctttatcc agtggattgt tagttcttct gctgttagga agccact 57  
 atg tct gga cgt gga aag caa ggc ggc aaa gct cgg gca aaa gct aaa 105  
 Met Ser Gly Arg Gly Lys Gln Gly Gly Lys Ala Arg Ala Lys Ala Lys  
 1 5 10 15  
 acg cgt tct tcc agg gcc ggt ctt cag ttt cca gtt ggc cgt gtg cac 153  
 Thr Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val His  
 20 25 30  
 cgc ctc ctc cgc aaa ggc aac tac tcc gaa cga gtc ggg gcc ggc gct 201  
 Arg Leu Leu Arg Lys Gly Asn Tyr Ser Glu Arg Val Gly Ala Gly Ala  
 35 40 45  
 cca gtg tac ctg gca gcg gtg ctg gaa tat ctg acg gcc gag atc tta 249  
 Pro Val Tyr Leu Ala Ala Val Leu Glu Tyr Leu Thr Ala Glu Ile Leu  
 50 55 60  
 gag cta gct ggc aac gcg gct cgc gac aat aag aag acc cgc atc atc 297  
 Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile Ile  
 65 70 75 80  
 ccg cgc cac ctg cag cta gcc atc cgc aac gac gag gag cta aat aag 345  
 Pro Arg His Leu Gln Leu Ala Ile Arg Asn Asp Glu Glu Leu Asn Lys  
 85 90 95  
 ctt cta ggt cgc gtg acc atc gcg cag ggc ggt gtc ctg cca aca tcc 393  
 Leu Leu Gly Arg Val Thr Ile Ala Gln Gly Gly Val Leu Pro Thr Ser  
 100 105 110  
 agg cc 398  
 Arg

<210> 1285  
 <211> 436  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 69..434

<400> 1285  
 gtttttgtkacacgaggtck gagagacaga ggcagcgtgt ttgagctgct ggtgcggtgg 60  
 tcagcgcg atg ccc aag gcc aag ggc aaa acc cgg agg cag aag ttt ggt 110  
 Met Pro Lys Ala Lys Gly Lys Thr Arg Arg Gln Lys Phe Gly  
 1 5 10  
 tac agt gtc aac cga aag cgt ctg aac cgg aat gct cga cgg aag gca 158

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Tyr Ser Val Asn Arg Lys Arg Leu Asn Arg Asn Ala Arg Arg Lys Ala
15          20          25          30
gcg ccg cgg atc gaa tgc tcc cac atc cga cat gcc tgg gac cac gct      206
Ala Pro Arg Ile Glu Cys Ser His Ile Arg His Ala Trp Asp His Ala
          35          40          45
aaa tcg gta cgg cag aac ctg gcc gag atg ggg ttg gct gtg gac ccc      254
Lys Ser Val Arg Gln Asn Leu Ala Glu Met Gly Leu Ala Val Asp Pro
          50          55          60
aac agg gcg gtg ccc ctc cgt aag aga aag gtg aag gcc atg gag gtg      302
Asn Arg Ala Val Pro Leu Arg Lys Arg Lys Val Lys Ala Met Glu Val
          65          70          75
gac ata gag gag agg cct aaa gag ctt gta cgg aag ccc tat gtg ctg      350
Asp Ile Glu Glu Arg Pro Lys Glu Leu Val Arg Lys Pro Tyr Val Leu
          80          85          90
aat gac ctg gag gca gaa gcc agc ctt cca gaa aag aaa gga aat act      398
Asn Asp Leu Glu Ala Glu Ala Ser Leu Pro Glu Lys Lys Gly Asn Thr
          95          100          105          110
ctg tct cgg gac ctc att gac tat gta cgc tac atg gt      436
Leu Ser Arg Asp Leu Ile Asp Tyr Val Arg Tyr Met
          115          120

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<210> 1286  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 190..420

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<400> 1286
gtcttctccc ggaaatggtc taagccccag ctcttgccgg asgagctagc ctgcgaattt      60
cagcatgagt gtactgctga ggtcagggtt ggggccgttg tgtgccgtgg cgcgcgcasc      120
attcctttta tttggagagg gaaatacttc agctccggga atgagcctgc agaaaacccg      180
gtgacgccg atg ctg cgg cat ctt atg tac aaa ata aag tct act ggt ccc      231
      Met Leu Arg His Leu Met Tyr Lys Ile Lys Ser Thr Gly Pro
          1          5          10
atc act gtg gcc gag tac atg aag gag gtg ttg act aat cca gcc aag      279
Ile Thr Val Ala Glu Tyr Met Lys Glu Val Leu Thr Asn Pro Ala Lys
15          20          25          30
ggg tat tat gtg tac cgt gac atg cta ggc gaa aaa gga gat ttc att      327
Gly Tyr Tyr Val Tyr Arg Asp Met Leu Gly Glu Lys Gly Asp Phe Ile
          35          40          45
act tca cct gaa ata agt caa atc ttt ggg gag cta cag gta tat ggt      375
Thr Ser Pro Glu Ile Ser Gln Ile Phe Gly Glu Leu Gln Val Tyr Gly
          50          55          60
tca tta gtg aat gga tgg cca ctg gaa aaa gca cag ctt tcc agc tg      422
Ser Leu Val Asn Gly Trp Pro Leu Glu Lys Ala Gln Leu Ser Ser
          65          70          75

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<210> 1287  
 <211> 361  
 <212> DNA



<213> Homo sapiens

<220>

<221> CDS

<222> 165..359

<400> 1287

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attaaaaagc ccaacytttc ctccatgtta ratgtgactt ggaaaatgag aaagatttag      60
caaaattcca ccgtatcttt tgccaggcta gagacagga gagcagagta aaaccctcag      120
gctgctgaaa tttctaggct gttaggaagc ccctcgaatt cagc atg atg ttt aaa      176
                                   Met Met Phe Lys
                                   1
cac ttt gac aag gac aag tct ggc agg ctg aac cat cag gag ttc aaa      224
His Phe Asp Lys Asp Lys Ser Gly Arg Leu Asn His Gln Glu Phe Lys
5                               10                               15                               20
tct tgc ctg cgc tcc ctg ggc tat gac ctg ccc atg gtg gag gaa ggg      272
Ser Cys Leu Arg Ser Leu Gly Tyr Asp Leu Pro Met Val Glu Glu Gly
                               25                               30                               35
gaa cct gac cct gag ttc gag gca atc ctg gac acg gtg gat ccg aac      320
Glu Pro Asp Pro Glu Phe Glu Ala Ile Leu Asp Thr Val Asp Pro Asn
                               40                               45                               50
aga gat ggc cat gtc tcc ttg caa gaa tac atg gct ttc at      361
Arg Asp Gly His Val Ser Leu Gln Glu Tyr Met Ala Phe
                               55                               60                               65
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<210> 1288

<211> 299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 107..298

<400> 1288

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gagttttcca gcggaagtgg ctctgtgaag gcagcaaggt agcgtggccg gcgcccagagc      60
tgggggttg tccctgctgg gctgccgttc cagctggact gccgcc atg gaa ctc      115
                                   Met Glu Leu
                                   1
agc gcc gaa tac ctc cgc gag aag ctg cag cgg gac ctg gag gcg gas      163
Ser Ala Glu Tyr Leu Arg Glu Lys Leu Gln Arg Asp Leu Glu Ala Xaa
5                               10                               15
atg tgg agg tgg agg aca cga ccc tca acc gtt gct cct gta gct tcc      211
Met Trp Arg Trp Arg Thr Arg Pro Ser Thr Val Ala Pro Val Ala Ser
20                               25                               30                               35
gag tcc tgg tgg tgt cgg cca agt tcg agg gga aac cgc tgc ttc aga      259
Glu Ser Trp Trp Cys Arg Pro Ser Ser Arg Gly Asn Arg Cys Phe Arg
                               40                               45                               50
gac aca ggt tct gta cag agt aat gag atg tgt gac ggc t      299
Asp Thr Gly Ser Val Gln Ser Asn Glu Met Cys Asp Gly
                               55                               60
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<210> 1289  
 <211> 606  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 100..606

<400> 1289  
 acgtcatttc ctgccgcttg tcttttccgt gctacctgca gaggggtcca tacggcggtg 60  
 ttctggattc ccgtcgtaac ttaaagggaa aytttcaca atg tcc gga gcc ctt 114  
 Met Ser Gly Ala Leu  
 1 5  
 gat gtc ctg caa atg aag gag gag gat gtc ctt aag ttc ctt gca gca 162  
 Asp Val Leu Gln Met Lys Glu Glu Asp Val Leu Lys Phe Leu Ala Ala  
 10 15 20  
 gga acc cac tta ggt ggc acc aat ctt gac ttc cag atg gaa cag tac 210  
 Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe Gln Met Glu Gln Tyr  
 25 30 35  
 atc tat aaa agg aaa agt gat ggc atc tat atc ata aat ctc aag agg 258  
 Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile Ile Asn Leu Lys Arg  
 40 45 50  
 acc tgg gag aag ctt ctg ctg gca gct cgt gca att gtt gcc att gaa 306  
 Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala Ile Val Ala Ile Glu  
 55 60 65  
 aac cct gct gat gtc agt gtt ata tcc tcc agg aat act ggc cag agg 354  
 Asn Pro Ala Asp Val Ser Val Ile Ser Ser Arg Asn Thr Gly Gln Arg  
 70 75 80 85  
 gct gtg ctg aag ttt gct gct gcc act gga gcc act cca att gct ggc 402  
 Ala Val Leu Lys Phe Ala Ala Ala Thr Gly Ala Thr Pro Ile Ala Gly  
 90 95 100  
 cgc ttc act cct gga acc ttc act aac cag atc cag gca gcc ttc cgg 450  
 Arg Phe Thr Pro Gly Thr Phe Thr Asn Gln Ile Gln Ala Ala Phe Arg  
 105 110 115  
 gag cca cgg ctt ctt gtg gtt act gac ccc agg gct gac cac cag cct 498  
 Glu Pro Arg Leu Leu Val Val Thr Asp Pro Arg Ala Asp His Gln Pro  
 120 125 130  
 ctc acg gag gca tct tat gtt aac cta cct acc att gcg ctg tgt aac 546  
 Leu Thr Glu Ala Ser Tyr Val Asn Leu Pro Thr Ile Ala Leu Cys Asn  
 135 140 145  
 aca gat tct cct ctg cgc tat gtg gac att gcc atc cca tgc aac aac 594  
 Thr Asp Ser Pro Leu Arg Tyr Val Asp Ile Ala Ile Pro Cys Asn Asn  
 150 155 160 165  
 aag gga gct cac 606  
 Lys Gly Ala His

<210> 1290  
 <211> 470  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 213..470

<400> 1290

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tttttttttc cgtgctacct gcagaggggt ccatacggcg ttgttctgga ttcccgtcgt      60
aacttaaagg gaaattttca caatgtccgg agcccttgat gtccctgcaaa tgaaggagga      120
ggatgtcctt aagttccttg cagcaggaac ccacttaggt ggcaccaatc ttgacttcca      180
gatggaacag tacatctata aaaggaaaag tg atg agg gct gtg ctg nmg ttt      233
                               Met Arg Ala Val Leu Xaa Phe
                               1           5

gct gct gcc act gga gcc act cca att gct ggc cgc ttc act cct gga      281
Ala Ala Ala Thr Gly Ala Thr Pro Ile Ala Gly Arg Phe Thr Pro Gly
      10           15           20

acc ttc act aac cag atc cag gca gcc ttc cgg gag cca cgg ctt cnt      329
Thr Phe Thr Asn Gln Ile Gln Ala Ala Phe Arg Glu Pro Arg Leu Xaa
      25           30           35

gtg gtt act gac ccc agg gct gac cac cag cct ctc acg gag gca tct      377
Val Val Thr Asp Pro Arg Ala Asp His Gln Pro Leu Thr Glu Ala Ser
      40           45           50           55

tat gtt aac cta cct acc att gcg ctg tgt aac aca gat tct cct ctg      425
Tyr Val Asn Leu Pro Thr Ile Ala Leu Cys Asn Thr Asp Ser Pro Leu
      60           65           70

cgc tat gtg gac att gcc atc cca tgc aac aac aag gga gct cac      470
Arg Tyr Val Asp Ile Ala Ile Pro Cys Asn Asn Lys Gly Ala His
      75           80           85

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<210> 1291  
<211> 487  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 230..487

<400> 1291

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acgtcatttc ctgccgcttg tcttttccgt gctacctgca gaggggtcca tacggcgcttg      60
ttctggattc ccgtcgtaac ttaaagggaa attttcacaa tgtccggagc ccttgatgtc      120
ctgcaaataa aggaggagga tgtccttaag ttccttgtag caggaaccca cttaggtggc      180
accaatcttg acttcagat ggaacagtac atctataaaa ggaaaagtg atg agg gct      238
                               Met Arg Ala
                               1

gtg ctg nmg ttt gct gct gcc act gga gcc act cca att gct ggc cgc      286
Val Leu Xaa Phe Ala Ala Ala Thr Gly Ala Thr Pro Ile Ala Gly Arg
      5           10           15

ttc act cct gga acc ttc act aac cag atc cag gca gcc ttc cgg gag      334
Phe Thr Pro Gly Thr Phe Thr Asn Gln Ile Gln Ala Ala Phe Arg Glu
      20           25           30           35

cca cgg ctt cnt gtg gtt act gac ccc agg gct gac cac cag cct ctc      382
Pro Arg Leu Xaa Val Val Thr Asp Pro Arg Ala Asp His Gln Pro Leu
      40           45           50

acg gag gca tct tat gtt aac cta cct acc att gcg ctg tgt aac aca      430

```

Thr Glu Ala Ser Tyr Val Asn Leu Pro Thr Ile Ala Leu Cys Asn Thr  
55 60 65  
gat tct cct ctg cgc tat gtg gac att gcc atc cca tgc aac aac aag 478  
Asp Ser Pro Leu Arg Tyr Val Asp Ile Ala Ile Pro Cys Asn Asn Lys  
70 75 80  
gga gct cac 487  
Gly Ala His  
85

<210> 1292  
<211> 391  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 149..391

<400> 1292  
acacaaaatg gtagecgcgcg tgggggatgt ccagtttttt ttcctcttcc caagtacaga 60  
cgcagagcag acttgtcttt ccgcttaacc tcaacctcgt gtgatctgcc agtttcgctc 120  
ccgacgccaa attccagcga aacagctg atg cca gcc agc ttg aag acc cct 172  
Met Pro Ala Ser Leu Lys Thr Pro  
1 5  
gcc aca gaa gaa ggg aat cag cat gag aat aca gct tct tca tct cgc 220  
Ala Thr Glu Glu Gly Asn Gln His Glu Asn Thr Ala Ser Ser Ser Arg  
10 15 20  
tgt ccc atg act tcg ccc tgt act ctt cag cca att aat gat ctc cac 268  
Cys Pro Met Thr Ser Pro Cys Thr Leu Gln Pro Ile Asn Asp Leu His  
25 30 35 40  
act tgg gac cac tct aaa acc ctt aag aac ctg aga ctc aaa gtc ctc 316  
Thr Trp Asp His Ser Lys Thr Leu Lys Asn Leu Arg Leu Lys Val Leu  
45 50 55  
ctg gag acg aat ttg agg ttt cct cct atc tgt gtt tgg tgn cct atg 364  
Leu Glu Thr Asn Leu Arg Phe Pro Pro Ile Cys Val Trp Xaa Pro Met  
60 65 70  
att aaa cct ctt tct ctt ctg caa cct 391  
Ile Lys Pro Leu Ser Leu Leu Gln Pro  
75 80

<210> 1293  
<211> 459  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 134..457

<400> 1293  
gagcgcagag cggtttggtc gttcgttggg cggtgctggt ttttcgctcg tcgactgcgg 60  
ctcttctcgc ggcagcggaa gcggcgcggc ggtcggagaa gtggcctaaa acttcggcgt 120

tggtgtgaaag	aaa	atg	gcc	cga	acc	aag	cag	act	gct	cgt	aag	tcc	acc	169		
	Met	Ala	Arg	Thr	Lys	Gln	Thr	Ala	Arg	Lys	Ser	Thr				
	1				5					10						
ggt	ggg	aaa	gcc	ccc	cgc	aaa	cag	ctg	gcc	acg	aaa	gcc	gcc	agg	aaa	217
Gly	Gly	Lys	Ala	Pro	Arg	Lys	Gln	Leu	Ala	Thr	Lys	Ala	Ala	Arg	Lys	
	15				20					25						
agc	gct	ccc	tct	acc	ggc	ggg	gtg	aag	aag	cct	cat	cgc	tac	agg	ccc	265
Ser	Ala	Pro	Ser	Thr	Gly	Gly	Val	Lys	Lys	Pro	His	Arg	Tyr	Arg	Pro	
	30				35					40						
ggg	acc	gtg	gcg	ctt	cga	gag	att	cgt	cgt	tat	cag	aag	tcg	acc	gag	313
Gly	Thr	Val	Ala	Leu	Arg	Glu	Ile	Arg	Arg	Tyr	Gln	Lys	Ser	Thr	Glu	
	45				50					55					60	
ctg	ctc	atc	cgg	aag	ctg	ccc	ttc	cag	agg	ttg	gtg	agg	gag	atc	gcg	361
Leu	Leu	Ile	Arg	Lys	Leu	Pro	Phe	Gln	Arg	Leu	Val	Arg	Glu	Ile	Ala	
			65					70					75			
cag	gat	ttc	aaa	acc	gac	ctg	agg	ttt	cag	agc	gca	sca	tcg	gtg	cgc	409
Gln	Asp	Phe	Lys	Thr	Asp	Leu	Arg	Phe	Gln	Ser	Ala	Xaa	Ser	Val	Arg	
			80					85					90			
tgc	agg	agg	cta	gcg	aag	kya	cct	ggt	ggg	tct	gtt	cga	aga	tac	caa	457
Cys	Arg	Arg	Leu	Ala	Lys	Xaa	Pro	Gly	Gly	Ser	Val	Arg	Arg	Tyr	Gln	
	95						100					105				
cc																459

<210> 1294  
 <211> 285  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 115..285

<400> 1294	
tttccgcccgc	tggtggccac
cgccaggtag	tgatgtcgag
cgctcgagctc	ccaaaaccga
gctggtgagg	ggctgcaggt
ggcggcgcag	tctcggtagg
cggtacttct	tcag atg
	Met
	1
tat	aag
gaa	gag
ctg	gta
cca	ttc
aga	ctg
aaa	cta
ttc	caa
aaa	att
165	
Tyr	Lys
Glu	Glu
Leu	Val
Pro	Phe
Arg	Leu
Lys	Leu
Phe	Gln
Lys	Ile
	5
	10
	15
gag	gag
gag	gaa
ctc	ctc
cct	aac
tta	ttc
tat	gaa
gcc	agc
att	acc
213	
Glu	Glu
Glu	Glu
Leu	Leu
Pro	Asn
Leu	Phe
Tyr	Glu
Ala	Ser
Ile	Thr
	20
	25
	30
ctt	gac
att	aaa
atc	caa
caa	aga
tac	acc
aaa	aaa
aca	aaa
aaa	gaa
261	
Leu	Asp
Ile	Lys
Ile	Gln
Gln	Gln
Arg	Tyr
Thr	Lys
Lys	Lys
Thr	Lys
Lys	Lys
Glu	
	35
	40
	45
aaa	gaa
aac	ttc
aag	cca
ata	tcc
285	
Lys	Glu
Asn	Phe
Lys	Pro
Ile	Ser
	50
	55

<210> 1295  
 <211> 334  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 107..334

<400> 1295

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ttttcacttt tgttttcctg ctcccagcag ggttaggctt gctgaggggc aggcacagga      60
gtcctggctg agctcatggc ctgaggctgc ctagcggcca cgggga atg gtt gca      115
                               Met Val Ala
                               1
atg gcg gag gca gag gca ggg gtg gca gtg gag gtc cgt gga ctg ccc      163
Met Ala Glu Ala Glu Ala Gly Val Ala Val Glu Val Arg Gly Leu Pro
   5                               10                               15
cct gcc gtg ccc gac gag ctg ctc act ctc tac ttt gaa aac cgc cga      211
Pro Ala Val Pro Asp Glu Leu Leu Thr Leu Tyr Phe Glu Asn Arg Arg
  20                               25                               30                               35
cgc tct gga ggg gga cct gtg ttg agc tgg cag aga ctg ggc tgt ggg      259
Arg Ser Gly Gly Gly Pro Val Leu Ser Trp Gln Arg Leu Gly Cys Gly
                               40                               45                               50
ggc gtc ctc acc ttc aga gag cct gca gac gcc gag agg gtc ttg gcc      307
Gly Val Leu Thr Phe Arg Glu Pro Ala Asp Ala Glu Arg Val Leu Ala
                               55                               60                               65
cag gca gat cat gaa sta cat ggt gcc      334
Gln Ala Asp His Glu Xaa His Gly Ala
   70                               75
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<210> 1296

<211> 457

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 265..456

<400> 1296

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cagaaacaga gccagcagat tgcacaggat gagctgcggg tgcggcggta ccgagaggag      60
accacccgta tccgccagga gatccaagag ctcaaggcca gtcctaagat tttccaaaag      120
accaagtgca gcatctgtaa cagtgccttg gagttgccct cagtccactt cctgtgtggc      180
cactccttcc accaacactg ctttgagagt tactcggaaa gtgatgctga ctgccccacc      240
tgctccttg aaaaccggaa ggtc atg gat atg atc cgg gcc cag gaa cag      291
                               Met Asp Met Ile Arg Ala Gln Glu Gln
                               1                               5
aaa cga gat ctc cat gat caa ttc cag cat cag ctc aag tgc tcc aat      339
Lys Arg Asp Leu His Asp Gln Phe Gln His Gln Leu Lys Cys Ser Asn
  10                               15                               20                               25
gac agc ttt tct gtg att gct gac tac ttt ggc aga ggt gtt ttc aac      387
Asp Ser Phe Ser Val Ile Ala Asp Tyr Phe Gly Arg Gly Val Phe Asn
                               30                               35                               40
aaa ttg act ctg ckg acm gac cct ccc asa gcc aga ntg acc tcc agc      435
Lys Leu Thr Leu Xaa Thr Asp Pro Pro Xaa Ala Arg Xaa Thr Ser Ser
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45 50 55 457  
 ctg gaa gct ggg ctg caa cgc g  
 Leu Glu Ala Gly Leu Gln Arg  
 60

<210> 1297  
 <211> 396  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 100..396

<400> 1297  
 agacgcgccg cgggtccccgc ctgccgctgc tccgccgcag tcgccgctcc agtctatccg 60  
 gcactaggaa cagccccggg cggcgagacg gtccccgcc atg tct gcg gcc atg 114  
 Met Ser Ala Ala Met  
 1 5  
 agg gag agg ttc gac cgg ttc ctg cac gag aag aac tgc atg act gac 162  
 Arg Glu Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr Asp  
 10 15 20  
 ctt ctg gcc aag ctc gag gcc aaa acc ggc gtg aac agg agc ttc atc 210  
 Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe Ile  
 25 30 35  
 gct ctt ggt gtc atc gga ctg gtg gcc ttg tac ctg gtg ttc ggt tat 258  
 Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr  
 40 45 50  
 gga gcc tct ctc ctc tgc aac ctg ata gga ttt ggc tac cca gcc tac 306  
 Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr  
 55 60 65  
 atc tca att aaa gct ata gag agt ccc aac aaa gaa gat gat acc cag 354  
 Ile Ser Ile Lys Ala Ile Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln  
 70 75 80 85  
 tgg ctg acc tac tgg gta gtg tat ggt gtg ttc agc att gct 396  
 Trp Leu Thr Tyr Trp Val Val Tyr Gly Val Phe Ser Ile Ala  
 90 95

<210> 1298  
 <211> 456  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 110..454

<400> 1298  
 aatttcttgc ttggagctca gacaacaaag gcatagagag attgggttttc tttctctcag 60  
 catctccacc caaccagcag aaaaccggtc tctgaggttc caccaaat atg gaa ctt 118  
 Met Glu Leu  
 1

gat ttt gga cac ttt gac gaa aga gat aag aca tcc agg aac atg cga	166
Asp Phe Gly His Phe Asp Glu Arg Asp Lys Thr Ser Arg Asn Met Arg	
5 10 15	
ggc tcc cgg atg aat ggg ttg cct agc ccc act cac agc gcc cac tgt	214
Gly Ser Arg Met Asn Gly Leu Pro Ser Pro Thr His Ser Ala His Cys	
20 25 30 35	
agc ttc tac cga acc aga acc ttg cag gca ctg agt aat gag aag aaa	262
Ser Phe Tyr Arg Thr Arg Thr Leu Gln Ala Leu Ser Asn Glu Lys Lys	
40 45 50	
gcc aag aag gta mgt ttc tac cgc aat ggg gac cgc tac ttc aag ggg	310
Ala Lys Lys Val Xaa Phe Tyr Arg Asn Gly Asp Arg Tyr Phe Lys Gly	
55 60 65	
att gtg tac gct gtg tcc tct gac cgt ttt cgc agc ttt gac gcc ttg	358
Ile Val Tyr Ala Val Ser Ser Asp Arg Phe Arg Ser Phe Asp Ala Leu	
70 75 80	
ctg gct gac ctg acg cga tct cta nnt gac aac atc nac ctg cct cag	406
Leu Ala Asp Leu Thr Arg Ser Leu Xaa Asp Asn Ile Xaa Leu Pro Gln	
85 90 95	
gga gtg cgt tac att tac acc att gat gga tcc aag gaa gat cgg aag	454
Gly Val Arg Tyr Ile Tyr Thr Ile Asp Gly Ser Lys Glu Asp Arg Lys	
100 105 110 115	
ca	456

<210> 1299  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 163..381

<400> 1299	
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gcagcacggg caggcaagtg gtccctaggt tcgggagcag agcagcagcg cctcagtcct	120
gggtccccag tcccaagcct cacctgcctg cccagcgcca gg atg gcc acc atc	174
Met Ala Thr Ile	
1	
acc tgc acc cgc ttc acg gaa gag tac cag ctc ttc gag gaa ttg ggc	222
Thr Cys Thr Arg Phe Thr Glu Glu Tyr Gln Leu Phe Glu Glu Leu Gly	
5 10 15 20	
aag gga gcc ttc tcg gtg gtg cga agg tgt gtg aag gtg ctg gct ggc	270
Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val Lys Val Leu Ala Gly	
25 30 35	
cag gag tat gct gcc aag atc atc aac aca aag aag ctg tca gcc aga	318
Gln Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys Lys Leu Ser Ala Arg	
40 45 50	
gac cat cag aag ctg gag cgt gaa gcc cgc atc tgc cgc ctg ctg aag	366
Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys	
55 60 65	
cac ccc aac atc gtc	381
His Pro Asn Ile Val	
70	



<210> 1300  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 146..385

<400> 1300  
 attgcttctg gggttggggt gtgagaggat gcagagtggg agaccttaaa accgtctgat 60  
 ctggctgcta aagcagagtgt ctgacgacca cccattaaca ccagcgagta gcgtttgctc 120  
 acggcttttag gataagaagc ctgga atg gtc ccc cct ccg ccg gga gaa gaa 172  
 Met Val Pro Pro Pro Pro Gly Glu Glu  
 1 5  
 agc cag acg gtc atc ctt cca cct ggc tgg cag agc tac ctg tcg cct 220  
 Ser Gln Thr Val Ile Leu Pro Pro Gly Trp Gln Ser Tyr Leu Ser Pro  
 10 15 20 25  
 cag ggc cgg cgg tac tat gtc aac acg acc acc aat gag acc acc tgg 268  
 Gln Gly Arg Arg Tyr Tyr Val Asn Thr Thr Thr Asn Glu Thr Thr Trp  
 30 35 40  
 gaa cgt ccc agc agt tct cct ggg att cca gcc agc cct ggc tct cac 316  
 Glu Arg Pro Ser Ser Ser Pro Gly Ile Pro Ala Ser Pro Gly Ser His  
 45 50 55  
 agg agc tct ctg cct cca aca gtg aat gga tac cac gca tca ggg acc 364  
 Arg Ser Ser Leu Pro Pro Thr Val Asn Gly Tyr His Ala Ser Gly Thr  
 60 65 70  
 cca gcg cac cct cca gag act 385  
 Pro Ala His Pro Pro Glu Thr  
 75 80

<210> 1301  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 325..534

<400> 1301  
 attagcggcg cagacgtttg ggcctaagcg ctgggcgagg cgaggccctg cccctccccg 60  
 ccaacggcca ttctctggac ccgtctttct tyccgggagg cggtagacagc tgctgagacg 120  
 tggtgcagcc agagtctctc cgctttaatg cgctccatt agtgccgtcc cccactggaa 180  
 aaccgtggct tctgtattat ttgccatctt tggtgtgtag gagcagggag ggcttcctcc 240  
 cggggctcta ggcggcgggtg cagtcctctg tagaagaatt agagtagaag ttgtcggggg 300  
 ccgctcttag gacgcagccg cctc atg ggg gtc cag ggg ctc tgg aag ctg 351  
 Met Gly Val Gln Gly Leu Trp Lys Leu  
 1 5  
 ctg gag tgc tcc ggg cgg cag gtc agc ccc gaa gcg ctg gaa ggg aag 399  
 Leu Glu Cys Ser Gly Arg Gln Val Ser Pro Glu Ala Leu Glu Gly Lys

10	15	20	25	
atc ctg gct gtt gat att agc att tgg tta aac caa gca ctt aaa gga				447
Ile Leu Ala Val Asp Ile Ser Ile Trp Leu Asn Gln Ala Leu Lys Gly				
	30	35	40	
gtc cgg gat cgc cac ggg aac tca ata gaa aat cct cat ctt ctc act				495
Val Arg Asp Arg His Gly Asn Ser Ile Glu Asn Pro His Leu Leu Thr				
	45	50	55	
ttg ttt cat cgg ctc tgc aaa ctc tta ttt ttt cga atc c				535
Leu Phe His Arg Leu Cys Lys Leu Leu Phe Phe Arg Ile				
60	65	70		

<210> 1302  
 <211> 383  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 74..382

<400> 1302	
agcgtgatcg gtttccgggtc agtgggtgtgg taccgggtac ccggagacgt gtatcggacg	60
gtgggccgca gcc atg gcc gag aga aaa cct aac ggt ggc agc ggc ggc	109
Met Ala Glu Arg Lys Pro Asn Gly Gly Ser Gly Gly	
1 5 10	
gcc tcc act tcc tca tcg ggc act aac tta ctt ttc tcc tcc tcg gcc	157
Ala Ser Thr Ser Ser Ser Gly Thr Asn Leu Leu Phe Ser Ser Ser Ala	
15 20 25	
acg gag ttc agc ttc aat gtg ccc ttc atc cca gtc acc cag gcc tcc	205
Thr Glu Phe Ser Phe Asn Val Pro Phe Ile Pro Val Thr Gln Ala Ser	
30 35 40	
gct tct ccg gcc tcc ctg ctc tta ccg gga gag gat tcc aca gat gtt	253
Ala Ser Pro Ala Ser Leu Leu Leu Pro Gly Glu Asp Ser Thr Asp Val	
45 50 55 60	
ggg gag gag gac agc ttc ctt ggt cag act tct att cac aca tct gcc	301
Gly Glu Glu Asp Ser Phe Leu Gly Gln Thr Ser Ile His Thr Ser Ala	
65 70 75	
cca cag aca ttt agt tac ttc tct cag gta tca agc agc agt grt cct	349
Pro Gln Thr Phe Ser Tyr Phe Ser Gln Val Ser Ser Ser Ser Xaa Pro	
80 85 90	
ttt ggg aat att gga cag tca cca tta aca act g	383
Phe Gly Asn Ile Gly Gln Ser Pro Leu Thr Thr	
95 100	

<210> 1303  
 <211> 425  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 162..425

&lt;400&gt; 1303

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ctacgttcca attggggccg taccatggcg gagaagactc aaaagagtgt gaagattgct      60
cctggagcag ttgtatgtgt agaaagtgaa atcagaggag atgtaactat cgttaccag      120
ataatatcac tcttgacact gragatccag arccaaaacc t atg atc att ggc acc      176
                               Met Ile Ile Gly Thr
                               1           5
aat aat gtg ttt gaa gtt ggc tgt tat tcc caa gcc atg aag atg gga      224
Asn Asn Val Phe Glu Val Gly Cys Tyr Ser Gln Ala Met Lys Met Gly
                               10           15           20
gat aat aat gtc att gaa tca aaa gca tat gta ggc aga aat gta ata      272
Asp Asn Asn Val Ile Glu Ser Lys Ala Tyr Val Gly Arg Asn Val Ile
                               25           30           35
ttg aca agt ggc tgc atc att ggg gct tgt tgc aac cta aat aca ttt      320
Leu Thr Ser Gly Cys Ile Ile Gly Ala Cys Cys Asn Leu Asn Thr Phe
                               40           45           50
gaa gtc atc cct gag aat acg gtg atc tat ggt gca gac tgc ctt cgt      368
Glu Val Ile Pro Glu Asn Thr Val Ile Tyr Gly Ala Asp Cys Leu Arg
                               55           60           65
cgg gtg cag act gag cga ccg cag ccc cag aca cta cag ctg gat ttc      416
Arg Val Gln Thr Glu Arg Pro Gln Pro Gln Thr Leu Gln Leu Asp Phe
70                               75                               80                               85
ttg atg aaa
Leu Met Lys

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&lt;210&gt; 1304

&lt;211&gt; 458

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 199..456

&lt;400&gt; 1304

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attaaagcag ctccagccct gcgcactccc tgctgggggtg agcagcactg taaagatgaa      60
gctggctaac tggtactggc tgagctcagc tgttcttgcc acttacggtt ttttggttgt      120
ggcaaacaat gaaacagagg aaattaaaga tgaaagagca aaggatgtct gccagtgag      180
actagaaagc agaggggaa atg cga aga ggc agg gga gtg ccc cta cca ggt      231
                               Met Arg Arg Gly Arg Gly Val Pro Leu Pro Gly
                               1           5           10
aag cct gcc ccc ttg act att cag ctc ccg aag caa ttc agc agg atc      279
Lys Pro Ala Pro Leu Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile
                               15           20           25
gag gag gtg ttc aaa gaa gwm caa aac ctc aag gaa atc gta aat agt      327
Glu Glu Val Phe Lys Glu Xaa Gln Asn Leu Lys Glu Ile Val Asn Ser
                               30           35           40
cta aag aaa tct tgc caa gac tgc aag ctg cag gct gat gac aac gga      375
Leu Lys Lys Ser Cys Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly
                               45           50           55
gac cca ggc aga aac gga ctg ttg tta ccc agt aca gga gcc ccg gga      423
Asp Pro Gly Arg Asn Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly
60                               65                               70                               75

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gag gtt ggt gat aac aga gtt aga gaa tta gag ag 458  
 Glu Val Gly Asp Asn Arg Val Arg Glu Leu Glu  
 80 85

<210> 1305  
 <211> 445  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 13..444

<400> 1305  
 gacggaagga gc atg gcg tgg aga cac ctg caa aag cgg gcc cag gat gct 51  
 Met Ala Trp Arg His Leu Gln Lys Arg Ala Gln Asp Ala  
 1 5 10  
 gtg atc atc ctg ggg gga gga gga ctt ctc ttc gcc tcc tac ctg atg 99  
 Val Ile Ile Leu Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met  
 15 20 25  
 gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act ctg 147  
 Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu  
 30 35 40 45  
 cag ggg ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc ttc 195  
 Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe  
 50 55 60  
 acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac atg 243  
 Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met  
 65 70 75  
 ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga att 291  
 Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile  
 80 85 90  
 gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat aag 339  
 Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys  
 95 100 105  
 atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct cag 387  
 Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln  
 110 115 120 125  
 gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa gct 435  
 Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala  
 130 135 140  
 gtc att aac a 445  
 Val Ile Asn

<210> 1306  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 124..393

004220"666E7560

<400> 1306  
aacttttggg tcgggccctc cggaagatg gcggccgtgc aggcggccga ggtgaaagtg 60  
gatggcagcg agccgaaact gagcaagaag tggtggaat cattagttcc aggtgctct 120  
gcc atg ttg acg caa gct gct gta agg ctt gtt agg ggg tcc ctg cgc 168  
Met Leu Thr Gln Ala Ala Val Arg Leu Val Arg Gly Ser Leu Arg  
1 5 10 15  
aaa acc tcc tgg gca gag tgg ggt cac agg gaa ctg cga ctg ggt caa 216  
Lys Thr Ser Trp Ala Glu Trp Gly His Arg Glu Leu Arg Leu Gly Gln  
20 25 30  
ctt gct cct ttc aca gcg cct cac aag gac aag tca ttt tct gat caa 264  
Leu Ala Pro Phe Thr Ala Pro His Lys Asp Lys Ser Phe Ser Asp Gln  
35 40 45  
aga agt gag ctg aag aga cgc ctg aaa gct gag aag aaa gta gca gag 312  
Arg Ser Glu Leu Lys Arg Arg Leu Lys Ala Glu Lys Lys Val Ala Glu  
50 55 60  
aag gag gcc aaa cag aaa gag ctc agt gag aaa cag cta agc caa gcc 360  
Lys Glu Ala Lys Gln Lys Glu Leu Ser Glu Lys Gln Leu Ser Gln Ala  
65 70 75  
act gct gct gcc acc aac cac acc act gat aat 393  
Thr Ala Ala Ala Thr Asn His Thr Thr Asp Asn  
80 85 90

<210> 1307  
<211> 245  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 3..245

<400> 1307  
aa atg ctc tgg ggc gtg ccg cmg ccg tcg ctg cca cct ccc cta ccg 47  
Met Leu Trp Gly Val Pro Xaa Pro Ser Leu Pro Pro Pro Leu Pro  
1 5 10 15  
yta gtg gaa gaa gat ggc gga agg cgg asg gcg gat ctg gac acc cag 95  
Leu Val Glu Glu Asp Gly Gly Arg Arg Xaa Ala Asp Leu Asp Thr Gln  
20 25 30  
cgg tct gac atc gcg acg ctg ctc aaa acc tcg ctc cgg aaa ggg gac 143  
Arg Ser Asp Ile Ala Thr Leu Leu Lys Thr Ser Leu Arg Lys Gly Asp  
35 40 45  
acc tgg tac cta gtc ata gtc gct ggk tca aac agt gga aaa aat atg 191  
Thr Trp Tyr Leu Val Ile Val Ala Gly Ser Asn Ser Gly Lys Asn Met  
50 55 60  
ttg gct ttg aca gtt ggg aca aat acc aga tgg gag atc aaa atg tgt 239  
Leu Ala Leu Thr Val Gly Thr Asn Thr Arg Trp Glu Ile Lys Met Cys  
65 70 75  
atc ccg 245  
Ile Pro  
80

<210> 1308

<211> 491  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 231..491

<400> 1308  
ctttcccatc tggcgggcg ctcctgtcca gaccctgacc ctccctccca aggctcaacc 60  
gtccccaac aaccgccagc cttgtactga tgctggctgc gagagcctgt gcttaagtaa 120  
gaatcaggcc ttattggaga cattcaagca aagggtggac aactactttt ccagaacaga 180  
aaggaaactc atgcatcaga aaagggtgact aataaaggta ccagaagaat atg gct 236  
Met Ala  
1  
gca caa ata cca gaa tct gat cag ata aaa cag ttt aag gaa ttt ctg 284  
Ala Gln Ile Pro Glu Ser Asp Gln Ile Lys Gln Phe Lys Glu Phe Leu  
5 10 15  
ggg acc tac aat aaa ctt aca gag acc tgc ttt ttg gac tgt gtt aaa 332  
Gly Thr Tyr Asn Lys Leu Thr Glu Thr Cys Phe Leu Asp Cys Val Lys  
20 25 30  
gac ttc aca aca aga gaa gta aaa cct gaa gag acc acc tgt tca gaa 380  
Asp Phe Thr Thr Arg Glu Val Lys Pro Glu Glu Thr Thr Cys Ser Glu  
35 40 45 50  
cat tgc tta cag aaa tat tta aaa atg aca caa aga ata tcc atg aga 428  
His Cys Leu Gln Lys Tyr Leu Lys Met Thr Gln Arg Ile Ser Met Arg  
55 60 65  
ttt cag gaa tat cat att cag cag aat gaa gcc ctg gca gcc aaa gca 476  
Phe Gln Glu Tyr His Ile Gln Gln Asn Glu Ala Leu Ala Ala Lys Ala  
70 75 80  
gga ctc ctt ggc caa 491  
Gly Leu Leu Gly Gln  
85

<210> 1309  
<211> 376  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 165..374

<400> 1309  
gaaggaagag gaaattccag tagccgatca ggagtctgca aactccggtg gtaggggagc 60  
gcgctgctgt ttagagccac gagttaccgg agcgctgat tcctgcgccg aagtcagtgg 120  
tggccgaaag tccggagtcg ctgtaaaacc tgagattgtg agcc atg gtg ggg aga 176  
Met Val Gly Arg  
1  
tcc cgg cgg cgc gga gca gct aag tgg gca gct gtg cga gcc aag gca 224  
Ser Arg Arg Arg Gly Ala Ala Lys Trp Ala Ala Val Arg Ala Lys Ala  
5 10 15 20

ggt ccc acg ctc acc gac gaa aat gga gat gat tta gga ttg cca ccc	272
Gly Pro Thr Leu Thr Asp Glu Asn Gly Asp Asp Leu Gly Leu Pro Pro	
25 30 35	
tca cca ggg gac acc agc tac tac caa gat cag gta gat gac ttt cat	320
Ser Pro Gly Asp Thr Ser Tyr Tyr Gln Asp Gln Val Asp Asp Phe His	
40 45 50	
gag gca cga tcc cgg gcc gcc tta gct aag ggc tgg aat gaa gta cag	368
Glu Ala Arg Ser Arg Ala Ala Leu Ala Lys Gly Trp Asn Glu Val Gln	
55 60 65	
agt gga ga	376
Ser Gly	
70	

<210> 1310  
 <211> 433  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 151..432

<400> 1310	
ttctcgatt tgctcagctct tgccaaaacg gtgacgcagt ggtgtgttac ctgccgacag	60
cataaagcga ggcaaggtcc agctattcca cccggcatac aagcttatgg agcagcccc	120
tttgaagatc tccaggtgga cttcacagag atg tca aag tgt aga gat gat cga	174
Met Ser Lys Cys Arg Asp Asp Arg	
1 5	
gtg tgg atc aag gac tgg aaa gtt gcc tgt ttg tgt cca cgg tgg aaa	222
Val Trp Ile Lys Asp Trp Lys Val Ala Cys Leu Cys Pro Arg Trp Lys	
10 15 20	
gga ccc cag ayt gtc gtc ctg agc act ccc acc gct gtg aag gtg gaa	270
Gly Pro Gln Xaa Val Val Leu Ser Thr Pro Thr Ala Val Lys Val Glu	
25 30 35 40	
gga atc cca gcc tgg atc caa cac agc cat ata aaa cct gca gcg cct	318
Gly Ile Pro Ala Trp Ile Gln His Ser His Ile Lys Pro Ala Ala Pro	
45 50 55	
gaa acc tgg gag gca aga cca agc cca grt aac cct tgc aga gtg acc	366
Glu Thr Trp Glu Ala Arg Pro Ser Pro Xaa Asn Pro Cys Arg Val Thr	
60 65 70	
ctg aag aag ang aca agc cct gct cca gtc anc cgg aag ctg act agt	414
Leu Lys Lys Xaa Thr Ser Pro Ala Pro Val Xaa Arg Lys Leu Thr Ser	
75 80 85	
caa gca cgg ccg aag cct g	433
Gln Ala Arg Pro Lys Pro	
90	

<210> 1311  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 93..422

<400> 1311

tattccggaa ggtgctgcac agctgtggcg gcgggtactg cgtagtgat tagagtttct	60
tccctgccgg aggtgggata cacggtagca tc atg gtc gag gag gta cag aaa	113
Met Val Glu Glu Val Gln Lys	
1 5	
cat tct gta cac acc ctt gtg ttc agg tcg ttg aag agg acc cat gac	161
His Ser Val His Thr Leu Val Phe Arg Ser Leu Lys Arg Thr His Asp	
10 15 20	
atg ttt gta gct gat aat gga aaa cct gtg cct tta gat gaa gag agt	209
Met Phe Val Ala Asp Asn Gly Lys Pro Val Pro Leu Asp Glu Glu Ser	
25 30 35	
sac aaa cga aaa atg gca atc aag ctt cgt aat gag tat ggt cct gtg	257
Xaa Lys Arg Lys Met Ala Ile Lys Leu Arg Asn Glu Tyr Gly Pro Val	
40 45 50 55	
ttg cat atg cct act tca aaa gaa aat ctt aaa gag aag ggt cct cag	305
Leu His Met Pro Thr Ser Lys Glu Asn Leu Lys Glu Lys Gly Pro Gln	
60 65 70	
aat gca acg gat tca tat gtt cat aaa cag tac cct gcc aat caa gga	353
Asn Ala Thr Asp Ser Tyr Val His Lys Gln Tyr Pro Ala Asn Gln Gly	
75 80 85	
caa gaa gtt gaa tac ttt gtg gca ggt aca cat cca tac cca cca gga	401
Gln Glu Val Glu Tyr Phe Val Ala Gly Thr His Pro Tyr Pro Pro Gly	
90 95 100	
cct ggg gtt gct ttg aca gca ga	424
Pro Gly Val Ala Leu Thr Ala	
105 110	

<210> 1312  
<211> 444  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 56..442

<400> 1312

gaggacgtgt tccgaggaag ccagaccgg agccgtggcc tgccgggccc gcgac atg	58
Met	
1	
gat ccc ctg ttc cag caa acg cac aag cag gtc cac gag atc cag tct	106
Asp Pro Leu Phe Gln Gln Thr His Lys Gln Val His Glu Ile Gln Ser	
5 10 15	
tgc atg gga cgc ctg gag acg gsa gam aag sag yct gtg cac aka gta	154
Cys Met Gly Arg Leu Glu Thr Xaa Xaa Lys Xaa Xaa Val His Xaa Val	
20 25 30	
gaa aac gaa atc caa gca agc ata gac cag ata ttc agc cgt cta gaa	202
Glu Asn Glu Ile Gln Ala Ser Ile Asp Gln Ile Phe Ser Arg Leu Glu	
35 40 45	



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cgt ctg gag att ttg tcc agc aag gag ccc cct aac aaa agg caa aat      250
Arg Leu Glu Ile Leu Ser Ser Lys Glu Pro Pro Asn Lys Arg Gln Asn
50                      55                      60                      65
gcc aaa ctt cgg gtt gac cag tta aag tat gat gtc cag cac ctg cag      298
Ala Lys Leu Arg Val Asp Gln Leu Lys Tyr Asp Val Gln His Leu Gln
70                      75                      80
act gcg ctc aga aac ttc cag cat cgg cgc cat gca agg gag cag cag      346
Thr Ala Leu Arg Asn Phe Gln His Arg Arg His Ala Arg Glu Gln Gln
85                      90                      95
gag aga cag cga gaa gag ctt ctg tct cga acc ttc asc act aac grc      394
Glu Arg Gln Arg Glu Glu Leu Leu Ser Arg Thr Phe Xaa Thr Asn Xaa
100                     105                     110
tct ggm anc acc ata cca atg grc gat cac tgc agt tta act cct ccc      442
Ser Gly Xaa Thr Ile Pro Met Xaa Asp His Cys Ser Leu Thr Pro Pro
115                     120                     125
tc

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444

<210> 1313  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 103..345

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<400> 1313
ggggaagctg tcatggctgc tcctgtacgt agtcacggtc ttgtgctcta aggaaaacga      60
cagcacgtgt tctttttcac tagtagaagt gacgttggtt tc atg ttg aca act      114
                               Met Leu Thr Thr
                               1
ttg aag cca ttt gga agt gtt tca gtg gag agc aaa atg aat aac aaa      162
Leu Lys Pro Phe Gly Ser Val Ser Val Glu Ser Lys Met Asn Asn Lys
5                      10                      15                      20
gcg ggc tcc ttt ttc tgg aac ctt aga caa ttc agt aca tta gtt tca      210
Ala Gly Ser Phe Phe Trp Asn Leu Arg Gln Phe Ser Thr Leu Val Ser
25                      30                      35
aca agc aga act atg agg cta tgt tgt ttg gga ctt tgc aaa cca aaa      258
Thr Ser Arg Thr Met Arg Leu Cys Cys Leu Gly Leu Cys Lys Pro Lys
40                      45                      50
ata gtt cat tca aac tgg aac att tta aat aac ttt cat aac aga atg      306
Ile Val His Ser Asn Trp Asn Ile Leu Asn Asn Phe His Asn Arg Met
55                      60                      65
caa tca act gat atc att aga tat ctc ttt cag gat gca tt      347
Gln Ser Thr Asp Ile Ile Arg Tyr Leu Phe Gln Asp Ala
70                      75                      80

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<210> 1314  
 <211> 469  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 160..468

<400> 1314

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agatcttact agtattttact accaagctct actccagatt aaccatccca gtccttctgt      60
cagtctccga tgccatcatg cagcctggtt aggagcaaag gaaaggggaa aaagaaaaaac    120
gactaattca tcttttcctg atcgtcagga ccctaaaga atg gcc gag cct tgg      174
                               Met Ala Glu Pro Trp
                               1           5
ggg aac gag ttg gcg tcc gca gct gcc agg ggg gac cta gag caa ctt      222
Gly Asn Glu Leu Ala Ser Ala Ala Ala Arg Gly Asp Leu Glu Gln Leu
                               10           15           20
act agt ttg ttg caa aat aat gta aac gtc aat gca caa aat gga ttt      270
Thr Ser Leu Leu Gln Asn Asn Val Asn Val Asn Ala Gln Asn Gly Phe
                               25           30           35
gga agg act gcg ctg cag gtt atg aaa ctt gga aat ccc gag att gcc      318
Gly Arg Thr Ala Leu Gln Val Met Lys Leu Gly Asn Pro Glu Ile Ala
                               40           45           50
agg aga ctg cta ctt aga ggt gct aat ccc gat ttg aaa gac cga act      366
Arg Arg Leu Leu Leu Arg Gly Ala Asn Pro Asp Leu Lys Asp Arg Thr
                               55           60           65
ggt ttc gct gtc att cat gat gcg gcc aga gca ggt ttc ctg gac act      414
Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala Gly Phe Leu Asp Thr
70           75           80           85
tta cag act ttg ctg gag ttt caa gct gat gtt aac atc gag gat aat      462
Leu Gln Thr Leu Leu Glu Phe Gln Ala Asp Val Asn Ile Glu Asp Asn
                               90           95           100
gaa ggg a
Glu Gly

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<210> 1315  
<211> 233  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 75..233

<400> 1315

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agccgacgag gcaacaatta ggctttgggg ataaaacgag gtgcggagag cgggctgggg      60
catttctccc cgag atg gcg ggt ctg acg gcg gcg gcc ccg cgg gcc cgg      110
                               Met Ala Gly Leu Thr Ala Ala Ala Pro Arg Ala Arg
                               1           5           10
agt cct cct gct cct gct gtc cat cct cca ccc ctc tcg gcc tgg agg      158
Ser Pro Pro Ala Pro Ala Val His Pro Pro Pro Leu Ser Ala Trp Arg
                               15           20           25
ggt ccc tgg ggc cat tcc tgg tgg agt tcc tgg agg agt ctt tta tcc      206
Gly Pro Trp Gly His Ser Trp Trp Ser Ser Trp Arg Ser Leu Leu Ser
30           35           40
agg ggc tgg tct cgg agc cct tgg agg      233
Arg Gly Trp Ser Arg Ser Pro Trp Arg

```

45

50

&lt;210&gt; 1316

&lt;211&gt; 492

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 217..492

&lt;400&gt; 1316

ataaaggagc gggcggcgcg acagggggcg ctctttcctg ggtgggggtt gtgaagtcgt 60  
ggcccgttag caggaagcct aacagtcgcc ccgacgctag tgagggaccc aatctgagtc 120  
cccggccagc cgaatccaag ccgtgtgtac tgcgtgctca gcactgccc acagtcctag 180  
ctaaacttcg ccaactccgc tgcctttgcc gccacc atg ccc aaa acg atc agt 234  
Met Pro Lys Thr Ile Ser  
1 5  
gtg cgt gtg acc acc atg gat gca gag ctg gag ttt gcc atc cag ccc 282  
Val Arg Val Thr Thr Met Asp Ala Glu Leu Glu Phe Ala Ile Gln Pro  
10 15 20  
aac acc acc ggg aag cag cta ttt gac cag gtg gtg aaa act att ggc 330  
Asn Thr Thr Gly Lys Gln Leu Phe Asp Gln Val Val Lys Thr Ile Gly  
25 30 35  
ttg agg gaa gtt tgg ttc ttt ggt ctg cag tac cag gac act aaa ggt 378  
Leu Arg Glu Val Trp Phe Phe Gly Leu Gln Tyr Gln Asp Thr Lys Gly  
40 45 50  
ttc tcc acc tgg ctg aaa ctc aat aag aag gtg act gcc cag gat gtg 426  
Phe Ser Thr Trp Leu Lys Leu Asn Lys Lys Val Thr Ala Gln Asp Val  
55 60 65 70  
cgg aag gaa agc ccc ctg ctc ttt aag ttc cgt gcc aag ttc tac cct 474  
Arg Lys Glu Ser Pro Leu Leu Phe Lys Phe Arg Ala Lys Phe Tyr Pro  
75 80 85  
gag gat gtg tcc gag gaa 492  
Glu Asp Val Ser Glu Glu  
90

&lt;210&gt; 1317

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 144..335

&lt;400&gt; 1317

gagtgtcggg cgcggcagga ggacgaggca gggcggggcg gcgctctaag ggttctgctc 60  
tgactccagg ttgggacagc gtcttcgctg ctgctggata gtcgtgtttt cggggatcga 120  
ggatactcac cmagaaaccg aaa atg ccg aaa cca atc aat gtc cga gtt acc 173  
Met Pro Lys Pro Ile Asn Val Arg Val Thr  
1 5 10



<221> CDS  
<222> 108..506

<400> 1319

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aagaaggcgg gaggctggag tagasggaag cctgcaaccg gaagtgaagg cagatttccc      60
tccttcgctcg ctgttgctgc cgccatacgc gctctccctg tttagtt atg gca gag      116
                               Met Ala Glu
                               1
aac gat gtg gac aat gag ctc ttg gac tat gaa gat gat gag gtg gag      164
Asn Asp Val Asp Asn Glu Leu Leu Asp Tyr Glu Asp Asp Glu Val Glu
   5                               10                               15
aca gca gct ggg gga gat ggg gct gag gcc cct gcc aag aag gat gtc      212
Thr Ala Ala Gly Gly Asp Gly Ala Glu Ala Pro Ala Lys Lys Asp Val
  20                               25                               30                               35
aag ggc tcc tat gtc tcc atc cac agc tct ggc ttt cgt gac ttc ctg      260
Lys Gly Ser Tyr Val Ser Ile His Ser Ser Gly Phe Arg Asp Phe Leu
                               40                               45                               50
ctc aag cca gag ttg ctc cgg gcc att gtc gac tgt ggc ttt gag cat      308
Leu Lys Pro Glu Leu Leu Arg Ala Ile Val Asp Cys Gly Phe Glu His
                               55                               60                               65
ccg tca gaa gtc cag cat gag tgc atc cct cag gcc att ctg gga atg      356
Pro Ser Glu Val Gln His Glu Cys Ile Pro Gln Ala Ile Leu Gly Met
   70                               75                               80
gat gtc ctg tgc cag gcc aag tgc ggc atg gga aag aca gca gtg ttt      404
Asp Val Leu Cys Gln Ala Lys Ser Gly Met Gly Lys Thr Ala Val Phe
   85                               90                               95
gtc ttg gcc aca ctg caa cag ctg gag cca gtt act ggg cag gtg tct      452
Val Leu Ala Thr Leu Gln Gln Leu Glu Pro Val Thr Gly Gln Val Ser
  100                               105                               110                               115
gtr ctg gtg atg tgt cac act cgg gag ttg gct ttt cag atc agc aag      500
Val Leu Val Met Cys His Thr Arg Glu Leu Ala Phe Gln Ile Ser Lys
                               120                               125                               130
gaa tat ga
Glu Tyr
                               508

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<210> 1320  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 238..636

<400> 1320

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tccttcgctcg ctgttgctgc cgccatacgc gctctccctg tttagctctt ctgtagaaa      120
tagtatcttt gttttccttt gctgttcctc aatcccctac tcttcacccc ttgttttcac      180
ctatattgcg agaaccatc cagatcccc ttcccttctt cccctgccgg cccagtt      237
atg gca gag aac gat gtg gac aat gag ctc ttg gac tat gaa gat gat      285
Met Ala Glu Asn Asp Val Asp Asn Glu Leu Leu Asp Tyr Glu Asp Asp
  1                               5                               10                               15

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gag gtg gag aca gca gct ggg gga gat ggg gct gag gcc cct gcc aag 333  
 Glu Val Glu Thr Ala Ala Gly Gly Asp Gly Ala Glu Ala Pro Ala Lys  
 20 25 30  
 aag gat gtc aag ggc tcc tat gtc tcc atc cac agc tct ggc ttt cgt 381  
 Lys Asp Val Lys Gly Ser Tyr Val Ser Ile His Ser Ser Gly Phe Arg  
 35 40 45  
 gac ttc ctg ctc aag csa gag ttg ctc cgg gcc att gtc gac tgt ggc 429  
 Asp Phe Leu Leu Lys Xaa Glu Leu Leu Arg Ala Ile Val Asp Cys Gly  
 50 55 60  
 ttt gag cat ccg tca gaa gtc cag cat gag tgc atc cct cag gcc att 477  
 Phe Glu His Pro Ser Glu Val Gln His Glu Cys Ile Pro Gln Ala Ile  
 65 70 75 80  
 ctg gga atg gat gtc ctg tgc cag gcc aag tgc ggc atg gga aag aca 525  
 Leu Gly Met Asp Val Leu Cys Gln Ala Lys Ser Gly Met Gly Lys Thr  
 85 90 95  
 gca gtg ttt gtc ttg gcc aca ctg caa cag ctg gag cca gtt act ggg 573  
 Ala Val Phe Val Leu Ala Thr Leu Gln Gln Leu Glu Pro Val Thr Gly  
 100 105 110  
 cag gtg tct gtr ctg gtg atg tgt cac act cgg gag ttg gct ttt cag 621  
 Gln Val Ser Val Leu Val Met Cys His Thr Arg Glu Leu Ala Phe Gln  
 115 120 125  
 atc agc aag gaa tat ga 638  
 Ile Ser Lys Glu Tyr  
 130

<210> 1321  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 107..406

<400> 1321  
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 cgcttggttg ccggctgcgt gagtgccttag agcttttcgg tggaag atg ccg gac 115  
 Met Pro Asp  
 1  
 agt aac ttc gca gag cgc agn ngg gag cag gtg tct ggt gct aaa gtc 163  
 Ser Asn Phe Ala Glu Arg Xaa Xaa Glu Gln Val Ser Gly Ala Lys Val  
 5 10 15  
 atc gct cag gcc ctg aaa acg caa gat gtg gag tac ata ttt ggc atc 211  
 Ile Ala Gln Ala Leu Lys Thr Gln Asp Val Glu Tyr Ile Phe Gly Ile  
 20 25 30 35  
 gta ggc atc cca gtg acc gaa atc gcy att gct gcc cag cag cta ggc 259  
 Val Gly Ile Pro Val Thr Glu Ile Ala Ile Ala Ala Gln Gln Leu Gly  
 40 45 50  
 atc aag tac atc ggg atg agg aat gag caa gcg gct tgt tat gct gcc 307  
 Ile Lys Tyr Ile Gly Met Arg Asn Glu Gln Ala Ala Cys Tyr Ala Ala  
 55 60 65  
 tcc gcg att gga tat ctg aca agc agg cca gga gtc tgc ctt gtt gtt 355  
 Ser Ala Ile Gly Tyr Leu Thr Ser Arg Pro Gly Val Cys Leu Val Val

70	75	80	
tct ggc cca ggt ctc atc cat gcc ttg ggc ggt atg gca aat gca aac			403
Ser Gly Pro Gly Leu Ile His Ala Leu Gly Gly Met Ala Asn Ala Asn			
85	90	95	
atg aa			408
Met			
100			

<210> 1322  
 <211> 361  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 142..360

<400> 1322	
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cctggggcagg cagcagctgg ctgaccaagt ccaactggaag agaaggcttg tgccagccgg	120
gagaaggaag ccggggacag g atg aaa gca aca aca cct ttg cag aca gtc	171
Met Lys Ala Thr Thr Pro Leu Gln Thr Val	
1 5 10	
gac cgg ccc aag gac tgg tac aag acg atg ttt aag caa att cac atg	219
Asp Arg Pro Lys Asp Trp Tyr Lys Thr Met Phe Lys Gln Ile His Met	
15 20 25	
gtg cac aag ccg ggt ctg tac aac cca ccc tac agt gct cag tca cac	267
Val His Lys Pro Gly Leu Tyr Asn Pro Pro Tyr Ser Ala Gln Ser His	
30 35 40	
cct gct gca aag acc caa acc tac aga cct ctt tcc aaa agc cac tcc	315
Pro Ala Ala Lys Thr Gln Thr Tyr Arg Pro Leu Ser Lys Ser His Ser	
45 50 55	
gac aac agc ccc aat gcc ttt aag gat gcg tcc tcc cca gtg cct c	361
Asp Asn Ser Pro Asn Ala Phe Lys Asp Ala Ser Ser Pro Val Pro	
60 65 70	

<210> 1323  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 59..370

<400> 1323	
aaaatataac tgagtttacg cagacgcaga aaacgcaggc aaacctgagg tcctcaga	58
atg gcg ggc aca ggt ttg gtg gct gga gag gtt gtg gtg gat gcg ctg	106
Met Ala Gly Thr Gly Leu Val Ala Gly Glu Val Val Val Asp Ala Leu	
1 5 10 15	
ccg tat ttt gat caa ggt tat gaa gcc cct ggt gtg cgg gaa gcg gct	154
Pro Tyr Phe Asp Gln Gly Tyr Glu Ala Pro Gly Val Arg Glu Ala Ala	





cccacttcta ggcttggttg aaccgtgcag ataccttctc gaaacaaaag attttcctac 60  
 ctgcttatac ttggttaaccg aggggaattac taagacttct tgctcatttc tgagtattgt 120  
 ctttatatcc tgacactatg aaatgctact tgg atg cct ctw aag tct gtt ctc 174  
 Met Pro Leu Lys Ser Val Leu  
 1 5  
 tgg gga ggc agt aag ggg ccg tgg agc tgg cct cgg cct cgg cat cgg 222  
 Trp Gly Gly Ser Lys Gly Pro Trp Ser Trp Pro Arg Pro Arg His Arg  
 10 15 20  
 gag agg ctg gac ttc ctg tct ctc tgt gct gaa tgg ctg cga tgg cgc 270  
 Glu Arg Leu Asp Phe Leu Ser Leu Cys Ala Glu Trp Leu Arg Trp Arg  
 25 30 35  
 ccg ctc tca ctg acg cag cag ctg aag cnn wcc ata tcc ggt tca aac 318  
 Pro Leu Ser Leu Thr Gln Gln Leu Lys Xaa Xaa Ile Ser Gly Ser Asn  
 40 45 50 55  
 tgg ctc ccc cat cct cta ccc tg 341  
 Trp Leu Pro His Pro Leu Pro  
 60

<210> 1326  
 <211> 302  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 49..300

<400> 1326  
 tggaaaggca gagccgcgag ctggaccagc cgtgcaaadc tctagaag atg acg gtg 57  
 Met Thr Val  
 1  
 ttc ttt aaa acg ctt cga aat cac tgg aag aaa act aca gct ggg ctc 105  
 Phe Phe Lys Thr Leu Arg Asn His Trp Lys Lys Thr Thr Ala Gly Leu  
 5 10 15  
 tgc ctg ctg acc tgg gga ggc cat tgg ctc tat gga aaa cac tgt gat 153  
 Cys Leu Leu Thr Trp Gly Gly His Trp Leu Tyr Gly Lys His Cys Asp  
 20 25 30 35  
 aac ctc cta agg aga gca gcc tgt caa gaa gct cag gtg ttt ggc aat 201  
 Asn Leu Leu Arg Arg Ala Ala Cys Gln Glu Ala Gln Val Phe Gly Asn  
 40 45 50  
 caa ctc att cct ccc aat gca caa gtg aag nng gcc act gtt ttt ctc 249  
 Gln Leu Ile Pro Pro Asn Ala Gln Val Lys Xaa Ala Thr Val Phe Leu  
 55 60 65  
 aat cct gca gct tgc aaa gga aaa gcc agg act cta ttt gaa aaa aat 297  
 Asn Pro Ala Ala Cys Lys Gly Lys Ala Arg Thr Leu Phe Glu Lys Asn  
 70 75 80  
 gcg gc 302  
 Ala

<210> 1327  
 <211> 409  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 202..408

<400> 1327  
 aggcttgccg ggaaacttcc ttattattgt gacgccgaaa acggagaaac cccgggtccg 60  
 gcgagagggg ctgtgacagt cggagtccca agctgcgggt cggctgctgc cgagaactgc 120  
 aaggtgtgga atatttctgg cttctagtcc aatgccaaagt gtgtgacctg tggctamatg 180  
 attccctgaa agataagaac a atg tta tgt tgg gga tat tgg tct ctg ggc 231  
 Met Leu Cys Trp Gly Tyr Trp Ser Leu Gly  
 1 5 10  
 caa cct ggt atc agc acc aac ctg cag gga att gtg gct gag ccc cag 279  
 Gln Pro Gly Ile Ser Thr Asn Leu Gln Gly Ile Val Ala Glu Pro Gln  
 15 20 25  
 gtg tgt ggg ttc ata tct gac aga agt gtc aag gaa gtg gcc trt ggg 327  
 Val Cys Gly Phe Ile Ser Asp Arg Ser Val Lys Glu Val Ala Xaa Gly  
 30 35 40  
 gga aac cac tct gtg ttc ctg ctg gaa gat ggg gaa gtt tac aca tgt 375  
 Gly Asn His Ser Val Phe Leu Leu Glu Asp Gly Glu Val Tyr Thr Cys  
 45 50 55  
 ggt ttg aac acc aag ggg caa ctg ggc cat gag a 409  
 Gly Leu Asn Thr Lys Gly Gln Leu Gly His Glu  
 60 65

<210> 1328  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 206..418

<400> 1328  
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 cccctccgcc aaagcgcgca ctgagtgcga accccagagt caatccctgc ccggctccgc 120  
 ccccgcgccc gaatcccgcc cagccgggccc ctcaagccca gtcgggactc gagcctaggg 180  
 aggcgaggtt cccgcaccgg atagc atg ttt ttg gcc cag agg agc ctc tgc 232  
 Met Phe Leu Ala Gln Arg Ser Leu Cys  
 1 5  
 tct ctt agc ggt aga gca aaa ttc ctg aag aca att tct tct tcc aaa 280  
 Ser Leu Ser Gly Arg Ala Lys Phe Leu Lys Thr Ile Ser Ser Ser Lys  
 10 15 20 25  
 atc ctc gga ttc tct act tct gct aaa atg tca ctg aaa ttc aca aat 328  
 Ile Leu Gly Phe Ser Thr Ser Ala Lys Met Ser Leu Lys Phe Thr Asn  
 30 35 40  
 gca aaa cgg att gaa gga ctt gat agt aat gtg tgg att gaa ttt acc 376  
 Ala Lys Arg Ile Glu Gly Leu Asp Ser Asn Val Trp Ile Glu Phe Thr  
 45 50 55  
 aaa ttg gct gca gac cct tct gtt gtg aat ctt ggc caa ggc 418  
 Lys Leu Ala Ala Asp Pro Ser Val Val Asn Leu Gly Gln Gly

60

65

70

&lt;210&gt; 1329

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 210..581

&lt;400&gt; 1329

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cctccccctcc caaaaraaca cccctcatcc agtctcttcc agcctagaga tcctggccta      60
cccctccgcc aaagcgcgca ctgagtgcaa accccagagt caatccctgt cccgggtccg      120
ccccccgct ccgaatcccgc ccagccggg ccctcaagcc cagtcgggac tcgagcctag      180
ggaggcgagg ttcccgcacc ggatagaaa atg tca ctg aaa ttc aca aat gca      233
                               Met Ser Leu Lys Phe Thr Asn Ala
                               1           5
aaa cgg att gaa gga ctt gat agt aat gtg tgg att gaa ttt acc aaa      281
Lys Arg Ile Glu Gly Leu Asp Ser Asn Val Trp Ile Glu Phe Thr Lys
      10           15           20
ttg gct gca gac cct tct gtt gtg aat ctt ggc caa ggc ttt cca gat      329
Leu Ala Ala Asp Pro Ser Val Val Asn Leu Gly Gln Gly Phe Pro Asp
      25           30           35           40
ata tcc cct cct aca tat gta aaa gaa gaa tta tca aag att gca gca      377
Ile Ser Pro Pro Thr Tyr Val Lys Glu Glu Leu Ser Lys Ile Ala Ala
           45           50           55
atc gat agc ctg aat cag tat aca cga ggc ttt ggc cat cca tca ctt      425
Ile Asp Ser Leu Asn Gln Tyr Thr Arg Gly Phe Gly His Pro Ser Leu
           60           65           70
gtg aaa gct ctg tcc tat ctg tat gaa aag ctt tat caa aag caa att      473
Val Lys Ala Leu Ser Tyr Leu Tyr Glu Lys Leu Tyr Gln Lys Gln Ile
           75           80           85
gat tca aat aaa gaa atc ctt gtg aca gta gga gca tat gga tct ctt      521
Asp Ser Asn Lys Glu Ile Leu Val Thr Val Gly Ala Tyr Gly Ser Leu
           90           95           100
ttt aac acc att caa gca tta att gat gag gga gat gaa gtc ata cta      569
Phe Asn Thr Ile Gln Ala Leu Ile Asp Glu Gly Asp Glu Val Ile Leu
      105           110           115           120
ata gtg cct ttc
Ile Val Pro Phe

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&lt;210&gt; 1330

&lt;211&gt; 268

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 114..266

&lt;400&gt; 1330

atggtagcac cgccgagagt aaaggagggg tgggtgctaga cgtttcgggc agagctcggc 60  
 cgctgcggag gacaaggaac tctccctctc ccactagtct gacttcttcc aaa atg 116  
 Met  
 1  
 agc ggc ctg gat ggg ggc aac aag ctc cct ctc gcc caa acc ggc ggc 164  
 Ser Gly Leu Asp Gly Gly Asn Lys Leu Pro Leu Ala Gln Thr Gly Gly  
 5 10 15  
 ctg gct gct ccc gac cat gcc tca gga gat ccg gac cta gac cag tgc 212  
 Leu Ala Ala Pro Asp His Ala Ser Gly Asp Pro Asp Leu Asp Gln Cys  
 20 25 30  
 caa ggg ctc cgt gaa gaa acc gag gcg aca cag gtg atg gcg aac aca 260  
 Gln Gly Leu Arg Glu Glu Thr Glu Ala Thr Gln Val Met Ala Asn Thr  
 35 40 45  
 ggt ggg gg 268  
 Gly Gly  
 50

<210> 1331  
 <211> 513  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 152..511

<400> 1331  
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 agctccggcc tgccagttag cttctaccat c atg gac cta ttg ttc ggg cgc 172  
 Met Asp Leu Leu Phe Gly Arg  
 1 5  
 cgg aag acg cca gag gag cta ctg cgg cag aac cag agg gcc ctg aac 220  
 Arg Lys Thr Pro Glu Glu Leu Leu Arg Gln Asn Gln Arg Ala Leu Asn  
 10 15 20  
 cgt gcc atg cgg gag ctg gac cgc gag cga cag aaa cta gag acc cag 268  
 Arg Ala Met Arg Glu Leu Asp Arg Glu Arg Gln Lys Leu Glu Thr Gln  
 25 30 35  
 gag aag aaa atc att gca gac att aag aag atg gcc aag caa ggc cag 316  
 Glu Lys Lys Ile Ile Ala Asp Ile Lys Lys Met Ala Lys Gln Gly Gln  
 40 45 50 55  
 atg gat gct gtt cgc atc atg gca aaa gac ttg gtg cgc acc cgg cgc 364  
 Met Asp Ala Val Arg Ile Met Ala Lys Asp Leu Val Arg Thr Arg Arg  
 60 65 70  
 tat gtg cgc aag ttt gta ttg atg cgg gcc aac atc cag gct gtg tnc 412  
 Tyr Val Arg Lys Phe Val Leu Met Arg Ala Asn Ile Gln Ala Val Xaa  
 75 80 85  
 ctc aag atc cag aca ctc aag tcc aac aac tcg atg gca caa gcc atg 460  
 Leu Lys Ile Gln Thr Leu Lys Ser Asn Asn Ser Met Ala Gln Ala Met  
 90 95 100  
 aag ggt gtc acc aag gcc atg ggc acc atg aac aga cag ctg aag ttg 508  
 Lys Gly Val Thr Lys Ala Met Gly Thr Met Asn Arg Gln Leu Lys Leu  
 105 110 115

ccc ag  
Pro  
120

513

<210> 1332  
<211> 636  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 275..634

<400> 1332

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agctccgggtg	agtggccct	gctggaccgt	ggatcccggg	cgggcgtgcg	ggcggcagcg	180
tacgaggcct	tctactgcc	cgggtgtccg	gwgccmrct	tctccctggg	accctgtcgt	240
caacatcgag	gcctgccast	gagcttctac	catc atg gac cta ttg ttc ggg cgc			295

Met Asp Leu Leu Phe Gly Arg

cgg aag acg cca gag gag cta ctg cgg cag aac cag agg gcc ctg aac	343
Arg Lys Thr Pro Glu Glu Leu Leu Arg Gln Asn Gln Arg Ala Leu Asn	
10 15 20	
cgt gcc atg cgg gag ctg nac cgc gag cga cas aaa cta gag acc cag	391
Arg Ala Met Arg Glu Leu Xaa Arg Glu Arg Xaa Lys Leu Glu Thr Gln	
25 30 35	
gag aag aaa atc att gca gac att aag aag atg gcc aag caa ggc cag	439
Glu Lys Lys Ile Ile Ala Asp Ile Lys Lys Met Ala Lys Gln Gly Gln	
40 45 50 55	
atg gat gct gtt cgc atc atg gca aaa gac ttg gtg cgc acc cgg cgc	487
Met Asp Ala Val Arg Ile Met Ala Lys Asp Leu Val Arg Thr Arg Arg	
60 65 70	
tat gtg cgc aag ttt gta ttg atg cgg gcc aac atc cag gct gtg tnc	535
Tyr Val Arg Lys Phe Val Leu Met Arg Ala Asn Ile Gln Ala Val Xaa	
75 80 85	
ctc aag atc cag aca ctc aag tcc aac aac tcg atg gca caa gcc atg	583
Leu Lys Ile Gln Thr Leu Lys Ser Asn Asn Ser Met Ala Gln Ala Met	
90 95 100	
aag ggt gtc acc aag gcc atg ggc acc atg aac aga cag ctg aag ttg	631
Lys Gly Val Thr Lys Ala Met Gly Thr Met Asn Arg Gln Leu Lys Leu	
105 110 115	

ccc ag  
Pro  
120

636

<210> 1333  
<211> 721  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

<222> 360..719

<400> 1333

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gcaagtcggg gatcccagaa agagaagcgt gacccggaag cggaaacggg tgtccgtccs 120  
akctccggtg agtggccctt ggaccgtgga tccygggagg gcgtgcgggc ggcagcgta 180  
gaggccttct actcgcccggtgtgtccggtg cctcgcttct ccttgggacc ctgtcgta 240  
catcgaggtc tccaacacca ccttgccttg gtgcccgggc cactgactgt cctcggtg 300  
tagtgcgacc gaatctccat catcccgctc tcagtgcctg ccagtgcgtt tctaccatc 359  
atg gac cta ttg ttc ggg cgc cgg aag acg cca gag gag cta ctg cgg 407  
Met Asp Leu Leu Phe Gly Arg Arg Lys Thr Pro Glu Glu Leu Leu Arg  
1 5 10 15  
cag aac cag agg gcc ctg aac cgt gcc atg cgg gan stg gac cgc gag 455  
Gln Asn Gln Arg Ala Leu Asn Arg Ala Met Arg Xaa Xaa Asp Arg Glu  
20 25 30  
cga cag aaa cta gag acc cag gag aag aaa atc att gca gac att aag 503  
Arg Gln Lys Leu Glu Thr Gln Glu Lys Lys Ile Ile Ala Asp Ile Lys  
35 40 45  
aag atg gcc aag caa ggc cag atg gat gct gtt cgc atc atg gca aaa 551  
Lys Met Ala Lys Gln Gly Gln Met Asp Ala Val Arg Ile Met Ala Lys  
50 55 60  
gac ttg gtg cgc acc cgg cgc tat gtg cgc aag ttt gta ttg atg cgg 599  
Asp Leu Val Arg Thr Arg Arg Tyr Val Arg Lys Phe Val Leu Met Arg  
65 70 75 80  
gcc aac atc cag gct gtg tnc ctc aag atc cag aca ctc aag tcc aac 647  
Ala Asn Ile Gln Ala Val Xaa Leu Lys Ile Gln Thr Leu Lys Ser Asn  
85 90 95  
aac tcg atg gca caa gcc atg aag ggt gtc acc aag gcc atg ggc acc 695  
Asn Ser Met Ala Gln Ala Met Lys Gly Val Thr Lys Ala Met Gly Thr  
100 105 110  
atg aac aga cag ctg aag ttg ccc ag 721  
Met Asn Arg Gln Leu Lys Leu Pro  
115 120

<210> 1334

<211> 437

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 111..437

<400> 1334

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gggggcgacg cggctgaggg cttctcgtcg gggtcggggc tgcagccgtc atg ccg 116  
Met Pro  
1  
ggg ata gtg gag ctg ccc act cta gag gag ctg aaa gta gat gag gtg 164  
Gly Ile Val Glu Leu Pro Thr Leu Glu Glu Leu Lys Val Asp Glu Val  
5 10 15  
aaa att agt tct gct gtg ctt aaa gct gcg gcc cat cac tat gga gct 212

Lys	Ile	Ser	Ser	Ala	Val	Leu	Lys	Ala	Ala	Ala	His	His	Tyr	Gly	Ala		
20						25					30						
caa	tgt	gat	aag	ccc	aac	aag	gaa	ttt	atg	ctc	tgc	cgc	tgg	gaa	gag		260
Gln	Cys	Asp	Lys	Pro	Asn	Lys	Glu	Phe	Met	Leu	Cys	Arg	Trp	Glu	Glu		
35					40					45				50			
aaa	gat	ccg	agg	cgg	tgt	tta	gag	gaa	ggc	aaa	ctg	gtc	aac	aag	tgt		308
Lys	Asp	Pro	Arg	Arg	Cys	Leu	Glu	Glu	Gly	Lys	Leu	Val	Asn	Lys	Cys		
				55					60				65				
gct	ttg	gac	ttc	ttt	agg	cag	ata	aaa	cgt	cac	tgt	gca	gag	cct	ttt		356
Ala	Leu	Asp	Phe	Phe	Arg	Gln	Ile	Lys	Arg	His	Cys	Ala	Glu	Pro	Phe		
			70					75				80					
aca	gaa	tat	tgg	act	tgc	att	gat	tat	act	ggc	cag	cag	tta	ttt	cgt		404
Thr	Glu	Tyr	Trp	Thr	Cys	Ile	Asp	Tyr	Thr	Gly	Gln	Gln	Leu	Phe	Arg		
		85				90					95						
cac	tgt	cgc	aaa	cag	cag	gca	aag	ttt	gac	gag							437
His	Cys	Arg	Lys	Gln	Gln	Ala	Lys	Phe	Asp	Glu							
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									Met	Ala	Asp	Lys					
									1								
gtc	ctg	aag	gag	aag	aga	aag	ctg	ttt	atc	cat	tcc	atg	ggt	gaa	ggt		104
Val	Leu	Lys	Glu	Lys	Arg	Lys	Leu	Phe	Ile	His	Ser	Met	Gly	Glu	Gly		
5					10					15				20			
aca	ata	aat	ggc	tta	ctg	gat	gaa	tta	tta	cag	aca	agg	gtg	ctg	aac		152
Thr	Ile	Asn	Gly	Leu	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Arg	Val	Leu	Asn		
				25					30				35				
cag	gaa	gag	atg	gag	aaa	gta	aaa	cgt	gaa	aat	gct	aca	ggt	atg	gat		200
Gln	Glu	Glu	Met	Glu	Lys	Val	Lys	Arg	Glu	Asn	Ala	Thr	Val	Met	Asp		
			40					45				50					
aag	acc	cga	gct	ttg	att	gac	tcc	ggt	att	ccg	aaa	ggg	gca	cag	gca		248
Lys	Thr	Arg	Ala	Leu	Ile	Asp	Ser	Val	Ile	Pro	Lys	Gly	Ala	Gln	Ala		
		55				60						65					
tgc	caa	att	tgc	atc	aca	tac	att	tgt	gaa	gaa	gac	agt	tac	ctg	gca		296
Cys	Gln	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp	Ser	Tyr	Leu	Ala		
		70				75					80						
gag	acg	ctg	gga	ctc	tca	gca	gct	ctt	cag	gca	gtg	cag	gac	aac	cca		344
Glu	Thr	Leu	Gly	Leu	Ser	Ala	Ala	Leu	Gln	Ala	Val	Gln	Asp	Asn	Pro		
		85			90				95						100		
gct	atg	ccc	aca	tgc	tca												362
Ala	Met	Pro	Thr	Cys	Ser												
					105												

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 <212> DNA  
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<220>  
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 caagggccca ttgttggaag atg gag cgc tct ctc agg cag tct ctg ctg gag 173  
 Met Glu Arg Ser Leu Arg Gln Ser Leu Leu Glu  
 1 5 10  
 cca gtt ccc ccg agt tta ccm aam ntc tgt gct tgg ctg gtg tct gaa 221  
 Pro Val Pro Pro Ser Leu Pro Xaa Xaa Cys Ala Trp Leu Val Ser Glu  
 15 20 25  
 tta aga gtg ctc tgt aaa cta gag gaa aac gtg caa gca act aac agt 269  
 Leu Arg Val Leu Cys Lys Leu Glu Glu Asn Val Gln Ala Thr Asn Ser  
 30 35 40  
 ccg agt gaa gct gaa gaa ttc cag ctt gag gtg agt ggg cta cta ggg 317  
 Pro Ser Glu Ala Glu Glu Phe Gln Leu Glu Val Ser Gly Leu Leu Gly  
 45 50 55  
 gag atg aac tgc ccg tat ctt tca ctg aca tct ggg gat gtg acc aag 365  
 Glu Met Asn Cys Pro Tyr Leu Ser Leu Thr Ser Gly Asp Val Thr Lys  
 60 65 70 75  
 cgc ctt ctc att cag aag aac tgc ctc ctc ttg ctc aca tac ctc atc 413  
 Arg Leu Leu Ile Gln Lys Asn Cys Leu Leu Leu Leu Thr Tyr Leu Ile  
 80 85 90  
 tca gaa cta gaa gct gcc aga atg gct ctg tgt gaa tgc tcc tcc aaa 461  
 Ser Glu Leu Glu Ala Ala Arg Met Ala Leu Cys Glu Cys Ser Ser Lys  
 95 100 105  
 aaa ag 466  
 Lys

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 <211> 391  
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<220>  
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 <222> 166..390

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 cgaggcgcac gagcctagcc tccccgcgcc ctgggcagtg tggcc atg gag aat cag 177  
 Met Glu Asn Gln  
 1  
 gtg ttg acg ccg cat gtc tac tgg gct cag cga cac cgc gag cta tat 225



Val	Leu	Thr	Pro	His	Val	Tyr	Trp	Ala	Gln	Arg	His	Arg	Glu	Leu	Tyr		
5					10					15					20		
ctg	cgc	gtg	gag	ctg	agt	gac	gta	cag	aac	cct	gcc	atc	agc	atc	act		273
Leu	Arg	Val	Glu	Leu	Ser	Asp	Val	Gln	Asn	Pro	Ala	Ile	Ser	Ile	Thr		
			25						30					35			
gaa	aac	gtg	ctg	cat	ttc	aaa	gct	caa	gga	cat	ggg	gcc	aaa	gga	gac		321
Glu	Asn	Val	Leu	His	Phe	Lys	Ala	Gln	Gly	His	Gly	Ala	Lys	Gly	Asp		
		40						45				50					
aat	gtc	tat	gaa	ttt	cac	ctg	gag	ttc	tta	gac	ctt	gtg	aaa	cca	gag		369
Asn	Val	Tyr	Glu	Phe	His	Leu	Glu	Phe	Leu	Asp	Leu	Val	Lys	Pro	Glu		
		55					60					65					
cct	gtt	tac	aaa	ctg	acc	cag	a										391
Pro	Val	Tyr	Lys	Leu	Thr	Gln											
		70				75											

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<220>  
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agc	gtg	gcc	cgt	atc	gtg	aag	gtg	cag	ctc	cct	gca	tat	ctg	aag	cgg		104
Ser	Val	Ala	Arg	Ile	Val	Lys	Val	Gln	Leu	Pro	Ala	Tyr	Leu	Lys	Arg		
5					10					15					20		
ctc	cca	gtc	cct	gaa	agc	att	acc	ggg	ttc	gct	agg	ctc	aca	gtt	tca		152
Leu	Pro	Val	Pro	Glu	Ser	Ile	Thr	Gly	Phe	Ala	Arg	Leu	Thr	Val	Ser		
			25					30					35				
gaa	tgg	ctt	cgg	tta	ttg	cct	ttc	ctt	ggg	gta	ctc	gca	ctt	ctt	ggc		200
Glu	Trp	Leu	Arg	Leu	Leu	Pro	Phe	Leu	Gly	Val	Leu	Ala	Leu	Leu	Gly		
		40					45					50					
tac	ctt	gca	gtt	cgt	cca	ttc	ctc	ccg	aag	aag	aaa	caa	cag	aag	gat		248
Tyr	Leu	Ala	Val	Arg	Pro	Phe	Leu	Pro	Lys	Lys	Lys	Gln	Gln	Lys	Asp		
		55				60						65					
agc	ttg	att	aat	ctt	aaa	ata	caa	aag	gaa	aat	ccg	aaa	gta	gtg	aat		296
Ser	Leu	Ile	Asn	Leu	Lys	Ile	Gln	Lys	Glu	Asn	Pro	Lys	Val	Val	Asn		
		70			75					80							
gaa	ata	aac	att	gaa	gat	ttg	tgt	ctt	act	aaa	gca	gct	tat	tgt	agg		344
Glu	Ile	Asn	Ile	Glu	Asp	Leu	Cys	Leu	Thr	Lys	Ala	Ala	Tyr	Cys	Arg		
85				90					95					100			
tgt	tgg	cgt	tct	aaa	acg	ttt	cct	gcc	tgc	gat	ggg	tca	cat	aat	aaa		392
Cys	Trp	Arg	Ser	Lys	Thr	Phe	Pro	Ala	Cys	Asp	Gly	Ser	His	Asn	Lys		
			105					110					115				
cac	aat	gaa	ttg	aca	gga	gat	aat	gt									418
His	Asn	Glu	Leu	Thr	Gly	Asp	Asn										
			120														

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 75..353

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 tcattcccgt tggt atg gag ggc cac atc tgc cag agc ctg gag tct gcg 110  
                   Met Glu Gly His Ile Cys Gln Ser Leu Glu Ser Ala  
                   1                  5                  10  
 aag gcc ggg acc cgg ttc ccc ggc cca cag tgg ggg tgt gca aac ccg 158  
 Lys Ala Gln Thr Arg Phe Pro Gly Pro Gln Trp Gly Cys Ala Asn Pro  
                   15                  20                  25  
 aga gaa ctg ggc tgg agt gca atg gcg cga tct cgg ctc act gca acc 206  
 Arg Glu Leu Gly Trp Ser Ala Met Ala Arg Ser Arg Leu Thr Ala Thr  
                   30                  35                  40  
 tct gtc tcc cag gtt cag gaa aat ggc ttt gta aag aag ctt gag cct 254  
 Ser Val Ser Gln Val Gln Glu Asn Gly Phe Val Lys Lys Leu Glu Pro  
                   45                  50                  55                  60  
 aaa tct ggc tgg atg act ttt cta gaa gtt aca gga aag atc tgt gaa 302  
 Lys Ser Gly Trp Met Thr Phe Leu Glu Val Thr Gly Lys Ile Cys Glu  
                   65                  70                  75  
 atg ctc ttc tgt cct gaa gca ata ctg ttg acc aga aag gac act cca 350  
 Met Leu Phe Cys Pro Glu Ala Ile Leu Leu Thr Arg Lys Asp Thr Pro  
                   80                  85                  90  
 tat  
 Tyr 353

<210> 1340  
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<220>  
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 <222> 131..532

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 tactttctgg tcagagagaa gcaataatta ttattaacat ttattaacga tcaataaaac 120  
 tgattgcatt atg gcc agc act att aag gaa gcc tta tca gtt gtg agt 169  
                   Met Ala Ser Thr Ile Lys Glu Ala Leu Ser Val Val Ser  
                   1                  5                  10  
 gag gac cag tcg ttg ttt gag tgt gcc tac gga acg cca cac ctg gct 217  
 Glu Asp Gln Ser Leu Phe Glu Cys Ala Tyr Gly Thr Pro His Leu Ala  
                   15                  20                  25  
 aag aca gag atg acc gcg tcc tcc tcc agc gac tat gga cag act tcc 265  
 Lys Thr Glu Met Thr Ala Ser Ser Ser Ser Asp Tyr Gly Gln Thr Ser

30	35	40	45	
aag atg agc cca cgc gtc cct cag cag gat tgg ctg tct caa ccc cca				313
Lys Met Ser Pro Arg Val Pro Gln Gln Asp Trp Leu Ser Gln Pro Pro				
	50	55	60	
gcc agg gtc acc atc aaa atg gaa tgt aac cct agc cag gtg aat ggc				361
Ala Arg Val Thr Ile Lys Met Glu Cys Asn Pro Ser Gln Val Asn Gly				
	65	70	75	
tca agg aac tct cct gat gaa tgc agt gtg gcc aaa ggc ggg aag atg				409
Ser Arg Asn Ser Pro Asp Glu Cys Ser Val Ala Lys Gly Gly Lys Met				
	80	85	90	
gtg ggc agc cca gac acc gtt ggg atg aac tac ggc agt atn kat gga				457
Val Gly Ser Pro Asp Thr Val Gly Met Asn Tyr Gly Ser Xaa Xaa Gly				
	95	100	105	
aga gaa gca cat gcc acc ccc aaa cat gac cac gaa cga gcg cag agt				505
Arg Glu Ala His Ala Thr Pro Lys His Asp His Glu Arg Ala Gln Ser				
110	115	120	125	
tat cgt gcc agc aga tcc tac gct atg g				533
Tyr Arg Ala Ser Arg Ser Tyr Ala Met				
	130			

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<220>  
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 <222> 49..495

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	Met Ala Ala
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Gly Thr Leu Tyr Thr Tyr Pro Glu Asn Trp Arg Ala Phe Lys Ala Leu	
5	10
atc gct gct cag tac agc ggg gct cag gtc cgc gtg ctc tcc gca cca	153
Ile Ala Ala Gln Tyr Ser Gly Ala Gln Val Arg Val Leu Ser Ala Pro	
20	25
ccc cac ttc cat ttt ggc caa acc aac cgc acc cct gaa ttt ctc cgc	201
Pro His Phe His Phe Gly Gln Thr Asn Arg Thr Pro Glu Phe Leu Arg	
	40
aaa ttt cct gcc ggc aag gtc cca gca ttt gag ggt gat gat gga ttc	249
Lys Phe Pro Ala Gly Lys Val Pro Ala Phe Glu Gly Asp Asp Gly Phe	
	55
tgt gtg ttt gag agc aac gcc att gcc tac tat gtg agc aat gag gag	297
Cys Val Phe Glu Ser Asn Ala Ile Ala Tyr Tyr Val Ser Asn Glu Glu	
	70
ctg cgg gga agt act cca gag gca gca gcc cag gtg gtg cag tgg gtg	345
Leu Arg Gly Ser Thr Pro Glu Ala Ala Ala Gln Val Val Gln Trp Val	
	85
agc ttt gct gat tcc gat ata gtg ccc cca gcc agt acc tgg gtg ttc	393
Ser Phe Ala Asp Ser Asp Ile Val Pro Pro Ala Ser Thr Trp Val Phe	

100	105	110	115	
ccc acc ttg ggc atc atg cac cac aac aaa cag gcc act gag aat gca				441
Pro Thr Leu Gly Ile Met His His Asn Lys Gln Ala Thr Glu Asn Ala				
	120	125	130	
aag gag gaa gtg agg cga att ctg ggg gct gct gga tgc tta ctt gan				489
Lys Glu Glu Val Arg Arg Ile Leu Gly Ala Ala Gly Cys Leu Leu Xaa				
	135	140	145	
gac gag				495
Asp Glu				

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 <211> 578  
 <212> DNA  
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tgagttgcaa gcctaattgct cacctgcaga gacagaattc ctgagtgaac gaacagagca	180
gctcctcttc catctccaga aatgacctcc accttcaacc cccgagaatg taaactgtcc	240
aagcaagaag ggcaaaacta tggcttcttc ctgcgaantt gagaanggmc accgagggcc	300
acctggtccg ggtggttgag aagtgtagcc cagcagagaa ggctggcctt caagatggag	360
acagagttct taggatcaat ggtgtctttg tggacaaaga agaacat atg cag gtt	416
	Met Gln Val
	1
gtg gat ctg gtc aga aag agt ggg aat tca gtg act tta cta gtt ctg	464
Val Asp Leu Val Arg Lys Ser Gly Asn Ser Val Thr Leu Leu Val Leu	
5 10 15	
gat ggg gat tcc tat gag aaa gca gtg aaa aca cgg gtg gac ttg aaa	512
Asp Gly Asp Ser Tyr Glu Lys Ala Val Lys Thr Arg Val Asp Leu Lys	
20 25 30 35	
gag ttg ggt caa agt cag aag gag caa ggt ttg agt gat aat ata ctt	560
Glu Leu Gly Gln Ser Gln Lys Glu Gln Gly Leu Ser Asp Asn Ile Leu	
40 45 50	
tcc cct gtg atg aat gga	578
Ser Pro Val Met Asn Gly	
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<210> 1343  
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<220>  
 <221> CDS  
 <222> 171..509

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ccctccgctt cctctcctag gcgacgagac ccagtggtta gaagttcacc atg tct 176
                                     Met Ser
                                     1
att ctc aag atc cat gcc agg gag atc ttt gac tct cgc ggg aat ccc 224
Ile Leu Lys Ile His Ala Arg Glu Ile Phe Asp Ser Arg Gly Asn Pro
      5              10              15
act gtt gag gtt gat ctc ttc acc tca aaa ggt ctc ttc aga gct gct 272
Thr Val Glu Val Asp Leu Phe Thr Ser Lys Gly Leu Phe Arg Ala Ala
      20              25              30
gtg ccc agt ggt gct tca act ggt atc tat gag gcc cta gag ctc cgg 320
Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu Leu Arg
      35              40              45              50
gac aat gat aag act cgc tat atg ggg aag ggt gtc tca aag gct gtt 368
Asp Asn Asp Lys Thr Arg Tyr Met Gly Lys Gly Val Ser Lys Ala Val
      55              60              65
gag cac atc aat aaa act att gcg cct gcc ctg gtt agc aag aaa ctg 416
Glu His Ile Asn Lys Thr Ile Ala Pro Ala Leu Val Ser Lys Lys Leu
      70              75              80
aac gtc aca gaa caa gag aag att gac aaa ctg atg atc gag atg gat 464
Asn Val Thr Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met Asp
      85              90              95
gga aca gaa aat aaa tct aag ttt ggt gcg acg cca ttc tgg ggg tg 511
Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Thr Pro Phe Trp Gly
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 <212> DNA  
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<220>  
 <221> CDS  
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cttcaccctc cagtagtctc gtgggtcccc gagcgccass cgggaaccgg gaaaaggaaa 180
ccgtgtttgt tacgtaagat tcaggaaacg aaaccaggag ccgcgggtgt tggcgcaaag 240
gttactccca gacccttttc cggctgactt ctgagaaggt tgcgcascag ctgtgcccg 300
cagtctagag gcgcagaaga ggaagccatc gcctggcccc ggctctctgg acctgtctc 360
gctcgggagc ggaaacagcg gcagccagag aactgtttta atcatggaca aacaaaactc 420
acagatga atg ctt ctc acc cgg aaa caa act tgc cag ttg ggt atc ctc 470
      Met Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu
      1              5              10
ctc agt atc cac cga cag cat tcc aag caa gaa acc tcc ctg cgg gtc 518
Leu Ser Ile His Arg Gln His Ser Lys Gln Glu Thr Ser Leu Arg Val
      15              20              25              30
ccg gat ctc atc cag atg ttt gca act gwa gra tat gag cta gat aag 566
Pro Asp Leu Ile Gln Met Phe Ala Thr Xaa Xaa Tyr Glu Leu Asp Lys
      35              40              45

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 <211> 446  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 102..446

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 ggagactcga ttgttggtga cagcgaaaga acgataacaa a atg ccg gag cga gat 116  
 Met Pro Glu Arg Asp  
 1 5  
 agt gag ccg ttc tcc aac cct ttg gcc ccc gat ggc cac gat gtg gat 164  
 Ser Glu Pro Phe Ser Asn Pro Leu Ala Pro Asp Gly His Asp Val Asp  
 10 15 20  
 gat cct cac tcc ttc cac caa tca aaa ctc acc aat gaa gac ttc agg 212  
 Asp Pro His Ser Phe His Gln Ser Lys Leu Thr Asn Glu Asp Phe Arg  
 25 30 35  
 aaa ctt ctc atg acc ccc agg gct gca cct acc tct gca cca cct tct 260  
 Lys Leu Leu Met Thr Pro Arg Ala Ala Pro Thr Ser Ala Pro Pro Ser  
 40 45 50  
 aag tca cgt cac cat gag atg cca agg gag tac aat gag gat gaa gac 308  
 Lys Ser Arg His His Glu Met Pro Arg Glu Tyr Asn Glu Asp Glu Asp  
 55 60 65  
 cca gct gca cga agg agg aaa aag aaa agt tat tat gcc aag cta cgc 356  
 Pro Ala Ala Arg Arg Arg Lys Lys Lys Ser Tyr Tyr Ala Lys Leu Arg  
 70 75 80 85  
 caa caa gaa att gag aga gag aga gag cta gca gag aag tac cgg gat 404  
 Gln Gln Glu Ile Glu Arg Glu Arg Glu Leu Ala Glu Lys Tyr Arg Asp  
 90 95 100  
 cgt gcc aag gaa cgg aga gat gga gtg aac aaa gat tat gaa 446  
 Arg Ala Lys Glu Arg Arg Asp Gly Val Asn Lys Asp Tyr Glu  
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 <212> DNA  
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gtggagcaag tggagagtgg gcagtttccc ggagtgtgct ggg atg ata cag cta	175
Met Ile Gln Leu	
1	
aga cca tgt tcc gga ttc cct gga aac atg cag gcc tgg gca ata ttt	223
Arg Pro Cys Ser Gly Phe Pro Gly Asn Met Gln Ala Trp Ala Ile Phe	
5 10 15 20	
aag gga aag tat aag gag ggg gac aca gga ggt cca gct gtc tgg aag	271
Lys Gly Lys Tyr Lys Glu Gly Asp Thr Gly Gly Pro Ala Val Trp Lys	
25 30 35	
act cgc ctg cgc tgt gca ctc aac aag agt tct gaa ttt aag gag gtt	319
Thr Arg Leu Arg Cys Ala Leu Asn Lys Ser Ser Glu Phe Lys Glu Val	
40 45 50	
cct gag agg ggc cgc atg gat gtt gct gag ccc tac aag gtg tat cag	367
Pro Glu Arg Gly Arg Met Asp Val Ala Glu Pro Tyr Lys Val Tyr Gln	
55 60 65	
ttg ctg cca mca gga atc gtc tct kgc cag cca ggg act cag aaa gtm	415
Leu Leu Pro Xaa Gly Ile Val Ser Xaa Gln Pro Gly Thr Gln Lys Val	
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cat caa agc gac asa cag ttc	436
His Gln Ser Asp Xaa Gln Phe	
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<213> Homo sapiens	
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cagcaactca gg atg gca tca ggc agg gca cgc tgc acc cga aaa ctc cgg	111
Met Ala Ser Gly Arg Ala Arg Cys Thr Arg Lys Leu Arg	
1 5 10	
aac tgg gtg gtg gag caa gtg gag agt ggg cag ttt ccc gga gtg tgc	159
Asn Trp Val Val Glu Gln Val Glu Ser Gly Gln Phe Pro Gly Val Cys	
15 20 25	
tgg gat gat aca gct aag acc atg ttc cgg att ccc tgg aaa cat gca	207
Trp Asp Asp Thr Ala Lys Thr Met Phe Arg Ile Pro Trp Lys His Ala	
30 35 40 45	
ggc aag cag gac ttc cgg gag gac cag gat gct gcc ttc ttc aag gcc	255
Gly Lys Gln Asp Phe Arg Glu Asp Gln Asp Ala Ala Phe Phe Lys Ala	
50 55 60	
tgg gca ata ttt aag gga aag tat aag gag ggg gac aca gga ggt cca	303
Trp Ala Ile Phe Lys Gly Lys Tyr Lys Glu Gly Asp Thr Gly Gly Pro	
65 70 75	
gct gtc tgg aag act cgc ctg cgc tgt gca ctc aac aag agt tct gaa	351
Ala Val Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys Ser Ser Glu	
80 85 90	
ttt aag gag gtt cct gag agg ggc cgc atg gat gtt gct gag ccc tac	399
Phe Lys Glu Val Pro Glu Arg Gly Arg Met Asp Val Ala Glu Pro Tyr	

95	100	105	
aag gtg tat cag ttg ctg cca mca gga atc gtc tct kgc cag cca ggg			447
Lys Val Tyr Gln Leu Leu Pro Xaa Gly Ile Val Ser Xaa Gln Pro Gly			
110	115	120	125
act cag aaa gtm cat caa agc gac asa cag ttc			480
Thr Gln Lys Val His Gln Ser Asp Xaa Gln Phe			
130	135		

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 <212> DNA  
 <213> Homo sapiens

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cgtaccgtct gtgtggccgg tgggggacct gcggtcggag tgggagggcc agtctgcacc	120
caagaggtgg aagaggacgg gctttaggct ggaagcgct tagaggagcc attttccag	180
g atg cct ggt ttg ctt tta tgt gaa ccg aca gag ctt tac aac atc ctg	229
Met Pro Gly Leu Leu Leu Cys Glu Pro Thr Glu Leu Tyr Asn Ile Leu	
1 5 10 15	
aat cag gcc aca aaa ctc tcc aga tta aca gac ccc aac tat ctc tgt	277
Asn Gln Ala Thr Lys Leu Ser Arg Leu Thr Asp Pro Asn Tyr Leu Cys	
20 25 30	
tta ttg gat gtc cgt tcc aaa tgg gag tat gac gaa agc cat gtg atc	325
Leu Leu Asp Val Arg Ser Lys Trp Glu Tyr Asp Glu Ser His Val Ile	
35 40 45	
act gcc ctt cga gtg aag aag gta cat ggg cag cgt cag gat ctg ggg	373
Thr Ala Leu Arg Val Lys Lys Val His Gly Gln Arg Gln Asp Leu Gly	
50 55 60	
cag gct ggc tac ctt gca gtg ggg tgg gga aga gtg gga agt ttc acc	421
Gln Ala Gly Tyr Leu Ala Val Gly Trp Gly Arg Val Gly Ser Phe Thr	
65 70 75 80	
ctc aat cca gcg ggc agc aga agc agg act gtt ttc tat gtg ccc acc	469
Leu Asn Pro Ala Gly Ser Arg Ser Arg Thr Val Phe Tyr Val Pro Thr	
85 90 95	
gtg gtg gtc ttc cac acc tct cac cct cac aca ttt tct cag gtg tcc	517
Val Val Val Phe His Thr Ser His Pro His Thr Phe Ser Gln Val Ser	
100 105 110	
tcc cat ccc cca aga atg gtc aac aac tcc att ata caa a	557
Ser His Pro Pro Arg Met Val Asn Asn Ser Ile Ile Gln	
115 120 125	

<210> 1349  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS



<222> 87..479

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tttgtccttg atccttggtt aaggaa atg acc aac cag tac ggt att ctc ttc 113  
Met Thr Asn Gln Tyr Gly Ile Leu Phe  
1 5  
aaa caa gag caa gcc cat gat gat gcc att tgg tca gtt gct tgg ggg 161  
Lys Gln Glu Gln Ala His Asp Asp Ala Ile Trp Ser Val Ala Trp Gly  
10 15 20 25  
aca aac aag aag gaa aac tct gag aca gtg gtc aca ggs tcc cta gat 209  
Thr Asn Lys Lys Glu Asn Ser Glu Thr Val Val Thr Gly Ser Leu Asp  
30 35 40  
gac ctg gtg aag gtc tgg aaa tgg cgt gat gag agg ctg gac cta car 257  
Asp Leu Val Lys Val Trp Lys Trp Arg Asp Glu Arg Leu Asp Leu Gln  
45 50 55  
tgg agt ctg gag gga cat cag ctg gga gtg gtg tct gtg gac atc agc 305  
Trp Ser Leu Glu Gly His Gln Leu Gly Val Val Ser Val Asp Ile Ser  
60 65 70  
cac acc ctg ccc att gct gca tcc agc tct ctt gat gct cat att cgt 353  
His Thr Leu Pro Ile Ala Ala Ser Ser Ser Leu Asp Ala His Ile Arg  
75 80 85  
ctt tgg gac ttg gaa aat ggc aaa cag ata aag tcc ata gat gca gga 401  
Leu Trp Asp Leu Glu Asn Gly Lys Gln Ile Lys Ser Ile Asp Ala Gly  
90 95 100 105  
cct gtg gat gcc tgg act twg gcc ttt tct cct gat tcc cag tat ctg 449  
Pro Val Asp Ala Trp Thr Xaa Ala Phe Ser Pro Asp Ser Gln Tyr Leu  
110 115 120  
gcc aca gga act cat gtc ggg aaa gtg aac a 480  
Ala Thr Gly Thr His Val Gly Lys Val Asn  
125 130

<210> 1350

<211> 615

<212> DNA

<213> Homo sapiens

<220>

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<222> 97..615

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aggctctgag gccacgcag ggccatagggt ggggaag atg gca ggt ggg ggc ggc 114  
Met Ala Gly Gly Gly Gly  
1 5  
gac ctg agc acc agg atg ttc acg gaa gac cag ggt gta gat gac agg 162  
Asp Leu Ser Thr Arg Met Phe Thr Glu Asp Gln Gly Val Asp Asp Arg  
10 15 20  
ctg ctc tat gac att gta ttc aag cac ttc aaa aga aat aag gtg gag 210  
Leu Leu Tyr Asp Ile Val Phe Lys His Phe Lys Arg Asn Lys Val Glu  
25 30 35

att tca aat gca ata aaa aag aca ttt cca ttc ctc gag ggc ctc cgt	258
Ile Ser Asn Ala Ile Lys Lys Thr Phe Pro Phe Leu Glu Gly Leu Arg	
40 45 50	
gat cgt gat ctc atc aca aat aaa atg ttt gaa gat tct caa gat tct	306
Asp Arg Asp Leu Ile Thr Asn Lys Met Phe Glu Asp Ser Gln Asp Ser	
55 60 65 70	
tgt aga aac ctg gtc cct gta cag aga gtg gtg tac aat gtt ctt agt	354
Cys Arg Asn Leu Val Pro Val Gln Arg Val Val Tyr Asn Val Leu Ser	
75 80 85	
gaa ctg gag aag aca ttt aac ctg cca gtt ctg gaa gca ctg ttc agc	402
Glu Leu Glu Lys Thr Phe Asn Leu Pro Val Leu Glu Ala Leu Phe Ser	
90 95 100	
gat gtc aac atg cag gaa tac ccc gat tta att cac att tat aaa ggc	450
Asp Val Asn Met Gln Glu Tyr Pro Asp Leu Ile His Ile Tyr Lys Gly	
105 110 115	
ttt gaa aat gta atc cat gac aaa ttg cct ctc caa gaa agt gaa gaa	498
Phe Glu Asn Val Ile His Asp Lys Leu Pro Leu Gln Glu Ser Glu Glu	
120 125 130	
gaa gag agg gag gag agg tct ggc ctc caa cta agt ctt gaa caa gga	546
Glu Glu Arg Glu Glu Arg Ser Gly Leu Gln Leu Ser Leu Glu Gln Gly	
135 140 145 150	
act ggt gaa aac tct ttt cga agc ctg act tgg cca cct tcg ggt tcc	594
Thr Gly Glu Asn Ser Phe Arg Ser Leu Thr Trp Pro Pro Ser Gly Ser	
155 160 165	
cca tct cat gct ggt aca acc	615
Pro Ser His Ala Gly Thr Thr	
170	

<210> 1351  
 <211> 690  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 97..690

<400> 1351	
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aggctctgag gccacgcag ggcctagggg gggaag atg gca ggt ggg ggc ggc	114
Met Ala Gly Gly Gly Gly	
1 5	
gac ctg agc acc agg agg ctg aat gaa tgt att tca cca gta gca aat	162
Asp Leu Ser Thr Arg Arg Leu Asn Glu Cys Ile Ser Pro Val Ala Asn	
10 15 20	
gag atg aac cat ctt cct gca cac agc cac gat ttg caa agg atg ttc	210
Glu Met Asn His Leu Pro Ala His Ser His Asp Leu Gln Arg Met Phe	
25 30 35	
acg gaa gac cag ggt gta gat gac agg ctg ctc tat gac att gta ttc	258
Thr Glu Asp Gln Gly Val Asp Asp Arg Leu Leu Tyr Asp Ile Val Phe	
40 45 50	
aag cac ttc aaa aga aat aag gtg gag att tca aat gca ata aaa aag	306
Lys His Phe Lys Arg Asn Lys Val Glu Ile Ser Asn Ala Ile Lys Lys	

55	60	65	70	
aca ttt cca ttc ctc gag ggc ctc cgt gat cgt gat ctc atc aca aat				354
Thr Phe Pro Phe Leu Glu Gly Leu Arg Asp Arg Asp Leu Ile Thr Asn				
	75	80	85	
aaa atg ttt gaa gat tct caa gat tct tgt aga aac ctg gtc cct gta				402
Lys Met Phe Glu Asp Ser Gln Asp Ser Cys Arg Asn Leu Val Pro Val				
	90	95	100	
cag aga gtg gtg tac aat gtt ctt agt gaa ctg gag aag aca ttt aac				450
Gln Arg Val Val Tyr Asn Val Leu Ser Glu Leu Glu Lys Thr Phe Asn				
	105	110	115	
ctg cca gtt ctg gaa gca ctg ttc agc gat gtc aac atg cag gaa tac				498
Leu Pro Val Leu Glu Ala Leu Phe Ser Asp Val Asn Met Gln Glu Tyr				
	120	125	130	
ccc gat tta att cac att tat aaa ggc ttt gaa aat gta atc cat gac				546
Pro Asp Leu Ile His Ile Tyr Lys Gly Phe Glu Asn Val Ile His Asp				
	135	140	145	150
aaa ttg cct ctc caa gaa agt gaa gaa gaa gag agg gag gag agg tct				594
Lys Leu Pro Leu Gln Glu Ser Glu Glu Glu Arg Glu Glu Arg Ser				
	155	160	165	
ggc ctc caa cta agt ctt gaa caa gga act ggt gaa aac tct ttt cga				642
Gly Leu Gln Leu Ser Leu Glu Gln Gly Thr Gly Glu Asn Ser Phe Arg				
	170	175	180	
agc ctg act tgg cca cct tcg ggt tcc cca tct cat gct ggt aca acc				690
Ser Leu Thr Trp Pro Pro Ser Gly Ser Pro Ser His Ala Gly Thr Thr				
	185	190	195	

<210> 1352  
 <211> 485  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 253..483

<400> 1352	
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cttccttagt catcaggttc atcacttcga agcatagaag ctgtagactg acccgtcaa	120
cagaagggtc atttaagaca gtgctgatca ctcttaccat ggaatattag cttttgctgg	180
tgggaacatt agcttcttag tcaccaaata actgtatgtg ggataaaaact gaaccttgaa	240
ctgcctcata aa atg act tta tat ttt agg aca tgg gaa gaa cag aag aca	291
Met Thr Leu Tyr Phe Arg Thr Trp Glu Glu Gln Lys Thr	
1 5 10	
gag cat gct ctt tta agt ctg ata aca tgg ttt caa gcc cag ccc cca	339
Glu His Ala Leu Leu Ser Leu Ile Thr Trp Phe Gln Ala Gln Pro Pro	
15 20 25	
gcc ttt ctt acc aat caa gga ctc aga act gaa ggc aat tat ttc ttt	387
Ala Phe Leu Thr Asn Gln Gly Leu Arg Thr Glu Gly Asn Tyr Phe Phe	
30 35 40 45	
tgg tgg act tgg aat ctc cgt ttg tct aca ctg tcc tct tca cag tgg	435
Trp Trp Thr Trp Asn Leu Arg Leu Ser Thr Leu Ser Ser Ser Gln Trp	
50 55 60	
agt ctt ttt att tca gac cta cag att gtt ttg rra ttt gtt gtc aca	483

485

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tgc	tgc	ctg	atg	ctt	gct	ctg	tca	agg	cac	agc	cta	ttg	tct	cct	ttg			101
Ser	Ser	Leu	Met	Leu	Ala	Leu	Ser	Arg	His	Ser	Leu	Leu	Ser	Pro	Leu			
10					15					20					25			

gat tcc caa aag gac atg att gaa atc cct ttg cct cca tgg cag gag 197  
Asp Ser Gln Lys Asp Met Ile Glu Ile Pro Leu Pro Pro Trp Gln Glu  
45 50 55

agc aga aag agg gga atg ttg gaa aac tgc att ctt ctt agt ctt ttt 293  
 Ser Arg Lys Arg Gly Met Leu Glu Asn Cys Ile Leu Leu Ser Leu Phe  
 75 80 85

gac cgc ctg att aac gag cct agt aat gac tgr gat att tac tac tgg 389  
Asp Arg Leu Ile Asn Glu Pro Ser Asn Asp Xaa Asp Ile Tyr Tyr Trp  
110 115 120

gcc aca gaa gct aaa cca gcc cc  
Ala Thr Glu Ala Lys Pro Ala  
125

<220>  
<221> CDS  
<222> 31..390

914

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Met Ala Pro Gln Lys Asp Arg Lys
1 5
ccc aag agg tca acc tgg agg ttt aat ttg gac ctt act cat cca gta      102
Pro Lys Arg Ser Thr Trp Arg Phe Asn Leu Asp Leu Thr His Pro Val
10 15 20
gaa gat gga att ttt gat tct gga aat ttt gag caa ttt cta cgg gag      150
Glu Asp Gly Ile Phe Asp Ser Gly Asn Phe Glu Gln Phe Leu Arg Glu
25 30 35 40
aag gtt aaa gtc aat ggc aaa act gga aat ctc ggg aat gtt gtt cac      198
Lys Val Lys Val Asn Gly Lys Thr Gly Asn Leu Gly Asn Val Val His
45 50 55
att gaa cgc ttc aag aat aaa atc aca gtt gtt tct gag aaa cag ttc      246
Ile Glu Arg Phe Lys Asn Lys Ile Thr Val Val Ser Glu Lys Gln Phe
60 65 70
tct aaa agg tat ttg aaa tac ctt acc aag aaa tac ctt aag aag aac      294
Ser Lys Arg Tyr Leu Lys Tyr Leu Thr Lys Lys Tyr Leu Lys Lys Asn
75 80 85
aat ctt cgt gat tgg ctt cga gtg gtt gca tct gac aag gag acc tac      342
Asn Leu Arg Asp Trp Leu Arg Val Val Ala Ser Asp Lys Glu Thr Tyr
90 95 100
gaa ctt cgt tac ttc cag att agt caa gat gaa gat gaa tca gag tcg      390
Glu Leu Arg Tyr Phe Gln Ile Ser Gln Asp Glu Asp Glu Ser Glu Ser
105 110 115 120
ga
392

<210> 1355
<211> 416
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 140..415

<400> 1355
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gggaggtgga gtcgttgctg ttgctgtttg tgagcctgtg gcgcggcttc tgtgggccgg      120
aaccttaaag atagccgca atg gct gaa aat ggt gat aat gaa aag atg gct      172
Met Ala Glu Asn Gly Asp Asn Glu Lys Met Ala
1 5 10
gcc ctg gag gcc aaa atc tgt cat caa att gag tat tat ttt ggc gac      220
Ala Leu Glu Ala Lys Ile Cys His Gln Ile Glu Tyr Tyr Phe Gly Asp
15 20 25
ttc aat ttg cca cgg gac aag ttt cta aag gaa cag ata aaa ctg gat      268
Phe Asn Leu Pro Arg Asp Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp
30 35 40
gaa ggc tgg gta cct ttg gag ata atg ata aaa ttc aac agg ttg aac      316
Glu Gly Trp Val Pro Leu Glu Ile Met Ile Lys Phe Asn Arg Leu Asn
45 50 55
cgt cta aca aca gac ttt aat gta att gtg gaa gca ttg agc aaa tcc      364
Arg Leu Thr Thr Asp Phe Asn Val Ile Val Glu Ala Leu Ser Lys Ser
60 65 70 75

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aag gca gaa ctc atg gaa atc agt gaa gat aaa act aaa atc aga agg 412  
 Lys Ala Glu Leu Met Glu Ile Ser Glu Asp Lys Thr Lys Ile Arg Arg  
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tct c 416  
 Ser

<210> 1356  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<220>  
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                   Met Ala Ala Phe Ser Glu Met Gly Val Met Pro  
                   1                  5                  10  
 gag att gca caa gct gtg gaa gag atg gat tgg ctc ctc cca act gat 161  
 Glu Ile Ala Gln Ala Val Glu Glu Met Asp Trp Leu Leu Pro Thr Asp  
                   15                  20                  25  
 atc cag gct gaa tct atc cca ytg atc tta gga gga ggt gat gta ctt 209  
 Ile Gln Ala Glu Ser Ile Pro Leu Ile Leu Gly Gly Gly Asp Val Leu  
                   30                  35                  40  
 atg gct gca gaa aca gga agt ggc aaa act ggt gct ttt agt att cca 257  
 Met Ala Ala Glu Thr Gly Ser Gly Lys Thr Gly Ala Phe Ser Ile Pro  
                   45                  50                  55  
 gtt atc cag ata gtt tat gaa act ctg aaa gac caa cag gaa ggc aaa 305  
 Val Ile Gln Ile Val Tyr Glu Thr Leu Lys Asp Gln Gln Glu Gly Lys  
                   60                  65                  70                  75  
 aaa gga aaa aca aca att aaa act g 330  
 Lys Gly Lys Thr Thr Ile Lys Thr  
                   80

<210> 1357  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 133..390

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 gaggatgtga ag atg gcg gag ctg cag atg ctg ctg gaa gag gaa atc ccg 171  
                   Met Ala Glu Leu Gln Met Leu Leu Glu Glu Glu Ile Pro  
                   1                  5                  10  
 ggg ggc cgc cgg gcc ctc ttc gac agc tan aca aat ctg gaa cgg gtg 219

Gly	Gly	Arg	Arg	Ala	Leu	Phe	Asp	Ser	Xaa	Thr	Asn	Leu	Glu	Arg	Val		
15						20					25						
gcc	gat	tac	tgc	gag	aac	aac	tac	ata	cak	tca	gca	gat	aag	cag	aga	267	
Ala	Asp	Tyr	Cys	Glu	Asn	Asn	Tyr	Ile	Xaa	Ser	Ala	Asp	Lys	Gln	Arg		
30					35					40				45			
gcc	cta	gaa	gaa	acc	aaa	gcc	tac	acc	acc	caa	tcc	tta	gca	agt	gtk	315	
Ala	Leu	Glu	Glu	Thr	Lys	Ala	Tyr	Thr	Thr	Gln	Ser	Leu	Ala	Ser	Val		
				50					55				60				
gcc	tat	ctg	ata	aac	acc	ttg	gcc	aac	aat	gtc	ctg	cag	atg	ctg	gat	363	
Ala	Tyr	Leu	Ile	Asn	Thr	Leu	Ala	Asn	Asn	Val	Leu	Gln	Met	Leu	Asp		
			65					70					75				
atc	cag	gca	tcc	cag	cta	cga	agg	atg								390	
Ile	Gln	Ala	Ser	Gln	Leu	Arg	Arg	Met									
		80						85									

<210> 1358  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 56..307

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						Met											
						1											
aag	acg	cga	agg	act	acc	cgc	ctt	cag	cag	cag	cac	tca	gag	cag	cct	106	
Lys	Thr	Arg	Arg	Thr	Thr	Arg	Leu	Gln	Gln	Gln	His	Ser	Glu	Gln	Pro		
			5					10					15				
ccg	cta	cag	ccg	tct	cct	gtt	acg	acc	agg	aga	ggg	ctg	cgg	gac	tct	154	
Pro	Leu	Gln	Pro	Ser	Pro	Val	Thr	Thr	Arg	Arg	Gly	Leu	Arg	Asp	Ser		
		20				25						30					
cat	tcc	tct	gaa	gag	gat	gaa	gca	tct	tcc	caa	act	gat	tta	agc	caa	202	
His	Ser	Ser	Glu	Glu	Asp	Glu	Ala	Ser	Ser	Gln	Thr	Asp	Leu	Ser	Gln		
		35				40				45							
acg	atc	tca	aag	aaa	act	gtc	agg	agc	ata	caa	gag	gct	cca	gtg	agt	250	
Thr	Ile	Ser	Lys	Lys	Thr	Val	Arg	Ser	Ile	Gln	Glu	Ala	Pro	Val	Ser		
					55					60					65		
gaa	gat	ctt	gta	atc	agg	tta	cgt	cga	ccc	cct	cta	aga	tac	cca	aga	298	
Glu	Asp	Leu	Val	Ile	Arg	Leu	Arg	Arg	Pro	Pro	Leu	Arg	Tyr	Pro	Arg		
				70					75					80			
tat	gaa	gcc	ac													309	
Tyr	Glu	Ala															

<210> 1359  
 <211> 446  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 78..446

<400> 1359

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gggtggttgc tgccgaa atg ggc aag ttc atg aaa cct ggg aag gtg gtg      110
           Met Gly Lys Phe Met Lys Pro Gly Lys Val Val
           1           5           10
ctt gtc ctg gct gga cgc tac tcc gga cgc aaa gct gtc atc gtg aag      158
Leu Val Leu Ala Gly Arg Tyr Ser Gly Arg Lys Ala Val Ile Val Lys
           15           20           25
aac att gat gat ggc acc tca gat cgc ccc tac agc cat gct ctg gtg      206
Asn Ile Asp Asp Gly Thr Ser Asp Arg Pro Tyr Ser His Ala Leu Val
           30           35           40
gct gga att gac cgc tac ccc cgc aaa gtg aca gct gcc atg ggc aag      254
Ala Gly Ile Asp Arg Tyr Pro Arg Lys Val Thr Ala Ala Met Gly Lys
           45           50           55
aag aag atc gcc aag aga tca aag ata aaa tct ttt gtg aaa gtg tat      302
Lys Lys Ile Ala Lys Arg Ser Lys Ile Lys Ser Phe Val Lys Val Tyr
60           65           70           75
aac tac aat cac cta atg ccc aca agg tac tct gtg gat atc ccc ttg      350
Asn Tyr Asn His Leu Met Pro Thr Arg Tyr Ser Val Asp Ile Pro Leu
           80           85           90
gac aaa act gtc gtc aat aag gat gtc ttc aga gat cct gct ctt aaa      398
Asp Lys Thr Val Val Asn Lys Asp Val Phe Arg Asp Pro Ala Leu Lys
           95           100           105
cgc aag gcc cga cgg gag gcc aag gtc agt ttg aag aga gat aca gac      446
Arg Lys Ala Arg Arg Glu Ala Lys Val Ser Leu Lys Arg Asp Thr Asp
           110           115           120
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<210> 1360

<211> 687

<212> DNA

<213> Homo sapiens

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<222> 319..687

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cctagtttta atattgttgt gcctcgaggc aaaggtagga ccaagaagag ggagagagat      120
gggggaagtg ccagtgagtg gagcagtcag aacacacatt tgttgattaa gtttgcaacc      180
ttctatgggc acagtttgtg atgccccaaa acaattgcaa tagtaatatc acagatcact      240
gatcacggat aatcataaca aatataataa taaaaatttg aaaccttttt gctgtaggcc      300
cgggtggttg ctgccgaa atg ggc aag ttc atg aaa cct ggg aag gtg gtg      351
           Met Gly Lys Phe Met Lys Pro Gly Lys Val Val
           1           5           10
ctt gtc ctg gct gga cgc tac tcc gga cgc aaa gct gtc atc gtg aag      399
Leu Val Leu Ala Gly Arg Tyr Ser Gly Arg Lys Ala Val Ile Val Lys
           15           20           25
aac att gat gat ggc acc tca gat cgc ccc tac agc cat gct ctg gtg      447
Asn Ile Asp Asp Gly Thr Ser Asp Arg Pro Tyr Ser His Ala Leu Val
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30	35	40	
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Ala Gly Ile Asp Arg Tyr Pro Arg Lys Val Thr Ala Ala Met Gly Lys			
45	50	55	
aag aag atc gcc aag aga tca aag ata aaa tct ttt gtg aaa gtg tat			543
Lys Lys Ile Ala Lys Arg Ser Lys Ile Lys Ser Phe Val Lys Val Tyr			
60	65	70	75
aac tac aat cac cta atg ccc aca agg tac tct gtg gat atc ccc ttg			591
Asn Tyr Asn His Leu Met Pro Thr Arg Tyr Ser Val Asp Ile Pro Leu			
80	85	90	
gac aaa act gtc gtc aat aag gat gtc ttc aga gat cct gct ctt aaa			639
Asp Lys Thr Val Val Asn Lys Asp Val Phe Arg Asp Pro Ala Leu Lys			
95	100	105	
cgc aag gcc cga cgg gag gcc aag gtc agt ttg aag aga gat aca gac			687
Arg Lys Ala Arg Arg Glu Ala Lys Val Ser Leu Lys Arg Asp Thr Asp			
110	115	120	

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aaaggggata ctaagaataa tcgcagaatt aacatcggca aggtatgatc aggatgagga	180
cgtgagaaac gcagggctaa gagttgggag tcctggg atg aac ttc cca cct caa	235
Met Asn Phe Pro Pro Gln	
1	5
agc cca gca cga ggg tcc ctg gac gct gtc ggc ccc gga cgt ggg tcc	283
Ser Pro Ala Arg Gly Ser Leu Asp Ala Val Gly Pro Gly Arg Gly Ser	
10	15
ccg aga ctc gac tgc agc tca gag tgg cca mat ctg ccc tgc cag gct	331
Pro Arg Leu Asp Cys Ser Ser Glu Trp Pro Xaa Leu Pro Cys Gln Ala	
25	30
gcc gcg gag aca aca cgg agg agc acc tgt gag aac acc tgc	373
Ala Ala Glu Thr Thr Arg Arg Ser Thr Cys Glu Asn Thr Cys	
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	50

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 <222> 85..423

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<213> Homo sapiens
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<400> 1363

920

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Ser Pro Gln Pro Phe Tyr Gly Asn Asn Phe Glu  
80 85

<210> 1364  
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<220>  
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rgtggccttg tggagacaac gccttaaccc aaggaagtga ctcaaactgt gagaacttca 120  
ggttttccaa cctattggtg gt atg tct gac agt gga tca caa ctt ggt tca 172  
Met Ser Asp Ser Gly Ser Gln Leu Gly Ser  
1 5 10  
atg ggt agc ctc acc atg aaa tca cag ctt cag atc act gtc atc tca 220  
Met Gly Ser Leu Thr Met Lys Ser Gln Leu Gln Ile Thr Val Ile Ser  
15 20 25  
gca aaa ctt aag gaa aat aag aag aat tgg ttt gga cca agt cct tac 268  
Ala Lys Leu Lys Glu Asn Lys Lys Asn Trp Phe Gly Pro Ser Pro Tyr  
30 35 40  
gta gag gtc aca gta gat gga cag tca aag aag aca gaa aaa tgc aac 316  
Val Glu Val Thr Val Asp Gly Gln Ser Lys Lys Thr Glu Lys Cys Asn  
45 50 55  
aac aca aac agt ccc aag tgg aag caa ccc ctt aca gtt atc gtt acc c 365  
Asn Thr Asn Ser Pro Lys Trp Lys Gln Pro Leu Thr Val Ile Val Thr  
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<220>  
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gggttttcag caaatccagg gctggtctgg aggcgcgaaa acttaaggca tacagaacg 119  
atg gag tat atg gca gaa tcc acc gac cgc agc cct gga cac atc ttg 167  
Met Glu Tyr Met Ala Glu Ser Thr Asp Arg Ser Pro Gly His Ile Leu  
1 5 10 15  
tgc tgt gag tgt ggt gtt ccg ata agt cca aat cct gcc aat att tgt 215  
Cys Cys Glu Cys Gly Val Pro Ile Ser Pro Asn Pro Ala Asn Ile Cys  
20 25 30  
gtg gcc tgt ttg cga agt aaa gtg gac atc agc caa ggt att ccg aaa 263

Val	Ala	Cys	Leu	Arg	Ser	Lys	Val	Asp	Ile	Ser	Gln	Gly	Ile	Pro	Lys	
	35						40				45					
caa	gtc	tcg	att	tcg	ttc	tgc	aaa	caa	tgt	caa	agg	tat	ttt	caa	cca	311
Gln	Val	Ser	Ile	Ser	Phe	Cys	Lys	Gln	Cys	Gln	Arg	Tyr	Phe	Gln	Pro	
	50					55				60						
cca	gga	act	tgg	ata	cag	tgt	gct	tta	gaa	tcc	ag					346
Pro	Gly	Thr	Trp	Ile	Gln	Cys	Ala	Leu	Glu	Ser						
65					70				75							

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Met	Pro	Val	Ala	Arg	Ser	Trp	Val	Cys	Arg	Lys	Thr	Tyr	Val	Thr	Pro	
1			5					10					15			
cgg	aga	ccc	ttc	gag	aaa	tct	cgt	ctc	gac	caa	gag	ctg	aag	ctg	atc	155
Arg	Arg	Pro	Phe	Glu	Lys	Ser	Arg	Leu	Asp	Gln	Glu	Leu	Lys	Leu	Ile	
			20					25				30				
ggc	gag	tat	ggg	ctc	cgg	aac	aaa	cgt	gag	gtc	tgg	agg	gtc	aaa	ttt	203
Gly	Glu	Tyr	Gly	Leu	Arg	Asn	Lys	Arg	Glu	Val	Trp	Arg	Val	Lys	Phe	
		35				40				45						
acc	ctg	gcc	aag	atc	cgc	aag	gcc	gcc	cgg	gaa	ctg	ctg	acg	ctt	gat	251
Thr	Leu	Ala	Lys	Ile	Arg	Lys	Ala	Ala	Arg	Glu	Leu	Leu	Thr	Leu	Asp	
	50				55				60							
gag	aag	gac	cca	cgg	cgt	ctg	ttc	gaa	ggc	aac	gcc	ctg	ctg	cgg	cgg	299
Glu	Lys	Asp	Pro	Arg	Arg	Leu	Phe	Glu	Gly	Asn	Ala	Leu	Leu	Arg	Arg	
65				70				75				80				
ctg	gtc	cgc	att	ggg	gtg	ctg	gat	gag	ggc	aag	atg	aag	ctg	gat	tac	347
Leu	Val	Arg	Ile	Gly	Val	Leu	Asp	Glu	Gly	Lys	Met	Lys	Leu	Asp	Tyr	
			85					90				95				
atc	ctg	ggc	ctg	aag	ata	gag	gat	ttc	tta	gag	aga	cgc	ctg	cag	acc	395
Ile	Leu	Gly	Leu	Lys	Ile	Glu	Asp	Phe	Leu	Glu	Arg	Arg	Leu	Gln	Thr	
		100						105				110				
cag	gtc	ttc	aag	ctg	ggc	ttg	gcc	aag	tcc	atc	cac	cac	gct	cgc	gtg	443
Gln	Val	Phe	Lys	Leu	Gly	Leu	Ala	Lys	Ser	Ile	His	His	Ala	Arg	Val	
		115				120					125					
ctg	atc	cgc	cag	cgc	cat	atc	agg	gtc	cgc	aag	cag	gtg	gtg	aac	ats	491
Leu	Ile	Arg	Gln	Arg	His	Ile	Arg	Val	Arg	Lys	Gln	Val	Val	Asn	Xaa	
		130				135				140						
ccg	tcc	ttc	att	gtc	cgc	ctg	gat	tcc	agm	aag	cac	atc	gac	ttc	tct	539
Pro	Ser	Phe	Ile	Val	Arg	Leu	Asp	Ser	Xaa	Lys	His	Ile	Asp	Phe	Ser	
145				150				155				160				
ctg	cgc	tct	ccc	tac	ggg	ggg	ggc	cgc	ccg	ggc	cgc	gtg	aag	agg	a	585
Leu	Arg	Ser	Pro	Tyr	Gly	Gly	Gly	Arg	Pro	Gly	Arg	Val	Lys	Arg		
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<210> 1367  
 <211> 658  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 133..657

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 aagcggasca ac atg cca gtg gcc cgg agc tgg gtt tgt cgc aaa act tat 171  
 Met Pro Val Ala Arg Ser Trp Val Cys Arg Lys Thr Tyr  
 1 5 10  
 gtg acc ccg cgg aga ccc ttc gag aaa tct cgt ctc gac caa gag ctg 219  
 Val Thr Pro Arg Arg Pro Phe Glu Lys Ser Arg Leu Asp Gln Glu Leu  
 15 20 25  
 aag ctg atc ggc gag tat ggg ctc cgg aac aaa cgt gag gtc tgg agg 267  
 Lys Leu Ile Gly Glu Tyr Gly Leu Arg Asn Lys Arg Glu Val Trp Arg  
 30 35 40 45  
 gtc aaa ttt acc ctg gcc aag atc cgc aag gcc gcc cgg gaa ctg ctg 315  
 Val Lys Phe Thr Leu Ala Lys Ile Arg Lys Ala Ala Arg Glu Leu Leu  
 50 55 60  
 acg ctt gat gag aag gac cca cgg cgt ctg ttc gaa ggc aac gcc ctg 363  
 Thr Leu Asp Glu Lys Asp Pro Arg Arg Leu Phe Glu Gly Asn Ala Leu  
 65 70 75  
 ctg cgg cgg ctg gtc cgc att ggg gtg ctg gat gag ggc aag atg aag 411  
 Leu Arg Arg Leu Val Arg Ile Gly Val Leu Asp Glu Gly Lys Met Lys  
 80 85 90  
 ctg gat tac atc ctg ggc ctg aag ata gag gat ttc tta gag aga cgc 459  
 Leu Asp Tyr Ile Leu Gly Leu Lys Ile Glu Asp Phe Leu Glu Arg Arg  
 95 100 105  
 ctg cag acc cag gtc ttc aag ctg ggc ttg gcc aag tcc atc cac cac 507  
 Leu Gln Thr Gln Val Phe Lys Leu Gly Leu Ala Lys Ser Ile His His  
 110 115 120 125  
 gct cgc gtg ctg atc cgc cag cgc cat atc agg gtc cgc aag cag gtg 555  
 Ala Arg Val Leu Ile Arg Gln Arg His Ile Arg Val Arg Lys Gln Val  
 130 135 140  
 gtg aac ats ccg tcc ttc att gtc cgc ctg gat tcc agm aag cac atc 603  
 Val Asn Xaa Pro Ser Phe Ile Val Arg Leu Asp Ser Xaa Lys His Ile  
 145 150 155  
 gac ttc tct ctg cgc tct ccc tac ggg ggt ggc cgc ccg ggc cgc gtg 651  
 Asp Phe Ser Leu Arg Ser Pro Tyr Gly Gly Gly Arg Pro Gly Arg Val  
 160 165 170  
 aag agg a 658  
 Lys Arg  
 175

<210> 1368  
 <211> 453  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 144..452

<400> 1368

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cccgccagca ggcgaasagg gag atg tca gac tgc tac acg gag ctg gag aag      173
                Met Ser Asp Cys Tyr Thr Glu Leu Glu Lys
                  1                5                10
gca gtc att gtc ctg gtg gaa aac ttc tac aaa tat gtg tct aag tac      221
Ala Val Ile Val Leu Val Glu Asn Phe Tyr Lys Tyr Val Ser Lys Tyr
                15                20                25
agc ctg gtc aag aac aag atc agc aag agc agc ttc cgc gag atg ctc      269
Ser Leu Val Lys Asn Lys Ile Ser Lys Ser Ser Phe Arg Glu Met Leu
                30                35                40
cag aaa gag ctg aac cac atg ctg tgc gac aca ggg aac cgg mwg gct      317
Gln Lys Glu Leu Asn His Met Leu Ser Asp Thr Gly Asn Arg Xaa Ala
                45                50                55
gcg gat aag ctc atc cag aac ctg gat gcc aat cat gat ggg cgc atc      365
Ala Asp Lys Leu Ile Gln Asn Leu Asp Ala Asn His Asp Gly Arg Ile
                60                65                70
agc ttc gat gag tac wgg acc ttg ata ggc ggc atc acc ggc ccc atc      413
Ser Phe Asp Glu Tyr Xaa Thr Leu Ile Gly Gly Ile Thr Gly Pro Ile
                75                80                85                90
gcc aaa ctc atc cat gag cag gag cag cag agc agc agc t      453
Ala Lys Leu Ile His Glu Gln Glu Gln Gln Ser Ser Ser
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<210> 1369

<211> 361

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 164..361

<400> 1369

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tgtgccctct ggcagtctgc tgctgtgtcc agagtccgac tccagctggg ctgtaactgg      120
gcttggtccc cgccttaggc cccgccagca ggcgaasagg gag atg tca gac tgc      173
                Met Ser Asp Cys
                  1
tac acg gag ctg gag aag gca gtc att gtc ctg gtg gaa aac ttc tac      223
Tyr Thr Glu Leu Glu Lys Ala Val Ile Val Leu Val Glu Asn Phe Tyr
                5                10                15                20
aaa tat gtg tct aag tac agc ctg gtc aag aac aag atc agc aag agc      271
Lys Tyr Val Ser Lys Tyr Ser Leu Val Lys Asn Lys Ile Ser Lys Ser
                25                30                35

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agc ttc cgc gag atg ctc cag aaa gag ctg aac cac atg ctg tcg gta 319  
 Ser Phe Arg Glu Met Leu Gln Lys Glu Leu Asn His Met Leu Ser Val  
           40                          45                          50  
 agg cct ctc acc caa ggg cct tgc ctc cct ctc ccc ttc cct 361  
 Arg Pro Leu Thr Gln Gly Pro Cys Leu Pro Leu Pro Phe Pro  
           55                          60                          65

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 <211> 473  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 164..472

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 gcttggtcccc cgccttaggc cccgccagca ggcgaasagg gag atg tca gac tgc 175  
   Met Ser Asp Cys  
   1  
 tac acg gag ctg gag aag gca gtc att gtc ctg gtg gaa aac ttc tac 223  
 Tyr Thr Glu Leu Glu Lys Ala Val Ile Val Leu Val Glu Asn Phe Tyr  
   5                          10                          15                          20  
 aaa tat gtg tct aag tac agc ctg gtc aag aac aag atc agc aag agc 271  
 Lys Tyr Val Ser Lys Tyr Ser Leu Val Lys Asn Lys Ile Ser Lys Ser  
                           25                          30                          35  
 agc ttc cgc gag atg ctc cag aaa gag ctg aac cac atg ctg tcg gac 319  
 Ser Phe Arg Glu Met Leu Gln Lys Glu Leu Asn His Met Leu Ser Asp  
           40                          45                          50  
 aca ggg aac cgg aag gct gcg gat aag ctc atc cag aac ctg gat gcc 367  
 Thr Gly Asn Arg Lys Ala Ala Asp Lys Leu Ile Gln Asn Leu Asp Ala  
   55                          60                          65  
 aat cat gat ggg cgc atc agc ttc gat gag tac tgg acc ttg ata ggc 415  
 Asn His Asp Gly Arg Ile Ser Phe Asp Glu Tyr Trp Thr Leu Ile Gly  
   70                          75                          80  
 ggc atc acc ggc ccc atc gcc aaa ctc atc cat gag crg gag cag cag 463  
 Gly Ile Thr Gly Pro Ile Ala Lys Leu Ile His Glu Xaa Glu Gln Gln  
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 agc agc agc t  
 Ser Ser Ser 473

<210> 1371  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..373

0011220 666E1560

<400> 1371

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Met

gct ccc agc gtg cca gcg gca gaa ccc gag tat cct aaa ggc atc cgg 106  
Ala Pro Ser Val Pro Ala Ala Glu Pro Glu Tyr Pro Lys Gly Ile Arg

5 10 15  
gcc gtg ctg ctg ggg cct ccc ggg gcc ggt aaa ggg acc cag gca ccc 154  
Ala Val Leu Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Pro

20 25 30  
aga ttg gct gaa aac ttc tgt gtc tgc cat tta gct act ggg kac atg 202  
Arg Leu Ala Glu Asn Phe Cys Val Cys His Leu Ala Thr Gly Xaa Met

35 40 45  
ctg agg gcc atg gtg gct tct ggc tca gag cta gga aaa aag ctg aag 250  
Leu Arg Ala Met Val Ala Ser Gly Ser Glu Leu Gly Lys Lys Leu Lys

50 55 60 65  
gca act atg gat gct ggg aaa ctg gtg agt gat gaa atg gta gtg gag 298  
Ala Thr Met Asp Ala Gly Lys Leu Val Ser Asp Glu Met Val Val Glu

70 75 80  
ctc att gag aag aat ttg gag acc ccc ttg tgc aaa aat ggt ttt ctt 346  
Leu Ile Glu Lys Asn Leu Glu Thr Pro Leu Cys Lys Asn Gly Phe Leu

85 90 95  
ctg gat ggc ttc cct cgg act gtg agg c 374  
Leu Asp Gly Phe Pro Arg Thr Val Arg

<210> 1372

<211> 588

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 213..587

<400> 1372

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ccctgcccc tctcgagtcc accctccggg cttctgccc ctgatcgctt ggttttcctt 180  
gcagtcgct gctgctgtcg tcgggaggaa ag atg aat ggg agg gct gat ttt 233

Met Asn Gly Arg Ala Asp Phe  
1 5

cga gag ccg aat gca gag gtt cca aga cca att ccc cac ata ggg cct 281  
Arg Glu Pro Asn Ala Glu Val Pro Arg Pro Ile Pro His Ile Gly Pro

10 15 20  
gat tac att cca aca gag gaa gaa agg aga gtc ttc gca gaa tgc aat 329  
Asp Tyr Ile Pro Thr Glu Glu Glu Arg Arg Val Phe Ala Glu Cys Asn

25 30 35  
gat gaa agc ttc tgg ttc aga tct gtg cct ttg gct gca aca agt atg 377  
Asp Glu Ser Phe Trp Phe Arg Ser Val Pro Leu Ala Ala Thr Ser Met

40 45 50 55  
ttg att act caa gga tta att agt aaa gga ata ctt tca agt cat ccc 425  
Leu Ile Thr Gln Gly Leu Ile Ser Lys Gly Ile Leu Ser Ser His Pro

00420" 666E750



aaa tat ggt tcc atc cct aaa ctt ata ctt gct tgt atc atg gga tac	473
Lys Tyr Gly Ser Ile Pro Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr	
75 80 85	
ttt gct gga aaa ctt tct tat gtg aaa act tgc caa gag aaa ttc aag	521
Phe Ala Gly Lys Leu Ser Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys	
90 95 100	
aaa ctt gaa aat tcc ccc ctt gga gaa gct tta cga tca gga caa gca	569
Lys Leu Glu Asn Ser Pro Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala	
105 110 115	
cga cga tct tca cca cct g	588
Arg Arg Ser Ser Pro Pro	
120 125	
<210> 1373	
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Met Glu Phe Val Lys Cys Leu Gly His	
1 5	
ccc gaa gag ttc tac aac ctg gtg cgc tty cgg atc ggg ggc aag cgg	162
Pro Glu Glu Phe Tyr Asn Leu Val Arg Phe Arg Ile Gly Gly Lys Arg	
10 15 20 25	
aag gtg atg ccc aag atg gac cag gac tgc ctc agc agc agc ctg aaa	210
Lys Val Met Pro Lys Met Asp Gln Asp Ser Leu Ser Ser Ser Leu Lys	
30 35 40	
act tgc tac arg tat ctc aat cag acc agt cgc agt ttc gca gct gtt	258
Thr Cys Tyr Xaa Tyr Leu Asn Gln Thr Ser Arg Ser Phe Ala Ala Val	
45 50 55	
atc cag gcg ctg gat ggg gaa atg cgc aac gca gtg tgc ata ttt tat	306
Ile Gln Ala Leu Asp Gly Glu Met Arg Asn Ala Val Cys Ile Phe Tyr	
60 65 70	
ctg gtt ctc cga gct ctg gac aca ctg gaa gat gac atg acc atc agt	354
Leu Val Leu Arg Ala Leu Asp Thr Leu Glu Asp Asp Met Thr Ile Ser	
75 80 85	
gtg gaa aag aag gtc ccg ctg tta cac aac ttt cac tct ttc ctt tac	402
Val Glu Lys Lys Val Pro Leu Leu His Asn Phe His Ser Phe Leu Tyr	
90 95 100 105	
caa cca gac tgg ccg ttc atg gag agc aag gag aag gat cgc cag gtg	450
Gln Pro Asp Trp Arg Phe Met Glu Ser Lys Glu Lys Asp Arg Gln Val	
110 115 120	
ctg gag gac ttc cca acg atc tcc ct	476
Leu Glu Asp Phe Pro Thr Ile Ser	
125	

<210> 1374  
 <211> 353  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 94..351

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 Met Glu Glu Ala Ser Glu Gly  
 1 5  
 gga gga aat gat cgt gtg cgg aac ctg caa agt gag gtg gag gga gtt 162  
 Gly Gly Asn Asp Arg Val Arg Asn Leu Gln Ser Glu Val Glu Gly Val  
 10 15 20  
 aag aat att atg acc cag aat gtg gag cgg atc ctg gtc cgg ggg gaa 210  
 Lys Asn Ile Met Thr Gln Asn Val Glu Arg Ile Leu Val Arg Gly Glu  
 25 30 35  
 aac ttg gaa cat ctc cgc aac aag aca gag gat ctg gaa gcc aca tct 258  
 Asn Leu Glu His Leu Arg Asn Lys Thr Glu Asp Leu Glu Ala Thr Ser  
 40 45 50 55  
 gag cac ttc aag acg aca tcg cag aag gtg gct cga aaa ttc tgg tgg 306  
 Glu His Phe Lys Thr Thr Ser Gln Lys Val Ala Arg Lys Phe Trp Trp  
 60 65 70  
 aag aac gtg aag atg att gtc ctt atc tgc gtg att gtt ttt atc at 353  
 Lys Asn Val Lys Met Ile Val Leu Ile Cys Val Ile Val Phe Ile  
 75 80 85

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 Met Ala Ile Phe Ser Val Tyr Val  
 1 5  
 gtg aac aaa gct ggc ggc ttg att tac cag ttg gac agc tac gcg cca 101  
 Val Asn Lys Ala Gly Gly Leu Ile Tyr Gln Leu Asp Ser Tyr Ala Pro  
 10 15 20  
 cgg gct gag gct gag aaa act ttc agt tat ccg ctg gat ctg ctg ctc 149  
 Arg Ala Glu Ala Glu Lys Thr Phe Ser Tyr Pro Leu Asp Leu Leu Leu  
 25 30 35 40  
 aag cta cac gat gag cgt gtg ttg gtt gct ttc ggc cag cgg gac ggc 197  
 Lys Leu His Asp Glu Arg Val Leu Val Ala Phe Gly Gln Arg Asp Gly  
 45 50 55

atc cga gtg ggt cat gca gtg ctg gcc atc aat ggc atg gac gtg aat	245
Ile Arg Val Gly His Ala Val Leu Ala Ile Asn Gly Met Asp Val Asn	
60 65 70	
ggc agg tac acg gcc gac ggg maa gag gtg ctg agt atc tgg gta acc	293
Gly Arg Tyr Thr Ala Asp Gly Xaa Glu Val Leu Ser Ile Trp Val Thr	
75 80 85	
ctg cta att acc cgg tgt cca ttc gat ttg gcc ggc ccc gcc tca ctt	341
Leu Leu Ile Thr Arg Cys Pro Phe Asp Leu Ala Gly Pro Ala Ser Leu	
90 95 100	
cta atg aga agc tta tgc tgg cct cca tgt tcc act cgc tct ttg cca	389
Leu Met Arg Ser Leu Cys Trp Pro Pro Cys Ser Thr Arg Ser Leu Pro	
105 110 115 120	
tgc gct ccc agc tgt ctc ctg aac agg gaa gct cag gca ttg aka tgc	437
Ser Ala Pro Ser Cys Leu Leu Asn Arg Glu Ala Gln Ala Leu Xaa Cys	
125 130 135	
tgg aga cag aca cat tca aat tgc act gc	466
Trp Arg Gln Thr His Ser Asn Cys Thr	
140 145	

<210> 1376  
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 <212> DNA  
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atg gaa tat tat ctt gta aaa tgg aaa gga tgg cca gat tct aca aat	105
Met Glu Tyr Tyr Leu Val Lys Trp Lys Gly Trp Pro Asp Ser Thr Asn	
1 5 10 15	
act tgg gaa cct ttg caa aat ctg aag tgc ccg tta ctg ctt cag caa	153
Thr Trp Glu Pro Leu Gln Asn Leu Lys Cys Pro Leu Leu Leu Gln Gln	
20 25 30	
ttc tct aat gac aag cat aat tat tta tct cag gta aag aaa ggc aaa	201
Phe Ser Asn Asp Lys His Asn Tyr Leu Ser Gln Val Lys Lys Gly Lys	
35 40 45	
gcn ata act cca aaa gac aat aac aaa act ttg aaa cct gcc att gct	249
Ala Ile Thr Pro Lys Asp Asn Asn Lys Thr Leu Lys Pro Ala Ile Ala	
50 55 60	
gag tac att gtg aag aag gct aaa caa agg ata gct ctg cag aga tgg	297
Glu Tyr Ile Val Lys Lys Ala Lys Gln Arg Ile Ala Leu Gln Arg Trp	
65 70 75 80	
caa gat gaa ctc aac aga aga aag aat cat aaa gga atg ata ttt gtt	345
Gln Asp Glu Leu Asn Arg Arg Lys Asn His Lys Gly Met Ile Phe Val	
85 90 95	
gaa aat act gtt gat tta gag ggc	369
Glu Asn Thr Val Asp Leu Glu Gly	
100	

<210> 1377

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 108..515

<400> 1377

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tttttctttc tgtttttctt ctctttcttc tatttcttgt ggatatt atg gct aat      116
                                   Met Ala Asn
                                   1
aac aca aca agt tta ggg agt cca tgg cca gaa aac ttt tgg gag gac      164
Asn Thr Thr Ser Leu Gly Ser Pro Trp Pro Glu Asn Phe Trp Glu Asp
   5                                   10                                   15
ctt atc atg tcc ttc act gat cca tgg caa tcg ggc tgg tac ttg gag      212
Leu Ile Met Ser Phe Thr Asp Pro Trp Gln Ser Gly Trp Tyr Leu Glu
  20                                   25                                   30                                   35
gat tta ttt ggg ctg tgt tca ttt gtc tgt ctc gaa gaa gaa gag cca      260
Asp Leu Phe Gly Leu Cys Ser Phe Val Cys Leu Glu Glu Glu Glu Pro
   40                                   45                                   50
gtg ctc cca tct cac agt gga gtt caa gca gga gat cta ggt ctt ctt      308
Val Leu Pro Ser His Ser Gly Val Gln Ala Gly Asp Leu Gly Leu Leu
   55                                   60                                   65
aca ccc acg gcc tca aca gaa ctg gat ttt acc gcc aca gtg gct gtg      356
Thr Pro Thr Ala Ser Thr Glu Leu Asp Phe Thr Ala Thr Val Ala Val
   70                                   75                                   80
aac gtc gaa gca acc tca gcc tgg cca gtc tca cct tcc agc gac aag      404
Asn Val Glu Ala Thr Ser Ala Trp Pro Val Ser Pro Ser Ser Asp Lys
   85                                   90                                   95
ctt ccc tgg aac aag caa att cct ttc caa gaa aat caa gtt tca gag      452
Leu Pro Trp Asn Lys Gln Ile Pro Phe Gln Glu Asn Gln Val Ser Glu
  100                                   105                                   110                                   115
ctt cta ctt tcc atc cct ttc tgc aaa tgt cca cca ctt cct gtg gaa      500
Leu Leu Leu Ser Ile Pro Phe Cys Lys Cys Pro Pro Leu Pro Val Glu
   120                                   125                                   130
act gag agt cag ctg
Thr Glu Ser Gln Leu
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<210> 1378  
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 <212> DNA  
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<220>  
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 <222> 96..344

<400> 1378

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tg	ttt	ggg	ccc	ttg	cct	gtg	atg	gcc	ttg	ctg	tgc	tac		113		
							Met	Ala	Leu	Leu	Cys	Tyr				
							1				5					
aac	cgg	ggc	tgc	ggg	cag	cgc	ttc	gat	cct	gag	acc	aat	tcc	gac	gat	161
Asn	Arg	Gly	Cys	Gly	Gln	Arg	Phe	Asp	Pro	Glu	Thr	Asn	Ser	Asp	Asp	
			10					15				20				
gct	tgc	aca	tac	cac	cca	ggg	gtt	ccg	gtc	ttt	cac	gat	gca	tta	aag	209
Ala	Cys	Thr	Tyr	His	Pro	Gly	Val	Pro	Val	Phe	His	Asp	Ala	Leu	Lys	
			25				30					35				
ggg	tgg	tct	tgc	tgt	aag	aga	aga	aca	act	gat	ttt	tct	gat	ttc	tta	257
Gly	Trp	Ser	Cys	Cys	Lys	Arg	Arg	Thr	Thr	Asp	Phe	Ser	Asp	Phe	Leu	
			40			45				50						
agc	att	gta	ggc	tgt	aca	aaa	ggg	aga	cat	aat	agt	gag	aag	cca	cct	305
Ser	Ile	Val	Gly	Cys	Thr	Lys	Gly	Arg	His	Asn	Ser	Glu	Lys	Pro	Pro	
					60					65				70		
gag	cca	gtc	aaa	cct	gaa	gtc	aag	act	act	gag	aag	aag	ga			346
Glu	Pro	Val	Lys	Pro	Glu	Val	Lys	Thr	Thr	Glu	Lys	Lys				
				75					80							

<210> 1379  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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											Met	Leu	Asp	Gly	Ser	Val	Lys	Thr		
											1				5					
gtg	atg	gtg	gat	gat	tcc	aag	act	gtg	ggg	gag	ctc	ctg	gtc	act	att					101
Val	Met	Val	Asp	Asp	Ser	Lys	Thr	Val	Gly	Glu	Leu	Leu	Val	Thr	Ile					
						15					20									
tgt	agc	aga	ata	gga	ata	aca	aat	tat	gaa	gaa	tac	tcc	tta	atc	caa					149
Cys	Ser	Arg	Ile	Gly	Ile	Thr	Asn	Tyr	Glu	Glu	Tyr	Ser	Leu	Ile	Gln					
						30					35				40					
gaa	act	att	gaa	gaa	aag	aaa	gag	gaa	gga	acg	ggc	aca	ctc	aaa	aaa					197
Glu	Thr	Ile	Glu	Glu	Lys	Lys	Glu	Glu	Gly	Thr	Gly	Thr	Leu	Lys	Lys					
					45				50					55						
gac	agg	aca	ctg	tta	cga	gat	gag	ag												223
Asp	Arg	Thr	Leu	Leu	Arg	Asp	Glu													
						60														

<210> 1380  
 <211> 434  
 <212> DNA  
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<220>  
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 <222> 138..434

&lt;400&gt; 1380

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cttatcctgg cattgagggc gccggactgg cgcttttggc cgrcttggca ttgggtgggc      120
ggcttcttgg gacccac atg agc cag tgg cat cat ccc cgc agt ggc tgg      170
                Met Ser Gln Trp His His Pro Arg Ser Gly Trp
                1             5             10
ggc cgg aga cgc gac ttt tca gga cgc tcc tca gcc aag aag aag ggc      218
Gly Arg Arg Arg Asp Phe Ser Gly Arg Ser Ser Ala Lys Lys Lys Gly
                15             20             25
gga aac cac atc ccc gaa agg tgg aaa gac tat ctc cca gtt gga cag      266
Gly Asn His Ile Pro Glu Arg Trp Lys Asp Tyr Leu Pro Val Gly Gln
                30             35             40
cgg atg cct ggg act cgt ttc att gct ttc aaa gtt cct ttg caa aag      314
Arg Met Pro Gly Thr Arg Phe Ile Ala Phe Lys Val Pro Leu Gln Lys
                45             50             55
agt ttt gaa aag aaa ctt gct cca gaa gaa tgc ttt tcc cct ttg gat      362
Ser Phe Glu Lys Lys Leu Ala Pro Glu Glu Cys Phe Ser Pro Leu Asp
60             65             70             75
ctt ttt aac aaa atc cga gaa caa aat gaa gar ctt gga ctg att att      410
Leu Phe Asn Lys Ile Arg Glu Gln Asn Glu Glu Leu Gly Leu Ile Ile
                80             85             90
gat tta aca tat act caa cgc tat      434
Asp Leu Thr Tyr Thr Gln Arg Tyr
                95

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&lt;210&gt; 1381

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 115..483

&lt;400&gt; 1381

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ggctcccga agttccacgt cagtcagtct gacggtcagt ggatcgggtg gtttatctca      60
aggcctgagt agccggtaac aaacgagggt tcccgggatt ggaccgacgc agcc atg      117
                Met
                1
cct ctg cga ctt gat atc aaa aga aag cta act gct aga tct gat cga      165
Pro Leu Arg Leu Asp Ile Lys Arg Lys Leu Thr Ala Arg Ser Asp Arg
                5             10             15
gtt aag agt gtg gat ctg cat cct aca gag cca tgg atg ttg gca agt      213
Val Lys Ser Val Asp Leu His Pro Thr Glu Pro Trp Met Leu Ala Ser
                20             25             30
ctt tac aat ggc agt gtg tgt gtt tgg aat cat gaa aca cag aca ctg      261
Leu Tyr Asn Gly Ser Val Cys Val Trp Asn His Glu Thr Gln Thr Leu
                35             40             45
gtg aag aca ttt gaa gta tgt gat ctt cct gtt cga gct gca aag ttt      309
Val Lys Thr Phe Glu Val Cys Asp Leu Pro Val Arg Ala Ala Lys Phe
50             55             60             65

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gtt gca agg aag aat tgg gtt gtg aca gga gcg gat gac atg cag att	357
Val Ala Arg Lys Asn Trp Val Val Thr Gly Ala Asp Asp Met Gln Ile	
70 75 80	
aga gtg ttc aat tac aat act ctg gag aga gtt cat atg ttt gaa gca	405
Arg Val Phe Asn Tyr Asn Thr Leu Glu Arg Val His Met Phe Glu Ala	
85 90 95	
cac tca gac tac att cgc tgt att gct gtt cat cca acc cag cct ttc	453
His Ser Asp Tyr Ile Arg Cys Ile Ala Val His Pro Thr Gln Pro Phe	
100 105 110	
att cwa cta gca gtg atg aca tgc tta tta a	484
Ile Xaa Leu Ala Val Met Thr Cys Leu Leu	
115 120	

<210> 1382  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 54..401

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Met	
1	
tca tca ttg cca aga aga gcg aaa gta cag gtc cag gat gtg gta ctg	104
Ser Ser Leu Pro Arg Arg Ala Lys Val Gln Val Gln Asp Val Val Leu	
5 10 15	
aaa gat gaa ttt tct tca ttc tct gag tta tca tct gcc tct gaa gaa	152
Lys Asp Glu Phe Ser Ser Phe Ser Glu Leu Ser Ser Ala Ser Glu Glu	
20 25 30	
gat gac aag gaa gat agt gcc tgg gag ccc caa aag aaa gtt ccc aga	200
Asp Asp Lys Glu Asp Ser Ala Trp Glu Pro Gln Lys Lys Val Pro Arg	
35 40 45	
agc cgt aaa cag ccc cct ccc aag gaa tcc aaa cca aag agg atg cct	248
Ser Arg Lys Gln Pro Pro Pro Lys Glu Ser Lys Pro Lys Arg Met Pro	
50 55 60 65	
cgg gtg aag aag aat gcc cca cag atc agt gat ggc tca gaa gtc gtt	296
Arg Val Lys Lys Asn Ala Pro Gln Ile Ser Asp Gly Ser Glu Val Val	
70 75 80	
gtt gtt aag gag gag ctg aat agc tct gtg gct att gct gat act gct	344
Val Val Lys Glu Glu Leu Asn Ser Ser Val Ala Ile Ala Asp Thr Ala	
85 90 95	
tta gaa gac aga aaa aat aaa ttg gat act gta cag act ctg aaa aca	392
Leu Glu Asp Arg Lys Asn Lys Leu Asp Thr Val Gln Thr Leu Lys Thr	
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gcc aag aca aa	403
Ala Lys Thr	
115	

<210> 1383  
 <211> 372

004220"666EFS60

<212> DNA  
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<222> 37..372

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1 5  
gct gaa gag gaa ata aaa aca gaa cag gag gtg gta nra ggg cat gga 102  
Ala Glu Glu Glu Ile Lys Thr Glu Gln Glu Val Val Xaa Gly His Gly  
10 15 20  
tat ctc tac tcg ctc caa aga tcc tgg ctc tgc aga gag aac agc cca 150  
Tyr Leu Tyr Ser Leu Gln Arg Ser Trp Leu Cys Arg Glu Asn Ser Pro  
25 30 35  
gaa aag aaa gtt ccc cag ccc tcc aca ttc ttc caa tgg cca ctc gcc 198  
Glu Lys Lys Val Pro Gln Pro Ser Thr Phe Phe Gln Trp Pro Leu Ala  
40 45 50  
gca gac aca tca aca agc ccc att aaa aag aaa aag aaa cct ggc tta 246  
Ala Asp Thr Ser Thr Ser Pro Ile Lys Lys Lys Lys Lys Pro Gly Leu  
55 60 65 70  
ctg aac agt aac aat aag gag cag gat gga cgg aat gat ttc tac tgc 294  
Leu Asn Ser Asn Asn Lys Glu Gln Asp Gly Arg Asn Asp Phe Tyr Cys  
75 80 85  
tgg gtt tgt cac cgg gaa ggc caa gtc ctt tgc tgt gag ctc tgt ccc 342  
Trp Val Cys His Arg Glu Gly Gln Val Leu Cys Cys Glu Leu Cys Pro  
90 95 100  
cgg gtt tat cac gct aag tgt ctg aga ctg 372  
Arg Val Tyr His Ala Lys Cys Leu Arg Leu  
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<210> 1384  
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<212> DNA  
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ctctttgagg agaatcgtga ccaag atg tgg aac agt gga ttc gaa agc tat 172  
Met Trp Asn Ser Gly Phe Glu Ser Tyr  
1 5  
ggc agc tcc tca tac ggg gga gcc ggc ggc tac acg cag tcc ccg ggg 220  
Gly Ser Ser Ser Tyr Gly Gly Ala Gly Gly Tyr Thr Gln Ser Pro Gly  
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ggc ttt gga tcg ccc gca cct tct caa gcc gaa aag aaa tca aga gcc 268



Gly Phe Gly Ser Pro Ala Pro Ser Gln Ala Glu Lys Lys Ser Arg Ala	
30 35 40	
cga gcc cag cac att gtg ccc tgt act ata tct cag ctg ctt tct gcc	316
Arg Ala Gln His Ile Val Pro Cys Thr Ile Ser Gln Leu Leu Ser Ala	
45 50 55	
act ttg gtt gat gaa gtg ttc aga att ggg aat gtt gag att tca cag	364
Thr Leu Val Asp Glu Val Phe Arg Ile Gly Asn Val Glu Ile Ser Gln	
60 65 70	
gtc act att gtg ggg atc atc aga cat gca gag aag gct cca acc aac	412
Val Thr Ile Val Gly Ile Ile Arg His Ala Glu Lys Ala Pro Thr Asn	
75 80 85	
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Ile Val Tyr Lys Ile Asp Asp Met Thr	
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cag aca gcc tct ctc act gcc gcg tac ggt cag ctc agt aag ggc aag	101
Gln Thr Ala Ser Leu Thr Ala Ala Tyr Gly Gln Leu Ser Lys Gly Lys	
10 15 20	
cct gca gag tgc cga atg gac tcc cca aaa gaa atc agt caa gcc gga	149
Pro Ala Glu Cys Arg Met Asp Ser Pro Lys Glu Ile Ser Gln Ala Gly	
25 30 35	
ttc gaa tgg cag agg aca gag ggc aaa ctg aat gaa att ggg ctg aat	197
Phe Glu Trp Gln Arg Thr Glu Gly Lys Leu Asn Glu Ile Gly Leu Asn	
40 45 50	
gtc agc atg gac ggg caa cca aaa gat ggg ctt gtg awk aat gcc agc	245
Val Ser Met Asp Gly Gln Pro Lys Asp Gly Leu Val Xaa Asn Ala Ser	
55 60 65 70	
ttc ctg gag cag aac aag ctc tgc ttt ttt gag ggg aag cta gac aaa	293
Phe Leu Glu Gln Asn Lys Leu Cys Phe Phe Glu Gly Lys Leu Asp Lys	
75 80 85	
gag ctg agc att gaa atg cag gac aag gac tgt caa gaa gcc tca ggt	341
Glu Leu Ser Ile Glu Met Gln Asp Lys Asp Cys Gln Glu Ala Ser Gly	
90 95 100	
cac ctt gag agc agg tat gtg att tca gag acc tgc cat ccc ttg gag	389
His Leu Glu Ser Arg Tyr Val Ile Ser Glu Thr Cys His Pro Leu Glu	
105 110 115	
ggg aac tcg gta cac cag aag acc tcc gag ttc cat ctg gga ctc ata	437
Gly Asn Ser Val His Gln Lys Thr Ser Glu Phe His Leu Gly Leu Ile	
120 125 130	
gag ggg cca gac aaa aac aaa acc att cca gtt cag ggg aag gtg gca	485

Glu Gly Pro Asp Lys Asn Lys Thr Ile Pro Val Gln Gly Lys Val Ala  
 135 140 145 150  
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 Gly Lys Asn Gly Leu Glu Thr Lys Ser Gln Ser Asp  
 155 160

521

<210> 1386  
 <211> 165  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 Gly Arg Ala Leu Arg Leu Arg Gly Arg Ala Trp Val Arg Thr Thr Arg  
 15 20 25  
 gcc gcg gcg acc tct gat cgt cac cca agc tgt gcc ctc cca ttt cac 145  
 Ala Ala Ala Thr Ser Asp Arg His Pro Ser Cys Ala Leu Pro Phe His  
 30 35 40 45  
 gaa aat tat cac ctg ctg ag 165  
 Glu Asn Tyr His Leu Leu  
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 <212> DNA  
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 ttttaattttt cttttctagc ttcccatcga cggctcagtgc gcacgttgta atcagctgag 180  
 gcc atg tca gga gac gga gcc asg gag cag gca gct gag tat gtc cca 228  
 Met Ser Gly Asp Gly Ala Xaa Glu Gln Ala Ala Glu Tyr Val Pro  
 1 5 10 15  
 gag aag gtg aag aaa gcg gaa aag aaa tta gaa gag aat cca tat gac 276  
 Glu Lys Val Lys Lys Ala Glu Lys Lys Leu Glu Glu Asn Pro Tyr Asp  
 20 25 30  
 ctt gat gct tgg agc att ctc att cga gag gca cag aat caa cct ata 324  
 Leu Asp Ala Trp Ser Ile Leu Ile Arg Glu Ala Gln Asn Gln Pro Ile  
 35 40 45  
 gac aaa gca cgg aag act tat gaa cgc ctt gtt gcc cag ttc ccc agt 372

Asp Lys Ala Arg Lys Thr Tyr Glu Arg Leu Val Ala Gln Phe Pro Ser  
 50 55 60  
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 Ser Gly Arg Phe Trp Lys Leu Tyr Ile Glu Ala  
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406

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 24..380

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 Lys Leu Leu Arg Ala Leu Ala Leu Arg Pro Arg Phe Leu Ala Ala Gly  
 15 20 25  
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 Ser Gln Ala Val Gln Leu Thr Ser Arg Arg Trp Leu Asn Leu Gln Glu  
 30 35 40  
 tac cag agc aag aaa ctg atg tct gac aac gga gtg aga gtt caa aga 197  
 Tyr Gln Ser Lys Lys Leu Met Ser Asp Asn Gly Val Arg Val Gln Arg  
 45 50 55  
 ttc ttt gta gca gac act gca aat gaa gct ctc gag gct gct aag aga 245  
 Phe Phe Val Ala Asp Thr Ala Asn Glu Ala Leu Glu Ala Ala Lys Arg  
 60 65 70  
 cta aat gca aaa gaa att gtt tta aaa gcc cag atc tta gct gga gga 293  
 Leu Asn Ala Lys Glu Ile Val Leu Lys Ala Gln Ile Leu Ala Gly Gly  
 75 80 85 90  
 aga gga aaa ggt gtc ttc aat agt ggt ttg aaa gga ggt gtt cat tww 341  
 Arg Gly Lys Gly Val Phe Asn Ser Gly Leu Lys Gly Gly Val His Xaa  
 95 100 105  
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 <222> 2..244

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Met Gln Gly Gly Asn Ser Gly Val Arg Lys Arg Glu Glu Glu Gly Asp  
 1 5 10 15  
 ggg gct ggg gct gtg gct gcg ccg ccg gcc atc gac ttt ccc gcc gag 97  
 Gly Ala Gly Ala Val Ala Ala Pro Pro Ala Ile Asp Phe Pro Ala Glu  
 20 25 30  
 ggc ccg gac ccc gaa tat gac gaa tct gat gtt cca gca kaa atc cag 145  
 Gly Pro Asp Pro Glu Tyr Asp Glu Ser Asp Val Pro Ala Xaa Ile Gln  
 35 40 45  
 gtg tta aaa gaa ccc cta caa cag cca acc ttc cct ttt gca gtt gca 193  
 Val Leu Lys Glu Pro Leu Gln Gln Pro Thr Phe Pro Phe Ala Val Ala  
 50 55 60  
 aac caa ctc ttg ctg gtt tct ttg ctg gag cac ttg agc cac gtg cat 241  
 Asn Gln Leu Leu Leu Val Ser Leu Leu Glu His Leu Ser His Val His  
 65 70 75 80  
 gaa cc 246  
 Glu

<210> 1390  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 37..489

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 Met Gly Glu Leu Met Ala  
 1 5  
 ttc ctg tta cct ctc atc att gtg tta atg gtg aag cac agc gat tcc 102  
 Phe Leu Leu Pro Leu Ile Ile Val Leu Met Val Lys His Ser Asp Ser  
 10 15 20  
 cgg acg cac tct ctg aga tat ttt cgc ctg ggc gtt tcg gat ccc atc 150  
 Arg Thr His Ser Leu Arg Tyr Phe Arg Leu Gly Val Ser Asp Pro Ile  
 25 30 35  
 cat ggg gtc cct gaa ttt att tcg gtt ggg tac gtg gac tcg cac cct 198  
 His Gly Val Pro Glu Phe Ile Ser Val Gly Tyr Val Asp Ser His Pro  
 40 45 50  
 atc acc aca tat gac agt gtc act cgg cag aag gag cca cgg gcc cca 246  
 Ile Thr Thr Tyr Asp Ser Val Thr Arg Gln Lys Glu Pro Arg Ala Pro  
 55 60 65 70  
 tgg atg gca gag aac ctc gcg cct gat cac tgg gag agg tac act cag 294  
 Trp Met Ala Glu Asn Leu Ala Pro Asp His Trp Glu Arg Tyr Thr Gln  
 75 80 85  
 ctg ctg agg ggc tgg cag cag atg ttc aag gtg gaa ctg aag cgc cta 342  
 Leu Leu Arg Gly Trp Gln Gln Met Phe Lys Val Glu Leu Lys Arg Leu  
 90 95 100  
 cag agg cac tac aat cac tca ggg tct cac act tac cag aga atg att 390  
 Gln Arg His Tyr Asn His Ser Gly Ser His Thr Tyr Gln Arg Met Ile  
 105 110 115  
 ggc tgt gag ctg ctg gag gat gga agc acc aca gga ttt ctg cag tat 438  
 Gly Cys Glu Leu Leu Glu Asp Gly Ser Thr Thr Gly Phe Leu Gln Tyr

120	125	130	
gca tat gac ggg cag gat ttc ctg atc ttc aat aaa gac acc ctc tcc			486
Ala Tyr Asp Gly Gln Asp Phe Leu Ile Phe Asn Lys Asp Thr Leu Ser			
135	140	145	150
tgg ct			
Trp			491

<210> 1391  
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<220>  
 <221> CDS  
 <222> 22..219

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Met Asn Leu Gly Ala Arg Lys Ser Lys Lys	
1 5 10	
ttg gga aag tta aaa ggg att cac gag gag cag cca cag cag cag cag	99
Leu Gly Lys Leu Lys Gly Ile His Glu Glu Gln Pro Gln Gln Gln Gln	
15 20 25	
ccc cca ccc cca ccc cca ccc ccg caa agc cca gag gaa ggg aca acg	147
Pro Pro Pro Pro Pro Pro Pro Pro Gln Ser Pro Glu Glu Gly Thr Thr	
30 35 40	
tac atc gct cct gca aaa gaa ccc tcg gtc aac aca gca ctg gtt cct	195
Tyr Ile Ala Pro Ala Lys Glu Pro Ser Val Asn Thr Ala Leu Val Pro	
45 50 55	
cag ctc tcc aca atc tca cga acg	219
Gln Leu Ser Thr Ile Ser Arg Thr	
60 65	

<210> 1392  
 <211> 529  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 145..528

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agttgagacg tgattaccgg gttgggcggg ccccatcttg gaggggtttg tgggtgaact	120
cgggggtccac cgcccgtga ggag atg gat gag gac ggg ctt cct ctc atg	171
Met Asp Glu Asp Gly Leu Pro Leu Met	
1 5	
ggg tca ggc ata gac ctg acc aas gtg cca gct att caa cag aaa aga	219
Gly Ser Gly Ile Asp Leu Thr Xaa Val Pro Ala Ile Gln Gln Lys Arg	
10 15 20 25	
acg gtg gct ttt cta aac caa ttt gtg gtg cac act gta cag ttc ctc	267

Thr	Val	Ala	Phe	Leu	Asn	Gln	Phe	Val	Val	His	Thr	Val	Gln	Phe	Leu	
				30					35				40			
aac	cgc	ttt	tct	aca	gtt	tgt	gag	gag	aaa	ctg	gca	gac	ctt	tca	ctt	315
Asn	Arg	Phe	Ser	Thr	Val	Cys	Glu	Glu	Lys	Leu	Ala	Asp	Leu	Ser	Leu	
			45					50				55				
cgt	atc	caa	caa	att	gaa	aca	act	ctc	aat	att	tta	gat	gca	aag	ntg	363
Arg	Ile	Gln	Gln	Ile	Glu	Thr	Thr	Leu	Asn	Ile	Leu	Asp	Ala	Lys	Xaa	
		60					65				70					
tca	tct	atc	cca	ggc	cta	gat	gat	gtc	aca	gtt	gaa	gta	tct	cct	tta	411
Ser	Ser	Ile	Pro	Gly	Leu	Asp	Asp	Val	Thr	Val	Glu	Val	Ser	Pro	Leu	
	75					80				85						
aat	gtc	acc	agt	gtc	aca	aat	gga	gca	cat	cct	gaa	gcc	act	tca	gag	459
Asn	Val	Thr	Ser	Val	Thr	Asn	Gly	Ala	His	Pro	Glu	Ala	Thr	Ser	Glu	
	90				95				100						105	
caa	cca	cag	cag	aac	agt	aca	cga	gac	tct	gga	cta	cag	gaa	agt	gaa	507
Gln	Pro	Gln	Gln	Asn	Ser	Thr	Arg	Asp	Ser	Gly	Leu	Gln	Glu	Ser	Glu	
				110				115					120			
gta	tca	gca	gaa	aat	atc	tta	a									529
Val	Ser	Ala	Glu	Asn	Ile	Leu										
				125												

<210> 1393  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 79..369

<400> 1393																
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ggtttgcgga	stgctagg	atg	gag	cag	gtt	gcg	gag	gga	gca	agg	gtg	acc	111			
		Met	Glu	Gln	Val	Ala	Glu	Gly	Ala	Arg	Val	Thr				
		1				5					10					
gca	gtc	cct	gtg	tca	gct	gcc	gac	agc	act	gag	gag	ttg	gcc	gaa	gtc	159
Ala	Val	Pro	Val	Ser	Ala	Ala	Asp	Ser	Thr	Glu	Glu	Leu	Ala	Glu	Val	
		15					20					25				
gaa	gaa	gga	gtt	gga	gta	gtg	ggc	gaa	gat	aat	gac	gca	gcc	gcg	aga	207
Glu	Glu	Gly	Val	Gly	Val	Val	Gly	Glu	Asp	Asn	Asp	Ala	Ala	Ala	Arg	
		30					35				40					
gga	gcg	gag	gcc	ttt	ggc	gac	agt	gag	gag	gac	gga	gag	gat	gtg	ttc	255
Gly	Ala	Glu	Ala	Phe	Gly	Asp	Ser	Glu	Glu	Asp	Gly	Glu	Asp	Val	Phe	
	45				50				55							
gag	gtg	gag	aag	atc	ctg	gac	atg	aag	acc	gag	ggg	ggt	aaa	gtt	ctt	303
Glu	Val	Glu	Lys	Ile	Leu	Asp	Met	Lys	Thr	Glu	Gly	Gly	Lys	Val	Leu	
	60				65				70					75		
tac	aaa	gtt	cgc	tgg	aaa	ggc	tat	aca	tcg	gat	gat	gat	acc	tgg	gag	351
Tyr	Lys	Val	Arg	Trp	Lys	Gly	Tyr	Thr	Ser	Asp	Asp	Asp	Thr	Trp	Glu	
			80					85					90			
ccc	gag	att	cac	ctg	gag	ga										371
Pro	Glu	Ile	His	Leu	Glu											
				95												

<210> 1394  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 218..385

<400> 1394  
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 ttgtggagtg gcgtagacga gttaagtcct ggtctgcgtg gaggtcgacg actccgtcgc 120  
 agactacgga cctgtctggg tctcagccgc caaagacccc gtccggtagg tgagtggctc 180  
 actttgaggg caagccttct cggatcgagg cttcttc atg gcc gct cag atc gtg 235  
 Met Ala Ala Gln Ile Val  
 1 5  
 agc ggc cgg ggc tgc tct ctt tgc gga gga tgg cgt cta atg agc gca 283  
 Ser Gly Arg Gly Cys Ser Leu Cys Gly Gly Trp Arg Leu Met Ser Ala  
 10 15 20  
 gtt gat tgc agg tgg gcg ctg ggg cac gtc tcc ctt ttg gca tac tgt 331  
 Val Asp Ser Arg Trp Ala Leu Gly His Val Ser Leu Leu Ala Tyr Cys  
 25 30 35  
 ttg agg ggt act gag gtg aaa ggg cgg tca ctg ttc ggg tgc ttt tta 379  
 Leu Arg Gly Thr Glu Val Lys Gly Arg Ser Leu Phe Gly Ser Phe Leu  
 40 45 50  
 cac agc 385  
 His Ser  
 55

<210> 1395  
 <211> 494  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 147..494

<400> 1395  
 agtgcgtgcg cggggcatgc cgggagtggg tgtgtacggt ccgcagcggc aggtgaagcc 60  
 tagcagagga cgcggccagg cgattcgggtg aagcgattcc tgcaggcggtt gggtccctcc 120  
 tttgacctgg atttgaattt gttgaa atg agc agt cgt aaa tca aag agt aac 173  
 Met Ser Ser Arg Lys Ser Lys Ser Asn  
 1 5  
 agc tta att cac aca gag tgc ctt tca cag gta caa aga att tta cgt 221  
 Ser Leu Ile His Thr Glu Cys Leu Ser Gln Val Gln Arg Ile Leu Arg  
 10 15 20 25  
 gaa aga ttt tgt cgt cag agt cca cat agt aac cta ttt gga gtg caa 269  
 Glu Arg Phe Cys Arg Gln Ser Pro His Ser Asn Leu Phe Gly Val Gln  
 30 35 40  
 gta caa tac aaa cac tta agt gag ctg ctg aaa aga act gct ctc cat 317

Val	Gln	Tyr	Lys	His	Leu	Ser	Glu	Leu	Leu	Lys	Arg	Thr	Ala	Leu	His		
			45					50					55				
gga	gag	agt	aac	tct	gtc	ctt	att	atc	gga	ccc	cga	gga	tcn	gga	aaa		365
Gly	Glu	Ser	Asn	Ser	Val	Leu	Ile	Ile	Gly	Pro	Arg	Gly	Ser	Gly	Lys		
		60					65					70					
act	atg	tta	ata	agt	cat	gct	ttg	aaa	gar	ctc	atg	gaa	ata	gaa	gaa		413
Thr	Met	Leu	Ile	Ser	His	Ala	Leu	Lys	Glu	Leu	Met	Glu	Ile	Glu	Glu		
	75					80				85							
gtg	agt	gaa	aat	gta	tta	caa	gtt	cac	tta	aat	gga	ctg	ctg	cag	ats		461
Val	Ser	Glu	Asn	Val	Leu	Gln	Val	His	Leu	Asn	Gly	Leu	Leu	Gln	Xaa		
90					95				100					105			
rat	gac	aaa	atc	gcc	cta	aag	gaa	atc	aca	agg							494
Xaa	Asp	Lys	Ile	Ala	Leu	Lys	Glu	Ile	Thr	Arg							
			110					115									

<210> 1396

<211> 318

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..318

<400> 1396

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Met	Ala	Thr	Ser	Ala	Thr	Ser	Pro	His	Ala	Pro	Gly	Phe	Pro	Ala			
1				5				10					15				
gag	ggg	aga	tgc	ggg	tac	tat	gtg	gaa	aag	aaa	cgg	ttc	tgc	agg			96
Glu	Gly	Arg	Cys	Gly	Tyr	Tyr	Val	Glu	Lys	Lys	Lys	Arg	Phe	Cys	Arg		
			20				25					30					
atg	gtg	gtg	gcc	gca	ggg	aaa	aga	ttt	tgt	ggg	gaa	cac	gct	gga	gcc		144
Met	Val	Val	Ala	Ala	Gly	Lys	Arg	Phe	Cys	Gly	Glu	His	Ala	Gly	Ala		
		35				40					45						
atg	gag	gaa	gat	gct	cgg	aaa	aga	atc	ctg	tgt	cct	tta	gat	cca			192
Met	Glu	Glu	Glu	Asp	Ala	Arg	Lys	Arg	Ile	Leu	Cys	Pro	Leu	Asp	Pro		
	50					55					60						
aaa	cac	aca	gta	tat	gaa	gat	caa	cta	gsa	aag	cat	ttg	aaa	aaa	tgt		240
Lys	His	Thr	Val	Tyr	Glu	Asp	Gln	Leu	Xaa	Lys	His	Leu	Lys	Lys	Cys		
	65					70					75						
aac	tca	aga	gag	aaa	cca	aaa	cct	gat	ttc	tat	att	caa	gat	att	aat		288
Asn	Ser	Arg	Glu	Lys	Pro	Lys	Pro	Asp	Phe	Tyr	Ile	Gln	Asp	Ile	Asn		
80					85				90					95			
gca	ggc	tta	aga	gat	gaa	aca	gaa	ata	cct								318
Ala	Gly	Leu	Arg	Asp	Glu	Thr	Glu	Ile	Pro								
			100					105									

<210> 1397

<211> 540

<212> DNA

<213> Homo sapiens

<220>



<221> CDS  
<222> 120..539

<400> 1397

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ctcagtcctat sagggggggg aggggggtggc gcgcgcgcca tttctagtcg ttttcaaagc      60
gcctcgcgct gattctcacg ggccccgctg ccggcccccg ctctgccctg cataataaa      119
atg gct aat cag gtg aat ggt aat gcg gta cag tta aaa gaa gag gaa      167
Met Ala Asn Gln Val Asn Gly Asn Ala Val Gln Leu Lys Glu Glu Glu
1          5          10          15
gaa cca atg gat act tcc agt gta act cac aca gaa cac tac aag aca      215
Glu Pro Met Asp Thr Ser Ser Val Thr His Thr Glu His Tyr Lys Thr
20          25          30
ctg ata gag gca ggc ctc cca cag aag gtg gca gaa aga ctt gat gaa      263
Leu Ile Glu Ala Gly Leu Pro Gln Lys Val Ala Glu Arg Leu Asp Glu
35          40          45
ata ttt cag aca gga ttg gta gct tat gtc gat ctt gat gaa aga gca      311
Ile Phe Gln Thr Gly Leu Val Ala Tyr Val Asp Leu Asp Glu Arg Ala
50          55          60
att gat gct ctc agg gaa ttt aat gaa gwa gga gct ctg tct gta cta      359
Ile Asp Ala Leu Arg Glu Phe Asn Glu Xaa Gly Ala Leu Ser Val Leu
65          70          75          80
cag cag ttc aag gaa agt gac tta tca cat gtt cag aac aaa agt gca      407
Gln Gln Phe Lys Glu Ser Asp Leu Ser His Val Gln Asn Lys Ser Ala
85          90          95
ttt tta tgt gga gtt atg aag acc tac agg cag aga gag aaa cag ggg      455
Phe Leu Cys Gly Val Met Lys Thr Tyr Arg Gln Arg Glu Lys Gln Gly
100          105          110
agc aag gtg caa gag tcc aca aag gga cct gat gaa gcg aag atc aag      503
Ser Lys Val Gln Glu Ser Thr Lys Gly Pro Asp Glu Ala Lys Ile Lys
115          120          125
gcc ttg ctt gag aga act ggt tat act ctg gat gta a      540
Ala Leu Leu Glu Arg Thr Gly Tyr Thr Leu Asp Val
130          135          140

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<210> 1398  
<211> 329  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 27..329

<400> 1398

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tatttctcct cccctcccg gccaaag atg tct gac atg gag gat gat ttc atg      53
Met Ser Asp Met Glu Asp Asp Phe Met
1          5
tgc gat gat gag gag gac tac gac ctg gaa tac tct gaa gat agt aac      101
Cys Asp Asp Glu Glu Asp Tyr Asp Leu Glu Tyr Ser Glu Asp Ser Asn
10          15          20          25
tcc gag cca aat gtg gat ttg gaa aat cag tac tat aat tcc aaa gca      149
Ser Glu Pro Asn Val Asp Leu Glu Asn Gln Tyr Tyr Asn Ser Lys Ala

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	30	35	40	
tta aaa gaa gat gac cca aaa gcg gca tta agc agt ttc caa aag gtt				197
Leu Lys Glu Asp Asp Pro Lys Ala Ala Leu Ser Ser Phe Gln Lys Val				
	45	50	55	
ttg gaa ctt gaa ggt gaa aaa gga gaa tgg gga ttt aaa gca ctg aaa				245
Leu Glu Leu Glu Gly Glu Lys Gly Glu Trp Gly Phe Lys Ala Leu Lys				
	60	65	70	
caa atg att aag att aac ttc aag ttg aca aac ttt cca gaa atg atg				293
Gln Met Ile Lys Ile Asn Phe Lys Leu Thr Asn Phe Pro Glu Met Met				
	75	80	85	
aat aga tat aag cag cta ttg acc tat att cgg agt				329
Asn Arg Tyr Lys Gln Leu Leu Thr Tyr Ile Arg Ser				
90	95	100		
<210> 1399				
<211> 592				
<212> DNA				
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ctctctatca gccgctcact ccgtctcaat atgtctcaag atg gcg gcc aat gtg				55
			Met Ala Ala Asn Val	
			1 5	
gga tcg atg ttt caa tat tgg aag cgc ttt gat tta cag cag ctg cag				103
Gly Ser Met Phe Gln Tyr Trp Lys Arg Phe Asp Leu Gln Gln Leu Gln				
	10	15	20	
aga gaa ctc gat gcc acc gca acg gta ttg gcg aac cgg cag gat gaa				151
Arg Glu Leu Asp Ala Thr Ala Thr Val Leu Ala Asn Arg Gln Asp Glu				
	25	30	35	
agt gag cag tcc aga aag cgg ctt atc gaa cag agc cgg gag ttc aag				199
Ser Glu Gln Ser Arg Lys Arg Leu Ile Glu Gln Ser Arg Glu Phe Lys				
	40	45	50	
aag aac act cca gag gat ttg cgc aag cag gta gcg ccg ctg ctg aag				247
Lys Asn Thr Pro Glu Asp Leu Arg Lys Gln Val Ala Pro Leu Leu Lys				
	55	60	65	
agt ttc caa gga gag att gat gca ctg agt aaa aga agc aag gaa gct				295
Ser Phe Gln Gly Glu Ile Asp Ala Leu Ser Lys Arg Ser Lys Glu Ala				
	70	75	80	85
gaa gca gct ttc ttg aat gtc tac aaa aga ttg att gac gtc cca gat				343
Glu Ala Ala Phe Leu Asn Val Tyr Lys Arg Leu Ile Asp Val Pro Asp				
	90	95	100	
ccc gta cca gct ttg gat ctc gga cag caa ctc cag ctc aaa gtg cag				391
Pro Val Pro Ala Leu Asp Leu Gly Gln Gln Leu Gln Leu Lys Val Gln				
	105	110	115	
cgc ctg cac gat att gaa aca gag aac cag aaa ctt agg gaa act ctg				439
Arg Leu His Asp Ile Glu Thr Glu Asn Gln Lys Leu Arg Glu Thr Leu				
	120	125	130	
gaa gaa tac aac aag gaa ttt gct gaa gtg aaa aat caa gag gtt acg				487
Glu Glu Tyr Asn Lys Glu Phe Ala Glu Val Lys Asn Gln Glu Val Thr				



<220>  
 <221> CDS  
 <222> 99..470

<400> 1401

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ctttctctgt tcgcgatgtg acgtaacgcg cctgcggact gggcccagct tgtcctctat      60
gacttaccca gaaggcaacg cttctctttc tgggtcaaaa atg gct ggt aag cag gcc      116
                               Met Ala Gly Lys Gln Ala
                               1           5
gtt tca gca tca ggc aag tgg ctg gat ggt att cga aaa tgg tat tac      164
Val Ser Ala Ser Gly Lys Trp Leu Asp Gly Ile Arg Lys Trp Tyr Tyr
                10           15           20
aat gct gca gga ttc aat aaa ctg ggg tta atg cga gat gat aca ata      212
Asn Ala Ala Gly Phe Asn Lys Leu Gly Leu Met Arg Asp Asp Thr Ile
                25           30           35
tac gag gat gaa gat gta aaa gaa gcc ata aga aga ctt cct gag aac      260
Tyr Glu Asp Glu Asp Val Lys Glu Ala Ile Arg Arg Leu Pro Glu Asn
                40           45           50
ctt tat aat gac agg atg ttt cgc att aag agg gca ctg gac ctg aac      308
Leu Tyr Asn Asp Arg Met Phe Arg Ile Lys Arg Ala Leu Asp Leu Asn
                55           60           65           70
ttg aag cat cag atc ttg cct aaa gag cag tgg acc aaa tat gaa gag      356
Leu Lys His Gln Ile Leu Pro Lys Glu Gln Trp Thr Lys Tyr Glu Glu
                75           80           85
gta gca cag ctt tat cta cct gac agt gtt gct cat taw gga tgg agt      404
Val Ala Gln Leu Tyr Leu Pro Asp Ser Val Ala His Xaa Gly Trp Ser
                90           95           100
ttt aga rac aag aga aac atg ttc att tgc ata gtg tta gag ttc tct      452
Phe Arg Xaa Lys Arg Asn Met Phe Ile Cys Ile Val Leu Glu Phe Ser
                105           110           115
gag tca tgt caa ata aat a
Glu Ser Cys Gln Ile Asn
                120

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<210> 1402  
 <211> 254  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 40..252

<400> 1402

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                               Met Ala Pro Arg Lys
                               1           5
ggg aag gaa aag aag gaa gaa cag gtc atc agc ctc gga cct cag gtg      102
Gly Lys Glu Lys Lys Glu Glu Gln Val Ile Ser Leu Gly Pro Gln Val
                10           15           20
gct gaa gga gag aat gta ttt ggt gtc tgc cat atc ttt gca tcc ttc      150
Ala Glu Gly Glu Asn Val Phe Gly Val Cys His Ile Phe Ala Ser Phe

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	25		30		35		
aat gac act ttg tcc akc tca ctg atc ttt ckg gca agt gag tac ctg						198	
Asn Asp Thr Leu Ser Xaa Ser Leu Ile Phe Xaa Ala Ser Glu Tyr Leu							
	40		45		50		
ggt gga gag gca tcc agc tgg caa aag gct gag gaa ggc aat ggc tgg						246	
Gly Gly Glu Ala Ser Ser Trp Gln Lys Ala Glu Glu Gly Asn Gly Trp							
	55		60		65		
gac ggg ct						254	
Asp Gly							
70							
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<222>	115..678						
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acggcgtgtt ggtcccagcg gttcagctga ggtagggacg tgctgtaggc cgga atg						117	
					Met		
					1		
tta ccg gct gtt gga tct gyg gat gag gar gag gat cct gcg gag gag						165	
Leu Pro Ala Val Gly Ser Xaa Asp Glu Glu Glu Asp Pro Ala Glu Glu							
	5		10		15		
gat tgt cct gaa ttg gtt ccc att gag acg acg caa agc gag gag gag						213	
Asp Cys Pro Glu Leu Val Pro Ile Glu Thr Thr Gln Ser Glu Glu Glu							
	20		25		30		
gaa aag tct ggc ctc ggc gcc aag atc cca gtc aca att atc acc ggg						261	
Glu Lys Ser Gly Leu Gly Ala Lys Ile Pro Val Thr Ile Ile Thr Gly							
	35		40		45		
tat tta ggt gct ggg aag aca aca ctt ctg aac tat att ttg aca gag						309	
Tyr Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn Tyr Ile Leu Thr Glu							
	50		55		60		65
caa cat agt aaa aga gta gcg gtc att tta aat gaa tyt ggg gaa gga						357	
Gln His Ser Lys Arg Val Ala Val Ile Leu Asn Glu Xaa Gly Glu Gly							
	70		75		80		
agt gcg ctg gag aaa tcc tta gct gtc agc caa ggt gga gag ctc tat						405	
Ser Ala Leu Glu Lys Ser Leu Ala Val Ser Gln Gly Gly Glu Leu Tyr							
	85		90		95		
gaa gag tgg ctg gaa ctt aga aac ggt tgc ctc tgc tgt tca gtg aag						453	
Glu Glu Trp Leu Glu Leu Arg Asn Gly Cys Leu Cys Cys Ser Val Lys							
	100		105		110		
gac aat ggc ctt aga gct att gag aat ttg atg caa aag aag ggg aaa						501	
Asp Asn Gly Leu Arg Ala Ile Glu Asn Leu Met Gln Lys Lys Gly Lys							
	115		120		125		
ttt gat tac ata ctg tta gag acc act gga ttg gca gac cca ggt gca						549	
Phe Asp Tyr Ile Leu Leu Glu Thr Thr Gly Leu Ala Asp Pro Gly Ala							
	130		135		140		145
gtg gct tct atg ttt tgg gtt gat gct gaa tta ggg agt gat att tac						597	

Val	Ala	Ser	Met	Phe	Trp	Val	Asp	Ala	Glu	Leu	Gly	Ser	Asp	Ile	Tyr		
				150					155				160				
ctt	gat	ggt	atc	ata	act	ata	gtg	gat	tca	aaa	tat	gga	tta	aaa	cat	645	
Leu	Asp	Gly	Ile	Ile	Thr	Ile	Val	Asp	Ser	Lys	Tyr	Gly	Leu	Lys	His		
			165					170				175					
tta	gca	gaa	gag	aaa	cct	gat	ggc	ctt	atc	aat	g					679	
Leu	Ala	Glu	Glu	Lys	Pro	Asp	Gly	Leu	Ile	Asn							
		180					185										

<210> 1404  
 <211> 534  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 339..533

<400> 1404																
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ccagacctca	ctagacacaa	acttcctggc	accttgattt	tggaactcat	agcctctaga											120
actgtgctgg	gaagacaaca	cttctgaact	atattttgac	agagcaacat	agtaaaagag											180
tagcgggtcat	tttaaataaa	tttggggaag	gaagtgcgct	ggagaaatcc	ttagctgtca											240
gccaagggtgg	agagctctat	gaagagtggc	tggaacttag	aaacggttgc	ctctgctgtt											300
cagtgaagga	caatggcctt	agagctattg	agaatttg	atg	caa	aag	aag	ggg	aaa							356
					Met	Gln	Lys	Lys	Gly	Lys						
					1				5							
ttt	gat	tac	ata	ctg	tta	gag	acc	act	gga	ttg	gca	gac	cca	ggt	gca	404
Phe	Asp	Tyr	Ile	Leu	Leu	Glu	Thr	Thr	Gly	Leu	Ala	Asp	Pro	Gly	Ala	
			10					15				20				
gtg	gct	tct	atg	ttt	tgg	gtt	gat	gct	gaa	tta	ggg	agt	gat	att	tac	452
Val	Ala	Ser	Met	Phe	Trp	Val	Asp	Ala	Glu	Leu	Gly	Ser	Asp	Ile	Tyr	
		25				30					35					
ctt	gat	ggt	atc	ata	act	ata	gtg	gat	tca	aaa	tat	gga	tta	aaa	cat	500
Leu	Asp	Gly	Ile	Ile	Thr	Ile	Val	Asp	Ser	Lys	Tyr	Gly	Leu	Lys	His	
		40			45				50							
tta	gca	gaa	gag	aaa	cct	gat	ggc	ctt	atc	aat	g					534
Leu	Ala	Glu	Glu	Lys	Pro	Asp	Gly	Leu	Ile	Asn						
55				60				65								

<210> 1405  
 <211> 323  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 115..321

<400> 1405																
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acggcgtgtt	ggtcccagcg	gttcagctga	ggtagggacg	tgctgtaggc	cggga	atg										117

[illegible]

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<210> 1406
<211> 421
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 43..420
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[illegible]

120

125

<210> 1407  
 <211> 497  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 204..497

<400> 1407  
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 gatcagtgtg aacatgggta cgccctcttca ttcccgtcca tgccgagccc ccgactgcag 120  
 cattcaaagc cccacggag gtggaggcgk gtgtgagagg tcgcgsagag tgtgaacatg 180  
 gctacgcctc ttcattcccc tcc atg ccg agc ccc cga ctg cag cat tca aag 233  
 Met Pro Ser Pro Arg Leu Gln His Ser Lys  
 1 5 10  
 ccc cca cgg agg ttg agc cgg gca cag aaa cac agc agc ggg agc agc 281  
 Pro Pro Arg Arg Leu Ser Arg Ala Gln Lys His Ser Ser Gly Ser Ser  
 15 20 25  
 aac acc agc act gcc aac aga tct aca cac aat gag ctg gaa aag aat 329  
 Asn Thr Ser Thr Ala Asn Arg Ser Thr His Asn Glu Leu Glu Lys Asn  
 30 35 40  
 cga cga gct cat ctg cgc ctt tgt tta gaa cgc tta aaa gtt ctg att 377  
 Arg Arg Ala His Leu Arg Leu Cys Leu Glu Arg Leu Lys Val Leu Ile  
 45 50 55  
 cca cta gga cca gac tgc acc cgg cac aca aca ctt ggt ttg ctc aac 425  
 Pro Leu Gly Pro Asp Cys Thr Arg His Thr Thr Leu Gly Leu Leu Asn  
 60 65 70  
 aaa gcc aaa gca cac atc aag aaa ctt gaa gaa gct gaa aga aaa agc 473  
 Lys Ala Lys Ala His Ile Lys Lys Leu Glu Glu Ala Glu Arg Lys Ser  
 75 80 85 90  
 cag cac cag ctc gag aat ttg gaa 497  
 Gln His Gln Leu Glu Asn Leu Glu  
 95

<210> 1408  
 <211> 410  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 187..408

<400> 1408  
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 ctagaaaaga atcgtgacgg gcaggaaacc attacaccac cacctgggct gtgctctccg 120  
 gctcccgcgc ccacccccgc cctcgccttc gcctccgcct ccggtgcaca ttaaagatcc 180  
 aaagtc atg act gac tcc aag tat ttc aca acc aat aaa aaa gga gaa 228  
 Met Thr Asp Ser Lys Tyr Phe Thr Thr Asn Lys Lys Gly Glu



1	5	10	
ata ttt raa cta aaa gct gaa ctc aac aat gaa aag aaa gaa aag aga			276
Ile Phe Xaa Leu Lys Ala Glu Leu Asn Asn Glu Lys Lys Glu Lys Arg			
15	20	25	30
aag gag gct gtg aag aaa gtg att gcy gct atg acc gtg ggg aag gat			324
Lys Glu Ala Val Lys Lys Val Ile Ala Ala Met Thr Val Gly Lys Asp			
	35	40	45
gtt agt tct ctc ttt cca gac gta gtg aac tgt atg cag act gac aat			372
Val Ser Ser Leu Phe Pro Asp Val Val Asn Cys Met Gln Thr Asp Asn			
	50	55	60
ctg gaa cga gag aac twn cat cct tcc cca cgg tca ta			410
Leu Glu Arg Glu Asn Xaa His Pro Ser Pro Arg Ser			
65	70		

<210> 1409  
 <211> 286  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 118..285

<400> 1409	
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cggagccctt gcacgcctgc tctctttag cttctctcag cctagcccag catcact	117
atg gtg gac gct ttc ctg ggc acc tgg aag cta gtg gac agc aag aat	165
Met Val Asp Ala Phe Leu Gly Thr Trp Lys Leu Val Asp Ser Lys Asn	
1	5
ttc gat gac tac atg aag tca ctc ggt gtg ggt ttt gct acc agg cag	213
Phe Asp Asp Tyr Met Lys Ser Leu Gly Val Gly Phe Ala Thr Arg Gln	
	20
gtg gcc agc atg acc aag cct acc aca atc atc gaa aag aat ggg gac	261
Val Ala Ser Met Thr Lys Pro Thr Thr Ile Ile Glu Lys Asn Gly Asp	
	35
att ctc acc cta aaa aca cac agc a	286
Ile Leu Thr Leu Lys Thr His Ser	
	50
	55

<210> 1410  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 122..349

<400> 1410	
agaagggctc caggatggag gccgacctga cttctccgcc tcggtgggct gggtcggcgg	60
ctggagcatt acccctactg cgggtcccgcc tgctggcagc gctggaaact ggggtggacgg	120
c atg ggt tgg tct cag gat ttg ttc cgc gcc ttg tgg aga tcg ctg tca	169



&lt;400&gt; 1412

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ctcctcccag tgccacagag ccgaagcccg agctgccgcc gcagccacag ccgagggcac      60
t atg gct tct gga gtt aca gtg aat gat gaa gtc atc aaa gtt ttt aat      109
  Met Ala Ser Gly Val Thr Val Asn Asp Glu Val Ile Lys Val Phe Asn
    1           5           10           15
gat atg aaa gta agg aaa tct tct aca caa gag gag atc aaa aag aga      157
Asp Met Lys Val Arg Lys Ser Ser Thr Gln Glu Glu Ile Lys Lys Arg
           20           25           30
aag aaa gca gtt ctc ttc tgt tta agc gat gac aaa aga caa ata att      205
Lys Lys Ala Val Leu Phe Cys Leu Ser Asp Asp Lys Arg Gln Ile Ile
           35           40           45
gta gag gaa gca aag cag atc ttg gtg ggt gac att ggt gat act gta      253
Val Glu Glu Ala Lys Gln Ile Leu Val Gly Asp Ile Gly Asp Thr Val
           50           55           60
gag gac ccc tac aca tct ttt gtg aag ttg cta cct ctg aat gat tgc      301
Glu Asp Pro Tyr Thr Ser Phe Val Lys Leu Leu Pro Leu Asn Asp Cys
           65           70           75           80
cga tat gct ttg tac gat gc      321
Arg Tyr Ala Leu Tyr Asp
           85

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&lt;210&gt; 1413

&lt;211&gt; 279

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 56..277

&lt;400&gt; 1413

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acattttctc ggccctgccca gccccagga ggaaggtggg tctgaatcta gcacc atg      58
                                     Met
                                     1
acg gaa cta gag aca gcc atg ggc atg atc ata gac gtc ttt tcc cga      106
Thr Glu Leu Glu Thr Ala Met Gly Met Ile Ile Asp Val Phe Ser Arg
           5           10           15
tat tcg ggc agc gag ggc agc acg cag acc ctg acc aag ggg gag ctc      154
Tyr Ser Gly Ser Glu Gly Ser Thr Gln Thr Leu Thr Lys Gly Glu Leu
           20           25           30
aag gtg ctg atg gag aag gag cta cca ggc ttc ctg cag agt gga aaa      202
Lys Val Leu Met Glu Lys Glu Leu Pro Gly Phe Leu Gln Ser Gly Lys
           35           40           45
gac aag gat gcc gtg gat aaw ttg ctc aag gac ctg gac gcc aat gga      250
Asp Lys Asp Ala Val Asp Xaa Leu Leu Lys Asp Leu Asp Ala Asn Gly
           50           55           60           65
gat gcc cag gtg gac ttc agt gag ttc at      279
Asp Ala Gln Val Asp Phe Ser Glu Phe
           70

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&lt;210&gt; 1414

<211> 378  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..376

<400> 1414  
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 Met  
 1  
 acg gaa cta gag aca gcc atg ggc atg atc ata gac gtc ttt tcc cga 106  
 Thr Glu Leu Glu Thr Ala Met Gly Met Ile Ile Asp Val Phe Ser Arg  
 5 10 15  
 tat tcg ggc agc gag ggc agc acg cag acc ctg acc aag ggg gag ctc 154  
 Tyr Ser Gly Ser Glu Gly Ser Thr Gln Thr Leu Thr Lys Gly Glu Leu  
 20 25 30  
 aag gtg ctg atg gag aag gag cta cca ggc ttc ctg cag gtg agc cag 202  
 Lys Val Leu Met Glu Lys Glu Leu Pro Gly Phe Leu Gln Val Ser Gln  
 35 40 45  
 gcc ggc agt gct gga ctc agc ggg ggc tgg gga aga agg gga agg cgt 250  
 Ala Gly Ser Ala Gly Leu Ser Gly Gly Trp Gly Arg Arg Gly Arg Arg  
 50 55 60 65  
 ggc agg cag agg gct gag agc tgc ggt ggg gtc ggc ggt caa ggg gct 298  
 Gly Arg Gln Arg Ala Glu Ser Cys Gly Gly Val Gly Gly Gln Gly Ala  
 70 75 80  
 cag agg caa gag gga cag atc ctg aaa tgc cct gga agc cca gcc aag 346  
 Gln Arg Gln Glu Gly Gln Ile Leu Lys Cys Pro Gly Ser Pro Ala Lys  
 85 90 95  
 gaa cgg acc cac cct ggc ata aag gca ggg gg 378  
 Glu Arg Thr His Pro Gly Ile Lys Ala Gly  
 100 105

<210> 1415  
 <211> 279  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 116..277

<400> 1415  
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 ggggtggcct gagcgccggc gacaccttc ctggactata aattgagcac ctggg atg 118  
 Met  
 1  
 ggt agg ggg cca acg cag tca ccg ccg tcc gca gtc aca gtc cag cca 166  
 Gly Arg Gly Pro Thr Gln Ser Pro Pro Ser Ala Val Thr Val Gln Pro  
 5 10 15  
 ctg acc gca gca gcg ccc ttg cgt asa gcy gct tgc agc gag aac act 214

Leu Thr Ala Ala Ala Pro Leu Arg Xaa Ala Ala Cys Ser Glu Asn Thr  
 20 25 30  
 gaa ttg cca acg agc agg aga gtc tca agg cgc aag asg agg cca ggg 262  
 Glu Leu Pro Thr Ser Arg Arg Val Ser Arg Arg Lys Xaa Arg Pro Gly  
 35 40 45  
 ctc gac cca cag agc ac 279  
 Leu Asp Pro Gln Ser  
 50

<210> 1416  
 <211> 644  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 305..643

<400> 1416  
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 tggaaacagc agcttgtctc tgactaccgc gaggacatgg agcaccceaa ataggaactt 120  
 tagagggatt gaaatctggt gcctgttcca ctaggaatat tgtttgcaag gcacaagggtg 180  
 tcttttggtg gtgagcgcgc tctgcgcatg cgcaggtcca ttcgggaatt actgccagc 240  
 agccgactaa gttgcattcc ttgaatcttc gcagaaaaga caattctttt aatcagagtt 300  
 agta atg tgg aca gta caa aat cga gag agt ctg ggg ctt ctc tct ttc 349  
 Met Trp Thr Val Gln Asn Arg Glu Ser Leu Gly Leu Leu Ser Phe  
 1 5 10 15  
 cct gtg atg att acc atg gtc tgt tgt gca cac agc acc aat gaa ccc 397  
 Pro Val Met Ile Thr Met Val Cys Cys Ala His Ser Thr Asn Glu Pro  
 20 25 30  
 agc aac atg tca tac gtg aaa gag aca gtg gac aga ttg ctc aaa gga 445  
 Ser Asn Met Ser Tyr Val Lys Glu Thr Val Asp Arg Leu Leu Lys Gly  
 35 40 45  
 tat gac att cgc ttg cgg ccg gac ttc gga ggg ccc ccc gtc gac gtt 493  
 Tyr Asp Ile Arg Leu Arg Pro Asp Phe Gly Gly Pro Pro Val Asp Val  
 50 55 60  
 ggg atg cgg atc gat gtc gcc agc ata gac atg gtc tcc gaa gtg aat 541  
 Gly Met Arg Ile Asp Val Ala Ser Ile Asp Met Val Ser Glu Val Asn  
 65 70 75  
 atg gtg agt ggc ctc ccg agg ggc ccg gcg gtt cgg ctt acg cag atg 589  
 Met Val Ser Gly Leu Pro Arg Gly Pro Ala Val Arg Leu Thr Gln Met  
 80 85 90 95  
 gga aat gga cag gtc cct ttg ccc tct gcg ttt cat tgg cgg tca sct 637  
 Gly Asn Gly Gln Val Pro Leu Pro Ser Ala Phe His Trp Arg Ser Xaa  
 100 105 110  
 cgc ccc t 644  
 Arg Pro

<210> 1417  
 <211> 315  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 138..314

<400> 1417  
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 acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acggggaccg 120  
 cctcccgcgc cgmccacc atg ccc aac ttc tct ggc aac tgg aaa atc atc 170  
 Met Pro Asn Phe Ser Gly Asn Trp Lys Ile Ile  
 1 5 10  
 cga tcg gaa aac ttc gag gaa ttg ctc aaa gtg ctg ggg gtg aat gtg 218  
 Arg Ser Glu Asn Phe Glu Glu Leu Leu Lys Val Leu Gly Val Asn Val  
 15 20 25  
 atg ctg agg aag att gct gtg gct gca gcg tcc aag cca gca gtg gag 266  
 Met Leu Arg Lys Ile Ala Val Ala Ala Ser Lys Pro Ala Val Glu  
 30 35 40  
 atc aaa cag gag gga grs act ttc tac atc aaa acc tcc acc acc gtg c 315  
 Ile Lys Gln Glu Gly Xaa Thr Phe Tyr Ile Lys Thr Ser Thr Thr Val  
 45 50 55

<210> 1418  
 <211> 430  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 32..430

<400> 1418  
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 Met Thr Glu Pro Gly Ala Ser  
 1 5  
 ccc gag gac cct tgg gtc aag gtg gag tat gcc tac agc gac aac agc 100  
 Pro Glu Asp Pro Trp Val Lys Val Glu Tyr Ala Tyr Ser Asp Asn Ser  
 10 15 20  
 ctg gac ccc ggg ctt ttt gta gaa agc acc cgc aag ggn agt gta gtg 148  
 Leu Asp Pro Gly Leu Phe Val Glu Ser Thr Arg Lys Gly Ser Val Val  
 25 30 35  
 tcc aga gct aat agc atc ggt tcc acc agt gcc tct tct gtc ccc aac 196  
 Ser Arg Ala Asn Ser Ile Gly Ser Thr Ser Ala Ser Ser Val Pro Asn  
 40 45 50 55  
 aca gat gat gag gac agt gat tac cac cag gag gcc tac aag gag tcc 244  
 Thr Asp Asp Glu Asp Ser Asp Tyr His Gln Glu Ala Tyr Lys Glu Ser  
 60 65 70  
 tac aaa gac cgg cgg cgg cgc gca cac act cag gct gag cag aag agg 292  
 Tyr Lys Asp Arg Arg Arg Arg Ala His Thr Gln Ala Glu Gln Lys Arg  
 75 80 85  
 agg gac gcc atc aag aga ggc tat gat gac ctt cag acc atc gtc ccc 340  
 Arg Asp Ala Ile Lys Arg Gly Tyr Asp Asp Leu Gln Thr Ile Val Pro  
 90 95 100  
 act tgc cag cag cag gac ttc tcc att ggc tcc caa aag ctc agc aaa 388

004220"066ET50

Thr Cys Gln Gln Gln Asp Phe Ser Ile Gly Ser Gln Lys Leu Ser Lys  
 105 110 115  
 gcc atc gtt cta caa aag acc att gac tac att cag ttt ttg  
 Ala Ile Val Leu Gln Lys Thr Ile Asp Tyr Ile Gln Phe Leu  
 120 125 130

430

<210> 1419  
 <211> 461  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 70..459

<400> 1419

gctaccgccc ccgcccgcgc tgcgcctgct gctcctcgcc gtccgcgctg cagtgcgaag 60  
 ggctcgaag atg gcc ggt tgg cag agc tac gtg gat aac ctg atg tgc gat 111  
 Met Ala Gly Trp Gln Ser Tyr Val Asp Asn Leu Met Cys Asp  
 1 5 10  
 ggc tgc tgc cag gag gcc gcc att gtc ggc tac tgc gac gcc aaa tac 159  
 Gly Cys Cys Gln Glu Ala Ala Ile Val Gly Tyr Cys Asp Ala Lys Tyr  
 15 20 25 30  
 gtc tgg gca gcc acg gcc ggg ggc gtc ttt cag agc att acg cca ata 207  
 Val Trp Ala Ala Thr Ala Gly Gly Val Phe Gln Ser Ile Thr Pro Ile  
 35 40 45  
 gaa ata gat atg att gta gga aaa gac cgg gaa ggt ttc ttt acc aac 255  
 Glu Ile Asp Met Ile Val Gly Lys Asp Arg Glu Gly Phe Phe Thr Asn  
 50 55 60  
 ggt ttg act ctt ggc gcg aag aaa tgc tca gtg atc aga gat agt cta 303  
 Gly Leu Thr Leu Gly Ala Lys Lys Cys Ser Val Ile Arg Asp Ser Leu  
 65 70 75  
 tac gtc gat ggt gac tgc aca atg gac atc cgg aca aag agt caa ggt 351  
 Tyr Val Asp Gly Asp Cys Thr Met Asp Ile Arg Thr Lys Ser Gln Gly  
 80 85 90  
 ggg gag cca aca tac aat gtg gct gtc ggc aga gct ggt aga gtc ttg 399  
 Gly Glu Pro Thr Tyr Asn Val Ala Val Gly Arg Ala Gly Arg Val Leu  
 95 100 105 110  
 gtc ttt gta atg gga aaa gaa ggg gtc cat gga ggc gga ttg aat aag 447  
 Val Phe Val Met Gly Lys Glu Gly Val His Gly Gly Gly Leu Asn Lys  
 115 120 125  
 aag gca tac tca at 461  
 Lys Ala Tyr Ser  
 130

<210> 1420  
 <211> 296  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 124..294

&lt;400&gt; 1420

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tcgtggccca ccgctccttc gcggtccctg ccgccaccgt ccacgctcag cgttgtagag      120
aag atg gtg ggt cgg aac agc gcc atc gcc gcc ggt gta tgc ggg gcc      168
  Met Val Gly Arg Asn Ser Ala Ile Ala Ala Gly Val Cys Gly Ala
    1             5             10            15
ctt ttc att ggg tac tgc atc tac ttc gac cgc aaa aga cga agt gac      216
Leu Phe Ile Gly Tyr Cys Ile Tyr Phe Asp Arg Lys Arg Arg Ser Asp
              20              25              30
ccc aac ttc aag aac agg ctt cga gaa cga aga aag aaa cag aag ctt      264
Pro Asn Phe Lys Asn Arg Leu Arg Glu Arg Arg Lys Lys Gln Lys Leu
              35              40              45
gcc aag gag aga gct ggg ctt tcc aag tta cc      296
Ala Lys Glu Arg Ala Gly Leu Ser Lys Leu
    50              55

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&lt;210&gt; 1421

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 106..483

&lt;400&gt; 1421

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gtcagaacgg cggccaggac gccggacgtg cggcagttgc aggcgagcag gcgaggaatc      60
gccgtggcgt cttggtgttc tccacgctgg ttcgcaggtg aagag atg gcg ttt gtg      117
                               Met Ala Phe Val
                               1
aag agt ggc tgg ttg ctg cga cag agt act att ttg aag cgc tgg aag      165
Lys Ser Gly Trp Leu Arg Gln Ser Thr Ile Leu Lys Arg Trp Lys
  5             10             15            20
aag aac tgg ttt gat ctg tgg tcg gat ggt cac ctg atc tat tat gat      213
Lys Asn Trp Phe Asp Leu Trp Ser Asp Gly His Leu Ile Tyr Tyr Asp
              25              30              35
gac cag act cgg cag aat atc gag gat aag gtc cac atg cca atg gac      261
Asp Gln Thr Arg Gln Asn Ile Glu Asp Lys Val His Met Pro Met Asp
              40              45              50
tgc atc aac atc cgc acg ggg cag gaa tgt cgg gat act cag ccc ccg      309
Cys Ile Asn Ile Arg Thr Gly Gln Glu Cys Arg Asp Thr Gln Pro Pro
              55              60              65
gat gga aag tca aaa gac tgc atg ctc cag att gtt tgt cga gat ggg      357
Asp Gly Lys Ser Lys Asp Cys Met Leu Gln Ile Val Cys Arg Asp Gly
              70              75              80
aaa aca att agt ctt tgt gca gaa agc aca gat gat tgc ttg gcc tgg      405
Lys Thr Ile Ser Leu Cys Ala Glu Ser Thr Asp Asp Cys Leu Ala Trp
  85             90             95            100
aaa ttt aca ctc caa gat tct agg aca aac aca gcg tat gtg ggc tct      453
Lys Phe Thr Leu Gln Asp Ser Arg Thr Asn Thr Ala Tyr Val Gly Ser
              105              110              115

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 Ala Val Met Thr Asp Glu Thr Ser Val Val  
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484

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 Met Ala Arg Gly Pro Lys Lys His  
 1 5  
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 Leu Lys Arg Val Ala Ala Pro Lys His Trp Met Leu Asp Lys Leu Thr  
 10 15 20  
 ggt gta ttt gca cct cgt cca tcg aca ggt ccc cac aag ctg agg gaa 148  
 Gly Val Phe Ala Pro Arg Pro Ser Thr Gly Pro His Lys Leu Arg Glu  
 25 30 35 40  
 tgt ctt cct ctg atc gtc ttc ctc agg aat aga ctc aag tat gcg ttg 196  
 Cys Leu Pro Leu Ile Val Phe Leu Arg Asn Arg Leu Lys Tyr Ala Leu  
 45 50 55  
 act gga gat gag gta aag aag ata tgt atg caa cgt ttc atc aaa att 244  
 Thr Gly Asp Glu Val Lys Lys Ile Cys Met Gln Arg Phe Ile Lys Ile  
 60 65 70  
 gat ggc aag gtt cga gtg gat gtc aca tac cct gct gga ttc atg gat 292  
 Asp Gly Lys Val Arg Val Asp Val Thr Tyr Pro Ala Gly Phe Met Asp  
 75 80 85  
 gtc atc agc atc gag aag aca ggt gaa cat ttc cgc ctg gtc tat gac 340  
 Val Ile Ser Ile Glu Lys Thr Gly Glu His Phe Arg Leu Val Tyr Asp  
 90 95 100  
 acc aag ggc cgt ttt gct gtt cac cgc atc aca gtg gaa gag gca aag 388  
 Thr Lys Gly Arg Phe Ala Val His Arg Ile Thr Val Glu Glu Ala Lys  
 105 110 115 120  
 tac aag ttg tgc aaa gtg agg aag att act gtg gga gtg aag gga atc 436  
 Tyr Lys Leu Cys Lys Val Arg Lys Ile Thr Val Gly Val Lys Gly Ile  
 125 130 135  
 cct cac ctg gtg act cat gat gct cga acc atc cgc tac cca gat cct 484  
 Pro His Leu Val Thr His Asp Ala Arg Thr Ile Arg Tyr Pro Asp Pro  
 140 145 150  
 gtc atc aar gtg aac gat act gt 507  
 Val Ile Lys Val Asn Asp Thr  
 155

<210> 1423  
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atg tcc cta agg ggc agc ctc tcg cgt ctc ctc cag acg cga gtg cat	106					
Met Ser Leu Arg Gly Ser Leu Ser Arg Leu Leu Gln Thr Arg Val His						
1 5 10 15						
tcc atc ctg aag aaa tcc gtc cac tcc gtg gct gtg ata gga gcc ccg	154					
Ser Ile Leu Lys Lys Ser Val His Ser Val Ala Val Ile Gly Ala Pro						
20 25 30						
ttc tca caa ggg cag aaa aga aaa gga gtg gag cat ggt ccc gct gcc	202					
Phe Ser Gln Gly Gln Lys Arg Lys Gly Val Glu His Gly Pro Ala Ala						
35 40 45						
ata aga gaa gct ggc ttg atg aaa agg ctc tcc agt ttg ggc tgc cac	250					
Ile Arg Glu Ala Gly Leu Met Lys Arg Leu Ser Ser Leu Gly Cys His						
50 55 60						
cta aaa gac ttt gga gat ttg agt ttt act cca gtc ccc aaa gat gat	298					
Leu Lys Asp Phe Gly Asp Leu Ser Phe Thr Pro Val Pro Lys Asp Asp						
65 70 75 80						
ctc tac aac aac ctg ata gtg aat cca cgc tca gtg ggt ctt gcc aac	346					
Leu Tyr Asn Asn Leu Ile Val Asn Pro Arg Ser Val Gly Leu Ala Asn						
85 90 95						
cag gaa ctg gct gag gtg gtt agc aga gct gtg tca gat ggc tac agc	394					
Gln Glu Leu Ala Glu Val Val Ser Arg Ala Val Ser Asp Gly Tyr Ser						
100 105 110						
tgt gtc aca ctg gga gga gay cac agc ctg gca atc ggt acc att agt g	443					
Cys Val Thr Leu Gly Gly Asp His Ser Leu Ala Ile Gly Thr Ile Ser						
115 120 125						

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 143..391

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cagggagtct	gaagcgtggg	ac atg gac cgt tca ctg gga tgg caa ggg aat	172			
Met Asp Arg Ser Leu Gly Trp Gln Gly Asn						
1 5 10						
tct gtc cct gag gac agg act gaa gct ggg atc aag cgt ttc ctg gag	220					
Ser Val Pro Glu Asp Arg Thr Glu Ala Gly Ile Lys Arg Phe Leu Glu						
15 20 25						
gac acc acg gat gat gga gaa ctg agc aag ttc gtg aag gat ttc tca	268					
Asp Thr Thr Asp Asp Gly Glu Leu Ser Lys Phe Val Lys Asp Phe Ser						
30 35 40						

gga aat gcg agc tgc cac cca cca gag gct aag acc tgg gca tcc agg	316
Gly Asn Ala Ser Cys His Pro Pro Glu Ala Lys Thr Trp Ala Ser Arg	
45 50 55	
ccc caa gtc ccg gag cca agg ccc cag rcc ccg gac ctc tat gat gat	364
Pro Gln Val Pro Glu Pro Arg Pro Gln Xaa Pro Asp Leu Tyr Asp Asp	
60 65 70	
gac ctg gag ttc aga ccc ccc tcg cgg	391
Asp Leu Glu Phe Arg Pro Pro Ser Arg	
75 80	

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Met Ala Thr Val Trp Asp Glu Ala Glu	
1 5	
caa gat gga att ggg gag gag gtg ctc aag atg tcc acg gag gag atc	102
Gln Asp Gly Ile Gly Glu Glu Val Leu Lys Met Ser Thr Glu Glu Ile	
10 15 20 25	
atc cag cgc aca cgg ctg ctg gac agt gag atc aag atc atg aag agt	150
Ile Gln Arg Thr Arg Leu Leu Asp Ser Glu Ile Lys Ile Met Lys Ser	
30 35 40	
gaa gtg ttg aga gtc acc cat gag ctc caa gcc atg aag gac aag ata	198
Glu Val Leu Arg Val Thr His Glu Leu Gln Ala Met Lys Asp Lys Ile	
45 50 55	
aaa gag aac agt gag aaa atc aaa gtg aac aag acc ctg ccg tac ctt	246
Lys Glu Asn Ser Glu Lys Ile Lys Val Asn Lys Thr Leu Pro Tyr Leu	
60 65 70	
gtc tcc aac gtc atc gag ctc ctg gat gtt gat cct aat gac caa gag	294
Val Ser Asn Val Ile Glu Leu Leu Asp Val Asp Pro Asn Asp Gln Glu	
75 80 85	
gag gat ggt gcc aat att gac ctg gac tcc cag agg aag ggc aag tgt	342
Glu Asp Gly Ala Asn Ile Asp Leu Asp Ser Gln Arg Lys Gly Lys Cys	
90 95 100 105	
gct gtg atc aaa acc tct aca cga cag acg tac ttc ctt cct gtg att	390
Ala Val Ile Lys Thr Ser Thr Arg Gln Thr Tyr Phe Leu Pro Val Ile	
110 115 120	
ggg ttg gtg gat gct gaa aag cca aag cca gga gac ctg gtg ggt gtg	438
Gly Leu Val Asp Ala Glu Lys Pro Lys Pro Gly Asp Leu Val Gly Val	
125 130 135	
aac aaa gac tcc tat ctg atc ctg gag acg ctg ccc aca gag tat ga	485
Asn Lys Asp Ser Tyr Leu Ile Leu Glu Thr Leu Pro Thr Glu Tyr	
140 145 150	

<210> 1426  
 <211> 393

<212> DNA  
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<220>  
<221> CDS  
<222> 150..392

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tgcattctgtc tctcttagtc tgcttttttt ccaccgatgt aacagacctg gagccagcag 120  
gactcagagg aaaggactta atcaggttt atg tgt cct aaa ggt tat gaa gac 173  
Met Cys Pro Lys Gly Tyr Glu Asp  
1 5  
agt atg gag ttt cca gac cat agt aga cat ttg cta cag tgt ctg agc 221  
Ser Met Glu Phe Pro Asp His Ser Arg His Leu Leu Gln Cys Leu Ser  
10 15 20  
gag cag aga cac cag ggt ttt ctt tgt gac tgc act gtt ctg gtg gga 269  
Glu Gln Arg His Gln Gly Phe Leu Cys Asp Cys Thr Val Leu Val Gly  
25 30 35 40  
gat gcc cag ttc cga gcg cac cga gct gta ctg gct tca tgc agc atg 317  
Asp Ala Gln Phe Arg Ala His Arg Ala Val Leu Ala Ser Cys Ser Met  
45 50 55  
tat ttc cac ctc ttt tac aag gac cag ctg gac aaa aga gac att gtt 365  
Tyr Phe His Leu Phe Tyr Lys Asp Gln Leu Asp Lys Arg Asp Ile Val  
60 65 70  
cat ctg aac agc gac att gtt aca gcc c 393  
His Leu Asn Ser Asp Ile Val Thr Ala  
75 80

<210> 1427  
<211> 359  
<212> DNA  
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<220>  
<221> CDS  
<222> 143..358

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tgtcttgggc aaagtgtaga agaacaagaa gaaaggaagg cttttgttgt aacaccctga 120  
ctttaaaagt tatgaagaca gt atg gag ttt cca gac cat agt aga cat ttg 172  
Met Glu Phe Pro Asp His Ser Arg His Leu  
1 5 10  
cta cag tgt ctg agc gag cag aga cac cag ggt ttt ctt tgt gac tgc 220  
Leu Gln Cys Leu Ser Glu Gln Arg His Gln Gly Phe Leu Cys Asp Cys  
15 20 25  
act gtt ctg gtg gga gat gcc cag ttc cga gcg cac cga gct gta ctg 268  
Thr Val Leu Val Gly Asp Ala Gln Phe Arg Ala His Arg Ala Val Leu  
30 35 40  
gct tca tgc agc atg tat ttc cac ctc ttt tac aag gac cag ctg gac 316  
Ala Ser Cys Ser Met Tyr Phe His Leu Phe Tyr Lys Asp Gln Leu Asp

45	50	55	
aaa aga gac att gtt cat ctg aac agc gac att gtw aca gcc c			359
Lys Arg Asp Ile Val His Leu Asn Ser Asp Ile Val Thr Ala			
60	65	70	

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 74..736

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cccgcgcgcc aag atg ccg aaa gga aag aag gcc aag gga aag aag gtg	109
Met Pro Lys Gly Lys Lys Ala Lys Gly Lys Lys Val	
1 5 10	
gct ccg gcc cca gct gtc gtg aag aag cag gag gct aag aaa gtg gtg	157
Ala Pro Ala Pro Ala Val Val Lys Lys Gln Glu Ala Lys Lys Val Val	
15 20 25	
aat ccc ctg ttt gag aaa agg cct aag aat ttt ggc att gga cag gac	205
Asn Pro Leu Phe Glu Lys Arg Pro Lys Asn Phe Gly Ile Gly Gln Asp	
30 35 40	
atc cag ccc aaa aga gac ctc acc cgc ttt gtg aaa tgg ccc cgc tat	253
Ile Gln Pro Lys Arg Asp Leu Thr Arg Phe Val Lys Trp Pro Arg Tyr	
45 50 55 60	
atc agg ttg cag cgg cag aga gcc atc ctc tat aag cgg ctg aaa gtg	301
Ile Arg Leu Gln Arg Gln Arg Ala Ile Leu Tyr Lys Arg Leu Lys Val	
65 70 75	
cct cct gcg att aac cag ttc acc cag gcc ctg gac cgc caa aca gct	349
Pro Pro Ala Ile Asn Gln Phe Thr Gln Ala Leu Asp Arg Gln Thr Ala	
80 85 90	
act cag ctg ctt aag ctg gcc cac aag tac aga cca gag aca aag caa	397
Thr Gln Leu Lys Leu Ala His Lys Tyr Arg Pro Glu Thr Lys Gln	
95 100 105	
gag aag aag cag aga ctg ttg gcc cgg gcc gag aag aag gct gct ggc	445
Glu Lys Lys Gln Arg Leu Leu Ala Arg Ala Glu Lys Lys Ala Ala Gly	
110 115 120	
aaa ggg gac gtc cca acg aag aga cca cct gtc ctt cga gca gga gtt	493
Lys Gly Asp Val Pro Thr Lys Arg Pro Pro Val Leu Arg Ala Gly Val	
125 130 135 140	
aac acc gtc acc acc ttg gtg gag aac aag aaa gct cag ctg gtg gtg	541
Asn Thr Val Thr Thr Leu Val Glu Asn Lys Lys Ala Gln Leu Val Val	
145 150 155	
att gca cac gac gtg gat ccc atc gag ctg gtt gtc ttc ttg cct gcc	589
Ile Ala His Asp Val Asp Pro Ile Glu Leu Val Val Phe Leu Pro Ala	
160 165 170	
ctg tgt cgt aaa atg ggg gtm nct tac tgc att atc aag gga aag gca	637
Leu Cys Arg Lys Met Gly Val Xaa Tyr Cys Ile Ile Lys Gly Lys Ala	
175 180 185	
aga ctg gga cgt cta gtc cac agg aag acc tgc acc act gtc gcc ttc	685

004220" 666E7560

Arg	Leu	Gly	Arg	Leu	Val	His	Arg	Lys	Thr	Cys	Thr	Thr	Val	Ala	Phe	
190						195				200						
aca	cag	gtg	aac	tcg	gaa	gac	aaa	ggc	gct	ttg	gct	aag	ctg	gtg	gaa	733
Thr	Gln	Val	Asn	Ser	Glu	Asp	Lys	Gly	Ala	Leu	Ala	Lys	Leu	Val	Glu	
205					210					215					220	
gct	at															738
Ala																

<210> 1429  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 93..422

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gcccgcggtt	cgccgccccg	ctcgccgccg	cg	atg	cca	gkg	ttt	cat	acg	cgc						113	
						Met	Pro	Xaa	Phe	His	Thr	Arg					
						1					5						
acg	atc	gag	agc	atc	ctg	gag	ccg	gtg	gca	cag	cag	atc	tcc	cac	ctg	161	
Thr	Ile	Glu	Ser	Ile	Leu	Glu	Pro	Val	Ala	Gln	Gln	Ile	Ser	His	Leu		
		10					15					20					
gtg	ata	atg	cac	gag	gag	ggc	gag	gtg	gac	ggc	aaa	gcc	att	cct	gac	209	
Val	Ile	Met	His	Glu	Glu	Gly	Glu	Val	Asp	Gly	Lys	Ala	Ile	Pro	Asp		
		25				30					35						
ctc	acc	gcg	ccc	gtg	gcc	gcc	gtg	cag	gcg	gcn	gtc	agc	aac	ctc	gtc	257	
Leu	Thr	Ala	Pro	Val	Ala	Ala	Val	Gln	Ala	Ala	Val	Ser	Asn	Leu	Val		
40					45					50					55		
cgg	gtt	gga	aaa	gag	act	gtt	caa	acc	act	gag	gat	cag	att	ttg	aag	305	
Arg	Val	Gly	Lys	Glu	Thr	Val	Gln	Thr	Thr	Glu	Asp	Gln	Ile	Leu	Lys		
			60						65				70				
aga	gat	atg	cca	gca	ttt	att	aag	gtt	gag	aat	gct	tgc	acc	aag		353	
Arg	Asp	Met	Pro	Pro	Ala	Phe	Ile	Lys	Val	Glu	Asn	Ala	Cys	Thr	Lys		
			75					80					85				
ctt	gtc	cag	gca	gct	cag	atg	ctt	cag	tca	gac	cct	tan	tca	gtg	cct	401	
Leu	Val	Gln	Ala	Ala	Gln	Met	Leu	Gln	Ser	Asp	Pro	Xaa	Ser	Val	Pro		
		90					95					100					
gct	cga	gat	tat	cta	att	gat										422	
Ala	Arg	Asp	Tyr	Leu	Ile	Asp											
		105				110											

<210> 1430  
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 <212> DNA  
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<220>  
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accagccctt gatcatttcg cctaaaagag caaggactag agttcctgac ctccaggcca      180
gtccctgac cctgaccta atg tta tcg cgg aat gat gta aag agg ctg gag      232
                Met Leu Ser Arg Asn Asp Val Lys Arg Leu Glu
                  1             5             10
agg agc tgg gcc cag ggc tcc tca gag cag gna ctc cac tat gca tct      280
Arg Ser Trp Ala Gln Gly Ser Ser Glu Gln Xaa Leu His Tyr Ala Ser
                15             20             25
ctg cag agg ctg cca gtg ccc agc agt gag gga cct gac ctc agg ggc      328
Leu Gln Arg Leu Pro Val Pro Ser Ser Glu Gly Pro Asp Leu Arg Gly
                30             35             40
aga gac aag aga ggc acn aag gag gat cca aga gct gac tat gcc tgc      376
Arg Asp Lys Arg Gly Thr Lys Glu Asp Pro Arg Ala Asp Tyr Ala Cys
                45             50             55
att gct gag aac aaa ccc ac      396
Ile Ala Glu Asn Lys Pro
60                65

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&lt;210&gt; 1431

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 309..470

&lt;400&gt; 1431

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tcgatcccca aagaaaagag cgagtgggca ggcagstgcg agacagaacc ggagtgtgca      180
gggtccctag aggcgggttc ctggtctgtg ctgctctcct ggaagccatg gtacaggcag      240
agctcagggc gatccccagg tgagggcagc ggctctgcct gggattccac cgcagtacaa      300
ccgggtag atg cgg ggt nra gaa gaa agg atg ttg cct gca ctg ctc gcc      350
                Met Arg Gly Xaa Glu Glu Arg Met Leu Pro Ala Leu Leu Ala
                  1             5             10
aat agc acc ctg aga ggc ras att tgc aga agc agc agc agn nng aag      398
Asn Ser Thr Leu Arg Gly Xaa Ile Cys Arg Ser Ser Ser Xaa Xaa Lys
                15             20             25             30
aca cag cgc cgg tcc agg agg cgg ctc gan snr gtt cgt aaa gtc gcc      446
Thr Gln Arg Arg Ser Arg Arg Arg Leu Xaa Xaa Val Arg Lys Val Ala
                35             40             45
cga mag ctt ttt ctc cgt agt atg c      471
Arg Xaa Leu Phe Leu Arg Ser Met
                50

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&lt;210&gt; 1432

&lt;211&gt; 334

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> CDS  
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ccgaatagag	gggctggggc	cacgagcgcc	attgacaagc	a atg ggg aag aaa cag		176
				Met Gly Lys Lys Gln		
				1	5	
aaa aac aag agc gaa gac agc acc aag gat gac att gat ctt gat gcc						224
Lys Asn Lys Ser Glu Asp Ser Thr Lys Asp Asp Ile Asp Leu Asp Ala						
	10		15		20	
ttg gct gca gaa ata gaa gga gct ggt gct gcc aaa gaa cag gag cct						272
Leu Ala Ala Glu Ile Glu Gly Ala Gly Ala Ala Lys Glu Gln Glu Pro						
	25		30		35	
caa aag tca aaa ggg ama mag ana ana gag ana aaa rag crg gac ttt						320
Gln Lys Ser Lys Gly Xaa Xaa Xaa Xaa Glu Xaa Lys Xaa Xaa Asp Phe						
	40		45		50	
gat gaa gat gat at						334
Asp Glu Asp Asp						
55						

<210> 1433  
 <211> 497  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 195..497

<400> 1433

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gaattgctaa	gtttctaatt	tcatatggtt	gctgacaagg	aggtgcagac	aaggaccctc	180
ttgctttcct	cact atg gat agt ctg ttg cct cca tct aga ttc tct tat					230
	Met Asp Ser Leu Leu Pro Pro Ser Arg Phe Ser Tyr					
	1	5		10		
ttc aaa aaa tat cct ctc cat gca att agg aga tat tta tcg acg ctg						278
Phe Lys Lys Tyr Pro Leu His Ala Ile Arg Arg Tyr Leu Ser Thr Leu						
	15		20		25	
aga aac caa aga gcc gaa gaa cag gtt gca cgt ttt caa aaa ata cct						326
Arg Asn Gln Arg Ala Glu Glu Gln Val Ala Arg Phe Gln Lys Ile Pro						
	30		35		40	
aat ggt gaa aat gag aca atg att cct gta ttg aca tca aaa aaa gca						374
Asn Gly Glu Asn Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala						
	45		50		55	60
agt gaa tta cca gtc agt gaa gtt gca agc att ctc caa gct gat ctt						422
Ser Glu Leu Pro Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu						
	65		70		75	

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cag aat ggt cta aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat	470
Gln Asn Gly Leu Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His	
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ggc tgg aat gag ttt gat att agt gaa	497
Gly Trp Asn Glu Phe Asp Ile Ser Glu	
95 100	

<210> 1434  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 60..467

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atg aac cga ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc	107
Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Ser	
1 5 10 15	
ctg act gac tgc att ggc acg gtg gac agt aga gca gaa tcc att gac	155
Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp	
20 25 30	
aag aag att tct cga ttg gat gct gag cta gtg aag tat aag gat cag	203
Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln	
35 40 45	
atc aag aag atg aga gag ggt cct gca aag aat atg gtc aag cag aaa	251
Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys	
50 55 60	
gcc ttg cga gtt tta aag caa aag agg atg tat gag cag cag cgg gac	299
Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp	
65 70 75 80	
aat ctt gcc caa cag tca ttc aac atg gaa caa gcc aat tat acc atc	347
Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile	
85 90 95	
cag tct ttg aag gac acc aag acc acg gtt gat gct atg aaa ctg gga	395
Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly	
100 105 110	
gta aag gaa atg aag aag gca tac aag caa gtg aag atc gnc cag att	443
Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Xaa Gln Ile	
115 120 125	
gag gat tta caa gac cag cta gag	467
Glu Asp Leu Gln Asp Gln Leu Glu	
130 135	

<210> 1435  
 <211> 198  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 36..197

<400> 1435

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actcagggag ccggaggnga cgcgccggag gaaag atg gaa gac tac cag gct      53
                        Met Glu Asp Tyr Gln Ala
                        1          5
gcg gag gag act gct ttt gtt gtt gat gaa gtg agc aac att gta aaa      101
Ala Glu Glu Thr Ala Phe Val Val Asp Glu Val Ser Asn Ile Val Lys
                        10          15          20
gag gct ata gaa agc gca att ggt ggt aac gct tat caa cac agc aaa      149
Glu Ala Ile Glu Ser Ala Ile Gly Gly Asn Ala Tyr Gln His Ser Lys
                        25          30          35
gtg aac cag tgg acc aca aat gta gta gaa caa act tta agc caa ctc a      198
Val Asn Gln Trp Thr Thr Asn Val Val Glu Gln Thr Leu Ser Gln Leu
                        40          45          50

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<210> 1436

<211> 214

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..212

<400> 1436

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catgtgtttt attgtttctt tcagtt atg tat tct cat ttt gcc caa gac ctt      53
                        Met Tyr Ser His Phe Ala Gln Asp Leu
                        1          5
tgg tca gag cag agc ata aaa gat tct ttc caa aaa gtg ata cta aga      101
Trp Ser Glu Gln Ser Ile Lys Asp Ser Phe Gln Lys Val Ile Leu Arg
10          15          20          25
aga tat gaa aaa tgt aga cat gac aat tta cag tta aaa aaa ggc tgt      149
Arg Tyr Glu Lys Cys Arg His Asp Asn Leu Gln Leu Lys Lys Gly Cys
                        30          35          40
gaa agt gta gat gag tgt cca gtg cac aaa aga ggt tat aat gga ctt      197
Glu Ser Val Asp Glu Cys Pro Val His Lys Arg Gly Tyr Asn Gly Leu
                        45          50          55
aaa caa tgt ttg gca ac
Lys Gln Cys Leu Ala
                        60

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<210> 1437

<211> 432

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 270..431

&lt;400&gt; 1437

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gccgcgggcg cgcccccgct ctgcgctgtc tctccgatgg cgtccgcctc agggggccatg      60
gcgaacacga gcagatcctg gtcctcgatc cgccccacaga cctcaaattc aaaggcccct      120
tcacagatgt agtcactaca aatcttaaat tgcgaaatcc atcggataga aaagtgtgtt      180
tcaaagtga gactacagca cctcgccggt actgtgtgag gcccaacagt ggaattattg      240
accaggggtc aactgtgact gtttcagta atg cta cag ccc ttt gac tat gat      293
                        Met Leu Gln Pro Phe Asp Tyr Asp
                        1             5
ccg aat gaa aag agt aaa cac aag ttt atg gta cag aca att ttt gct      341
Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala
    10             15             20
cca cca aac act tca gat atg gaa gct gtg tgg aaa gag gca aaa cct      389
Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro
    25             30             35             40
gat raa tta atg gat tcc aaa ttg aga tgc gta ttt gaa atg c      432
Asp Xaa Leu Met Asp Ser Lys Leu Arg Cys Val Phe Glu Met
                45             50

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&lt;210&gt; 1438

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 54..248

&lt;400&gt; 1438

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gttatgtatt tatcatcaat cttattccac tgcattgtatt tgtgttggtta ctg atg      56
                        Met
                        1
cag aga tac agc aaa aga gtc tac ata gca tat agc act ttc tac att      104
Gln Arg Tyr Ser Lys Arg Val Tyr Ile Ala Tyr Ser Thr Phe Tyr Ile
    5             10             15
gtg ggt tta ata tta tca atg cag ata cct ttt gtg gga ttc cag cca      152
Val Gly Leu Ile Leu Ser Met Gln Ile Pro Phe Val Gly Phe Gln Pro
    20             25             30
atc aga aca agt gaa cac atg gca gct gca ggt gtc ttt gca ttg ctg      200
Ile Arg Thr Ser Glu His Met Ala Ala Ala Gly Val Phe Ala Leu Leu
    35             40             45
caa gct tat gct ttc ttg cag tat ctg aga gac cga tta aca aaa caa      248
Gln Ala Tyr Ala Phe Leu Gln Tyr Leu Arg Asp Arg Leu Thr Lys Gln
    50             55             60             65
ga

```

250

&lt;210&gt; 1439

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 145..336

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<400> 1439
aagcggcttc cgggtgctcg cgcgccgacc tggacgcaga gaagccagag actttcgctt      60
ccggctgccg caggscttcg ctggtgcaga cgcagtgtcg agcacacagc taccggacaa      120
agagtgcgcg ccggagctgg agtt atg gcg gct acg gag ccg atc ttg gcg      171
                               Met Ala Ala Thr Glu Pro Ile Leu Ala
                               1                               5

gcc act ggg agt ccc gcg gcg gtg cca ccg gag aaa ctg gaa gga gcc      219
Ala Thr Gly Ser Pro Ala Ala Val Pro Pro Glu Lys Leu Glu Gly Ala
10                               15                               20                               25
ggt tcg agc tca gcc cct gag cgt aac tgt gtg ggc tcc tcg ctg cca      267
Gly Ser Ser Ser Ala Pro Glu Arg Asn Cys Val Gly Ser Ser Leu Pro
                               30                               35                               40
gag gcc tca ccg cct gcc cct gag cct tcc agt ccc aac gcc gcg gtc      315
Glu Ala Ser Pro Pro Ala Pro Glu Pro Ser Ser Pro Asn Ala Ala Val
                               45                               50                               55
cct gaa gcc atc ccy acg ccc      336
Pro Glu Ala Ile Pro Thr Pro
                               60

<210> 1440
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..423

<400> 1440
agagttcygg gggccaggcg gccgccgcga gtctggatc ctgwgcttcg tgagttgagc      60
gctgctgctc cgcggtggag tcaccgcaca gtcgccggga tc atg gtg ttc tac      114
                               Met Val Phe Tyr
                               1

ttc acc agc agc agc gtt aat tca tct gcc tac act att tac atg gga      162
Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr Ile Tyr Met Gly
5                               10                               15                               20
aaa gat aaa tat gaa aat gaa gat ctg atc aag cat ggc trr cct gaa      210
Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His Gly Xaa Pro Glu
                               25                               30                               35
gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct cat gta tac ctt      258
Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala His Val Tyr Leu
                               40                               45                               50
cga tta cat aag gga gag aat ata gaa gac atc cca aag gaa gtg ctg      306
Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro Lys Glu Val Leu
                               55                               60                               65
atg gac tgt gbm aac ctt gtg aag gcc aat agc att caa ggc tgc aag      354
Met Asp Cys Xaa Asn Leu Val Lys Ala Asn Ser Ile Gln Gly Cys Lys
                               70                               75                               80
atg aac aac gtt aat gtg gta tat acg ccg tgg tct aac ctg aag aaa      402
Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser Asn Leu Lys Lys
85                               90                               95                               100

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aca gct gac atg gat gtg ggg c  
 Thr Ala Asp Met Asp Val Gly  
 105

424

<210> 1441  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 112..495

<400> 1441  
 tttttttcgt ttgtgacgcc agggagcgtg aggacgtggg gcttccgtga atgcgcagtg 60  
 ggtgcgtcgg ccacgacctt ttggccaggt tagggagggg gcgacgctga g atg ggg 117  
 Met Gly  
 1  
 gcg gcg gcg gcg gaa gcg gat cgc act ctc ttt gtg ggc aac ctt gaa 165  
 Ala Ala Ala Ala Glu Ala Asp Arg Thr Leu Phe Val Gly Asn Leu Glu  
 5 10 15  
 acg aaa gtg acc gag gag ctc ctt ttc gag ctt ttc cac cag gct ggg 213  
 Thr Lys Val Thr Glu Glu Leu Leu Phe Glu Leu Phe His Gln Ala Gly  
 20 25 30  
 cca gta ata aag gtg aaa att cca aaa gat aag gat ggt aaa cca aag 261  
 Pro Val Ile Lys Val Lys Ile Pro Lys Asp Lys Asp Gly Lys Pro Lys  
 35 40 45 50  
 cag ttt gcg ttt gtg aat ttc aaa cat gaa gtg tct gtt cct tat gca 309  
 Gln Phe Ala Phe Val Asn Phe Lys His Glu Val Ser Val Pro Tyr Ala  
 55 60 65  
 atg aat cta ctt aat gga atc aaa ctt tat gga agg cct atc aaa att 357  
 Met Asn Leu Leu Asn Gly Ile Lys Leu Tyr Gly Arg Pro Ile Lys Ile  
 70 75 80  
 caa ttt aga tca gga agt agt cat gcc cca caa gat gtc agt ttg tca 405  
 Gln Phe Arg Ser Gly Ser Ser His Ala Pro Gln Asp Val Ser Leu Ser  
 85 90 95  
 tat ccc caa cat cat gtt gga aat tca agc cct acc tcc aca tct cct 453  
 Tyr Pro Gln His His Val Gly Asn Ser Ser Pro Thr Ser Thr Ser Pro  
 100 105 110  
 agc agg tac gaa agg act atg gat aac atg act tca tca gca 495  
 Ser Arg Tyr Glu Arg Thr Met Asp Asn Met Thr Ser Ser Ala  
 115 120 125

<210> 1442  
 <211> 319  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 108..317

&lt;400&gt; 1442

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gccgctggct tccggtcccc tgagactggg gcctcgctcg ctcccgaccc ggttgcaagt    60
gttgcgggtgg gagaaagtcg cgtccgcacg ggaggggaag cgccgctc atg cct aag    116
                                   Met Pro Lys
                                   1
tat tat gag gac aag ccg cag gcg cgn ngc gtg csg ggc ctg aag gag    164
Tyr Tyr Glu Asp Lys Pro Gln Ala Arg Xaa Val Xaa Gly Leu Lys Glu
   5                10                15
gac ctg ggc gcg tgt ctg ctg cag tcg gac tgt gtg gtc cag gaa gga    212
Asp Leu Gly Ala Cys Leu Leu Gln Ser Asp Cys Val Val Gln Glu Gly
  20                25                30                35
aaa tca cct cgg cag tgt ttg aag gaa gga tac tgc aac tct ttg aag    260
Lys Ser Pro Arg Gln Cys Leu Lys Glu Gly Tyr Cys Asn Ser Leu Lys
               40                45                50
tac gca ttt ttt gag tgt aaa aga tca gtg ttg gat aac agg gca aga    308
Tyr Ala Phe Phe Glu Cys Lys Arg Ser Val Leu Asp Asn Arg Ala Arg
               55                60                65
ttc aga gga ag
Phe Arg Gly
   70

```

&lt;210&gt; 1443

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 69..356

&lt;400&gt; 1443

```

gccacattcg ctctctgctt tcggtgtgtc tgttggtgtc tgttgcgggc accgcagtcg    60
ccgtgaag atg gcg tct acc agc cgt ttg gat gct ctt cca aga gtc aca    110
      Met Ala Ser Thr Ser Arg Leu Asp Ala Leu Pro Arg Val Thr
      1                5                10
tgt cca aac cat cca gat gcg att tta gtg gag gac tac aga gcc ggt    158
Cys Pro Asn His Pro Asp Ala Ile Leu Val Glu Asp Tyr Arg Ala Gly
  15                20                25                30
gat atg atc tgt cct gaa tgt ggc ttg gtt gta ggt gac cgg gtt att    206
Asp Met Ile Cys Pro Glu Cys Gly Leu Val Gly Asp Arg Val Ile
               35                40                45
gat gtg gga tct gaa tgg cga act ttc agc aat gac aaa gca aca aaa    254
Asp Val Gly Ser Glu Trp Arg Thr Phe Ser Asn Asp Lys Ala Thr Lys
               50                55                60
gat cca tct cga gtt gga gat tct cag aat cct ctt ctg agt gat gga    302
Asp Pro Ser Arg Val Gly Asp Ser Gln Asn Pro Leu Leu Ser Asp Gly
               65                70                75
gat ttg tct acc atg att ggc aag ggc aca gga gck gca agt ttt gac    350
Asp Leu Ser Thr Met Ile Gly Lys Gly Thr Gly Ala Ala Ser Phe Asp
               80                85                90
gaa gtt tg
Glu Val
   95

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<210> 1444  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 72..356

<400> 1444  
 agcggcgccc tcaccggaag tcccgcctct gccgtgggcc tgcgagaatc gaggcactcg 60  
 ctggcgctacc c atg tat cga aat gag ttc acg gcc tgg tac cgg cgg atg 110  
                   1                  5                  10  
 tcg gtg gtc tac ggg atc ggc acc tgg tct gtg ttg ggc tca ctg ctt 158  
 Ser Val Val Tyr Gly Ile Gly Thr Trp Ser Val Leu Gly Ser Leu Leu  
           15                  20                  25  
 tac tat agc cgg aca atg gcg aag tgc tca gac caa aag gat ggc tca 206  
 Tyr Tyr Ser Arg Thr Met Ala Lys Ser Ser Asp Gln Lys Asp Gly Ser  
           30                  35                  40                  45  
 gca agt gaa gta ccc agt gaa ctc tct gaa cgc cca aaa gga ttt tat 254  
 Ala Ser Glu Val Pro Ser Glu Leu Ser Glu Arg Pro Lys Gly Phe Tyr  
                   50                  55                  60  
 gtg gaa aca gtt gtc aca tat aaa gaa gat ttt gtt cca aat aca gaa 302  
 Val Glu Thr Val Val Thr Tyr Lys Glu Asp Phe Val Pro Asn Thr Glu  
                   65                  70                  75  
 aag atc ctc aac tat tgg aaa tca tgg act ggt ggc ctg gta cag aac 350  
 Lys Ile Leu Asn Tyr Trp Lys Ser Trp Thr Gly Gly Leu Val Gln Asn  
                   80                  85                  90  
 cat gac t 357  
 His Asp  
           95

<210> 1445  
 <211> 404  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 142..402

<400> 1445  
 gagagaggcg tgacagcgct gtgttttgca gcgggagcra ngkggcgccg gctgggggtgt 60  
 gtgctcctga gctcttcaga aaccaggctg ctttcaggaa cattgctgtg gattcccagg 120  
 gcctattccr ctagaagcaa g atg gct gaa ctc aat act cat gtg aat gtc 171  
                   1                  5                  10  
 aag gaa aag atc tat gca gtt aga tca gtt gtt ccc aac aaa agc aat 219  
 Lys Glu Lys Ile Tyr Ala Val Arg Ser Val Val Pro Asn Lys Ser Asn  
                   15                  20                  25

aat gaa ata gtc ctg gtg ctc caa cag ttt gat ttt aat gtg gat aaa	267
Asn Glu Ile Val Leu Val Leu Gln Gln Phe Asp Phe Asn Val Asp Lys	
30 35 40	
gcc gtg caa gcc ttt gtg gat ggc agt gca att caa gtt cta aaa gaa	315
Ala Val Gln Ala Phe Val Asp Gly Ser Ala Ile Gln Val Leu Lys Glu	
45 50 55	
tgg aat atg aca gga aaa aag aag aac aat aaa aga aaa aga agc aag	363
Trp Asn Met Thr Gly Lys Lys Lys Asn Asn Lys Arg Lys Arg Ser Lys	
60 65 70	
tcc aag cag cat caa ggc aac aaa gat gct aaa gac aag gt	404
Ser Lys Gln His Gln Gly Asn Lys Asp Ala Lys Asp Lys	
75 80 85	

<210> 1446  
 <211> 517  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 83..517

<400> 1446	
gaaggcggtg gtagegcctc agtgggtgtgg gcttgcgccc tgcccaggtg cccgcagaga	60
gcagccgggc tgccagcggtt tc atg atc aac atg gga gac tcc cac gtg gac	112
Met Ile Asn Met Gly Asp Ser His Val Asp	
1 5 10	
acc agc tcc acc gtg tcc gag gcg gtg gcc gaa gaa gta tct ctt ttc	160
Thr Ser Ser Thr Val Ser Glu Ala Val Ala Glu Glu Val Ser Leu Phe	
15 20 25	
agc atg acg gac atg att ctg ntt tgc ctc atc gtg ggt ctc cta acc	208
Ser Met Thr Asp Met Ile Leu Xaa Ser Leu Ile Val Gly Leu Leu Thr	
30 35 40	
tac tgg ttc ctc ttc aga aag aaa gaa gaa gtc ccc gag ttc acc	256
Tyr Trp Phe Leu Phe Arg Lys Lys Lys Glu Glu Val Pro Glu Phe Thr	
45 50 55	
aaa att cag aca ttg acc tcc tct gtc aga gag agc agc ttt gtg gaa	304
Lys Ile Gln Thr Leu Thr Ser Ser Val Arg Glu Ser Ser Phe Val Glu	
60 65 70	
aag atg aag aaa acg ggg agg aac atc atc gtg ttc tac ggc tcc cag	352
Lys Met Lys Lys Thr Gly Arg Asn Ile Ile Val Phe Tyr Gly Ser Gln	
75 80 85 90	
acg ggg act gca gag gag ttt gcn aac cgc ctg tcc aag gac gcc cac	400
Thr Gly Thr Ala Glu Glu Phe Ala Asn Arg Leu Ser Lys Asp Ala His	
95 100 105	
cgc tac ggg atg cga ggc atg tca gcg gac cct gag gag tat gac ctg	448
Arg Tyr Gly Met Arg Gly Met Ser Ala Asp Pro Glu Glu Tyr Asp Leu	
110 115 120	
gcc gac ctg agc agc ctg cca gag atc gac nac gcc ctg gtg gtt ttc	496
Ala Asp Leu Ser Ser Leu Pro Glu Ile Asp Xaa Ala Leu Val Val Phe	
125 130 135	
tgc atg gcc acc tac ggt gag	517
Cys Met Ala Thr Tyr Gly Glu	

004220"666T560



140

145

<210> 1447  
 <211> 476  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 189..476

<400> 1447  
 agtttgggct tggatggtaa cgtttatttt ccttggcaga gaagctgac gtcgaagggc 60  
 atctaacc aa agcggtagaa gaaacaaagc tttcaaaaga aaatcagaca agagcaaaag 120  
 aatctgattt ttcagatact ctgagtccaa gcaaggaaaa aagcagtgac gacactacag 180  
 ayycccaa atg gat gag caa gac cta aat gag cct ctt gcc aaa gtg tcc 230  
 Met Asp Glu Gln Asp Leu Asn Glu Pro Leu Ala Lys Val Ser  
 1 5 10  
 ctt tta aaa gat gac ttg cag ggt gca cag tca gaa att gag gca aag 278  
 Leu Leu Lys Asp Asp Leu Gln Gly Ala Gln Ser Glu Ile Glu Ala Lys  
 15 20 25 30  
 caa gam ata cag cat ctt cga aag gaa ttg atc gaa gcc cag gag cta 326  
 Gln Xaa Ile Gln His Leu Arg Lys Glu Leu Ile Glu Ala Gln Glu Leu  
 35 40 45  
 gct aga aca agt aaa caa aaa tgc ttt gaa ctt caa gct ctt ttg gaa 374  
 Ala Arg Thr Ser Lys Gln Lys Cys Phe Glu Leu Gln Ala Leu Leu Glu  
 50 55 60  
 gaa gaa aga naa gcc tat cga rat caa gtt gag gaw tcc act aaa caa 422  
 Glu Glu Arg Xaa Ala Tyr Arg Xaa Gln Val Glu Xaa Ser Thr Lys Gln  
 65 70 75  
 ata cng gtt ctt caa gcc caa ttg cag agg tta cac atc gat act gag 470  
 Ile Xaa Val Leu Gln Ala Gln Leu Gln Arg Leu His Ile Asp Thr Glu  
 80 85 90  
 aat ctc 476  
 Asn Leu  
 95

<210> 1448  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 164..427

<400> 1448  
 atagggttgt aacaggaagg ctgttgattc tggcttcatt gttgggcccag tcatttgtga 60  
 gctggtggcc ggaccacagg ccacacactt cttccgtgca aatcttcatg tattgaaact 120  
 gcctgtgtat tgtttttacg attggagact tggccaagaa aag atg agt tcc ggg 175  
 Met Ser Ser Gly  
 1

```

aac gcg tcc tat cgc tgc tct atg tct tcc tct gcg gat ttt tcc gat      223
Asn Ala Ser Tyr Arg Cys Ser Met Ser Ser Ser Ala Asp Phe Ser Asp
5          10          15          20
gag gat gat ttc agc cag aaa tct ggc tcc gca tcc cca gct ccg gga      271
Glu Asp Asp Phe Ser Gln Lys Ser Gly Ser Ala Ser Pro Ala Pro Gly
          25          30          35
gac acc tta ccc tgg aat ttg cct aaa cat gag aga tcg aaa aga aag      319
Asp Thr Leu Pro Trp Asn Leu Pro Lys His Glu Arg Ser Lys Arg Lys
          40          45          50
att caa ggg ggc tca gtg ctg gac cct gcc gag agg gca gtg ctt cgg      367
Ile Gln Gly Gly Ser Val Leu Asp Pro Ala Glu Arg Ala Val Leu Arg
          55          60          65
ata gca gat gaa cgg aca aag ttc aga ara aac att tac aaa atg gat      415
Ile Ala Asp Glu Arg Thr Lys Phe Arg Xaa Asn Ile Tyr Lys Met Asp
          70          75          80
aaa tca gca tct c
Lys Ser Ala Ser
85

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<210> 1449  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 209..385

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<400> 1449
aaagatgctg atgagggggt gcagcatgca attcacttca ccagcagtca ctaaggtctg      60
atctcttttc taaccatacc tggaagatgg aatgctggac ccaggaaggc tttgacatat      120
caatgcacca gggatcttac caaactaaat tttaagcact tatagctcaa gattctccct      180
ctgagatgaa acatacttcc accctgtc atg tgt cag ctt cag aag ata tca      232
                               Met Cys Gln Leu Gln Lys Ile Ser
                               1          5
att gct caa gaa agt gtt gga caa gca gaa aag cac act gaa cat ttc      280
Ile Ala Gln Glu Ser Val Gly Gln Ala Glu Lys His Thr Glu His Phe
          10          15          20
tgg act tgt gaa aga gct ctg aat atg gat ctc tca ggg ata ttc cat      328
Trp Thr Cys Glu Arg Ala Leu Asn Met Asp Leu Ser Gly Ile Phe His
          25          30          35          40
ccc cac caa tgc ttt acc aat gcg aga gct ggc cag gct gag aca ttt      376
Pro His Gln Cys Phe Thr Asn Ala Arg Ala Gly Gln Ala Glu Thr Phe
          45          50          55
aat gat aac
Asn Asp Asn
385

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<210> 1450  
 <211> 611  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 181..609

<400> 1450

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gtgttccgca ttctgcaagc ctccggagcg cacgtcggca gtcgggtccc tcgttgaccg      60
aatcaccgac ctctctcccc agctgtatctt ccaaaatgtc gctttctaac aagctgacgc      120
tggaacaagct ggacgttaaa gggaagcggg tcgttatgag agtcgcactt caatgttcct      180
atg aag aac aac cag ata aca aac aac cag agg att aag gct gct gtc      228
Met Lys Asn Asn Gln Ile Thr Asn Asn Gln Arg Ile Lys Ala Ala Val
1          5          10          15
cca agc atc aaa ttc tgc ttg gac aat gga gcc aag tcg gta gtc ctt      276
Pro Ser Ile Lys Phe Cys Leu Asp Asn Gly Ala Lys Ser Val Val Leu
20          25          30
atg agc cac cta ggc cgg cct gat ggt gtg ccc atg cct gac aag tac      324
Met Ser His Leu Gly Arg Pro Asp Gly Val Pro Met Pro Asp Lys Tyr
35          40          45
tcc tta gag cca gtt gct gta gaa ctc aaa tct ctg ctg ggc aag gat      372
Ser Leu Glu Pro Val Ala Val Glu Leu Lys Ser Leu Leu Gly Lys Asp
50          55          60
gtt ctg ttc ttg aag gac tgt gta ggc cca gaa gtg gag aaa gcc tgt      420
Val Leu Phe Leu Lys Asp Cys Val Gly Pro Glu Val Glu Lys Ala Cys
65          70          75          80
gcc aac cca gct gct ggg tct gtc atc ctg ctg gag aac ctc cgc ttt      468
Ala Asn Pro Ala Ala Gly Ser Val Ile Leu Leu Glu Asn Leu Arg Phe
85          90          95
cat gtg gag gaa gaa ggg aag gga aaa gat gct tct ggg aac aag gtt      516
His Val Glu Glu Glu Gly Lys Gly Lys Asp Ala Ser Gly Asn Lys Val
100          105          110
aaa gcc gag cca gcc aaa ata gaa gct ttc cga gct tca ctt tcc aag      564
Lys Ala Glu Pro Ala Lys Ile Glu Ala Phe Arg Ala Ser Leu Ser Lys
115          120          125
cta ggg gat gtc tat gtc aat gat gct ttt ggc act gct cac aga gc      611
Leu Gly Asp Val Tyr Val Asn Asp Ala Phe Gly Thr Ala His Arg
130          135          140

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<210> 1451  
<211> 232  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 75..230

<400> 1451

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attaccatgg ttaccaggca cagagtccag tgccccaacc tggacgttcc agaagaggcc      60
agggaggatc tgag atg gcc ttc ttc aac ttg tat cta ttg gga tat caa      110
Met Ala Phe Phe Asn Leu Tyr Leu Leu Gly Tyr Gln
1          5          10
aat tcc ttt cag aac aag aaa agg aac aca act gaa gaa aca aac cag      158
Asn Ser Phe Gln Asn Lys Lys Arg Asn Thr Thr Glu Glu Thr Asn Gln
15          20          25

```

aag gaa cca gag cct act agg ctt ccc ccc att atc tca aaa gat ggg 206  
 Lys Glu Pro Glu Pro Thr Arg Leu Pro Pro Ile Ile Ser Lys Asp Gly  
 30 35 40  
 aat tat tcc gtg cac cag aat agc ca 232  
 Asn Tyr Ser Val His Gln Asn Ser  
 45 50

<210> 1452  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 179..391

<400> 1452  
 aagttttact tctccctaga gcaggggtgt ttgccagcag cctgcactct cagaaatcag 60  
 acttgagtgg ccggaaccct tgagaccaga ggcttaccat gctgctccct aggagggcca 120  
 ggaactgctg acgtgaccac tggacagtta ttcgtgtctc ttacaattac caaacaga 178  
 atg gac aag ctt aat aaa ata acc gtc ccc gcc agt cag aag ttg agg 226  
 Met Asp Lys Leu Asn Lys Ile Thr Val Pro Ala Ser Gln Lys Leu Arg  
 1 5 10 15  
 cag ctt caa aag atg gtc cat gat att aaa aac aat gaa ggt gga ata 274  
 Gln Leu Gln Lys Met Val His Asp Ile Lys Asn Asn Glu Gly Gly Ile  
 20 25 30  
 atg aat aaa atc aaa aag cta aaa gtc aaa gca cct cca agt gtt cct 322  
 Met Asn Lys Ile Lys Lys Leu Lys Val Lys Ala Pro Pro Ser Val Pro  
 35 40 45  
 cga agg gac tac gct tca gag agc cct gct gac gaa gag gag cag tgg 370  
 Arg Arg Asp Tyr Ala Ser Glu Ser Pro Ala Asp Glu Glu Glu Gln Trp  
 50 55 60  
 tcc gat gac ttt gac agc gac 391  
 Ser Asp Asp Phe Asp Ser Asp  
 65 70

<210> 1453  
 <211> 427  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 68..427

<400> 1453  
 gagaaggcgc gatgttgacg gggtcctaag atggctgctg ggcgaccact tectgacaga 60  
 agaaaag atg tgg agt ggg ctg cta cct cct ggc cta aat gaa agt gac 109  
 Met Trp Ser Gly Leu Leu Pro Pro Gly Leu Asn Glu Ser Asp  
 1 5 10  
 gct gag tca aac tcg gaa gat gaa gct acg ttg gag aac tct gga ctt 157  
 Ala Glu Ser Asn Ser Glu Asp Glu Ala Thr Leu Glu Asn Ser Gly Leu

15	20	25	30	
aac tta cag gaa gat aaa gag gat gag agc atc aga aaa aca gaa atc				205
Asn Leu Gln Glu Asp Lys Glu Asp Glu Ser Ile Arg Lys Thr Glu Ile				
	35	40	45	
ata gat ttc tca aca gat gaa cca aaa act gaa aca gag tca aat gta				253
Ile Asp Phe Ser Thr Asp Glu Pro Lys Thr Glu Thr Glu Ser Asn Val				
	50	55	60	
aat gcc tat gaa gag tgt cct tct gga att ccc ata gat atg tgg aat				301
Asn Ala Tyr Glu Glu Cys Pro Ser Gly Ile Pro Ile Asp Met Trp Asn				
	65	70	75	
aaa ttt caa gaa ttg cat aaa aaa cat tct gaa cag aaa agc aca acc				349
Lys Phe Gln Glu Leu His Lys Lys His Ser Glu Gln Lys Ser Thr Thr				
	80	85	90	
tca aga ttc aga ggg aaa aga mga aaa cgc tcc aga aaa gat ama ttg				397
Ser Arg Phe Arg Gly Lys Arg Arg Lys Arg Ser Arg Lys Asp Xaa Leu				
	95	100	105	110
amg aat gar aaa gaa tta cat agt gam cgt				427
Xaa Asn Glu Lys Glu Leu His Ser Xaa Arg				
	115	120		

<210> 1454  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 148..378

<400> 1454  
 agaactgcag gagactatct ttctagacaa ggcagttgag gaggagggag cgcttgaggg 60  
 ggactggcct ggcgtgcact ccgcacctcg gggacattat tgcgcgtgga acggctgctt 120  
 ttggaagact attgcccaga agaaaag atg ttt ggt ttt cac aag cca aag atg 174  
 Met Phe Gly Phe His Lys Pro Lys Met

	1	5	
tac cga agt ata gag ggc tgc tgt att tgc aga gct aag tcc tcc agt			222
Tyr Arg Ser Ile Glu Gly Cys Cys Ile Cys Arg Ala Lys Ser Ser Ser			
	10	15	20
tct cga ttc act gac agt aaa cgc tat gaa aag gac ttc cag agc tgt			270
Ser Arg Phe Thr Asp Ser Lys Arg Tyr Glu Lys Asp Phe Gln Ser Cys			
	30	35	40
ttt gga ttg cat gag act cgt tca gga gac atc tgc aat gcc tgt gtc			318
Phe Gly Leu His Glu Thr Arg Ser Gly Asp Ile Cys Asn Ala Cys Val			
	45	50	55
ctg ctt gtg aaa aga tgg aag aag ttg cca gca gga tca aaa aaa aac			366
Leu Leu Val Lys Arg Trp Lys Lys Leu Pro Ala Gly Ser Lys Lys Asn			
	60	65	70
tgg aat cat gtg g			379
Trp Asn His Val			
	75		

<210> 1455  
 <211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 269..499

<400> 1455

agcagagaaa ggaagtcctc tccctggagg cctatctccc tcagaactgc gcgagaagcg 60  
agaccttaga aggcagsgct tcccgcgaag gaccggaaag gagcgctac taaggacgcc 120  
gtcgargtcc gggsgcctc aactctatag ctctaactgg ctagaagtgc ccaacgtgga 180  
atgtttcttt tttaaaggcg gctcttgaag cgacccggaa gcggaagtgg aagaaagttc 240  
tagtggcttg agattaagcc tgatcaag atg aca acc tcc caa aag cac cga 292  
Met Thr Thr Ser Gln Lys His Arg  
1 5  
gac ttc gtg gca gag ccc atg ggg gag aag cca gtg ggg agc ctg gct 340  
Asp Phe Val Ala Glu Pro Met Gly Glu Lys Pro Val Gly Ser Leu Ala  
10 15 20  
ggg att ggt gaa gtc ctg ggc aag aag ctg gag gaa agg ggt ttt gac 388  
Gly Ile Gly Glu Val Leu Gly Lys Lys Leu Glu Glu Arg Gly Phe Asp  
25 30 35 40  
ang gcc tat gtt gtc ctt ggc cag ttt ctg gtg cta aag aaa gat gaa 436  
Xaa Ala Tyr Val Val Leu Gly Gln Phe Leu Val Leu Lys Lys Asp Glu  
45 50 55  
gac ctc ttc cgg gaa tgg ctg aaa gac act tgt ggc gcc aac gcc aag 484  
Asp Leu Phe Arg Glu Trp Leu Lys Asp Thr Cys Gly Ala Asn Ala Lys  
60 65 70  
cag tcc cgg gac tgc tt 501  
Gln Ser Arg Asp Cys  
75

<210> 1456

<211> 411

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 140..409

<400> 1456

aaagaaagtt ctagtggctt gaggtatccg caggagcggc cgggtggcgg gaggaaccgt 60  
tacgggaact gaagttgcgg gcctatgttg tccttggcca gtttctggtg ctaaagaaag 120  
rtgaagacct cttccggga atg gct gaa aga cam ttg tkg gsg cca acg cca 172  
Met Ala Glu Arg Xaa Leu Xaa Xaa Pro Thr Pro  
1 5 10  
agc agt ccc ggg ayt gct tgc gat gcc ttc gag agt ggt gcg acg cct 220  
Ser Ser Pro Gly Xaa Ala Ser Asp Ala Phe Glu Ser Gly Ala Thr Pro  
15 20 25  
tct tgt gat gct ctc tgg gaa gct ctc aat ccc cag ccc tca tcc aga 268  
Ser Cys Asp Ala Leu Trp Glu Ala Leu Asn Pro Gln Pro Ser Ser Arg  
30 35 40

**Q**uestions **A**nswers **I**nterviews **E**xercises **P**roblems **S**olutions

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<220>  
<221> CDS  
<222> 141..458
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<210> 1458
<211> 326
<212> DNA
<213> Homo sapiens
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981

&lt;400&gt; 1458

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ctnytganng gtaggcggta gtggcggaag aggttcggcg gctgatggcg gatcaggatc 60
ggaagcctgc gtaactttct cccttgatcc gggagtcttt ccactggatt caca atg 117
                                     Met
                                     1
aca tcc ttt caa gaa gtc cca ttg cag act tcc aac ttt gcc cat gtc 165
Thr Ser Phe Gln Glu Val Pro Leu Gln Thr Ser Asn Phe Ala His Val
                    5                    10                    15
atc ttt caa aat gtg gcc aag agt tac ctt cct aat gca cac ctg gaa 213
Ile Phe Gln Asn Val Ala Lys Ser Tyr Leu Pro Asn Ala His Leu Glu
                    20                    25                    30
tgt cat tac acc tta act cca tcg gcg gct gat ata aaa att ttt ttc 261
Cys His Tyr Thr Leu Thr Pro Ser Ala Ala Asp Ile Lys Ile Phe Phe
                    35                    40                    45
tgt aga aac aga gtc tcc ctc tgt tgc cca ggc tgg agt gca gtg tta 309
Cys Arg Asn Arg Val Ser Leu Cys Cys Pro Gly Trp Ser Ala Val Leu
50                    55                    60                    65
ctg tct cag ttc act gc 326
Leu Ser Gln Phe Thr
                    70

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&lt;210&gt; 1459

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 24..431

&lt;400&gt; 1459

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attaccaggc acgcgcagga aac atg gcg gcg gcg ggt gtt gtg agc ggg aag 53
                                     Met Ala Ala Ala Gly Val Val Ser Gly Lys
                                     1                    5                    10
att ata tat gaa caa gaa gga gta tat att cac tca tct tgt gga aag 101
Ile Ile Tyr Glu Gln Glu Gly Val Tyr Ile His Ser Ser Cys Gly Lys
                    15                    20                    25
acc aat gac caa gac ggc ttg att tca gga ata tta cgt gtt tta gaa 149
Thr Asn Asp Gln Asp Gly Leu Ile Ser Gly Ile Leu Arg Val Leu Glu
                    30                    35                    40
aag gat gcc gaa gta ata gtg gac tgg aga cca ttg gat gat gca tta 197
Lys Asp Ala Glu Val Ile Val Asp Trp Arg Pro Leu Asp Asp Ala Leu
                    45                    50                    55
gat tcc tct agt att ctc tat gct aga aag gac tcc agt tca gtt gta 245
Asp Ser Ser Ser Ile Leu Tyr Ala Arg Lys Asp Ser Ser Ser Val Val
                    60                    65                    70
gaa tgg act cag gcc cca aaa gaa aga ggt cat cga gga tca gaa cat 293
Glu Trp Thr Gln Ala Pro Lys Glu Arg Gly His Arg Gly Ser Glu His
75                    80                    85                    90
ctg aac agt tac gaa gca gaa tgg gac atg gtt aat aca gtt tca ttt 341
Leu Asn Ser Tyr Glu Ala Glu Trp Asp Met Val Asn Thr Val Ser Phe
                    95                    100                    105

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**06-09-2017**

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<220>  
<221> CDS  
<222> 54..425
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<210> 1461
<211> 506
<212> DNA
<213> Homo sapiens
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983

<400> 1461

tgcgagctcc cggggaaaag caacagtgtc ctctaagcc tgaggccacc gcgaccgagc 60  
cgagccaggc taagggacca gtgtctccct gccccccmc ccacctctag grgctctgga 120  
gccttaggac catggacgct ctcaatagga accaaatagg ccctgg atg cca gac 175  
Met Pro Asp  
1

cca gac cat ggt gca gaa agg acc ctt gga cct gat cga gac agg caa 223  
Pro Asp His Gly Ala Glu Arg Thr Leu Gly Pro Asp Arg Asp Arg Gln  
5 10 15

agg gct gaa agt gca aac gac aaa ccc cac ctg gtg agc ctg ggc agt 271  
Arg Ala Glu Ser Ala Asn Asp Lys Pro His Leu Val Ser Leu Gly Ser  
20 25 30 35

ggg cga ctc agc aca gcc atc acc ctc ctg ccg ctg gag gaa ggg agg 319  
Gly Arg Leu Ser Thr Ala Ile Thr Leu Pro Leu Glu Glu Gly Arg  
40 45 50

acg gtg att ggc tct gca gcc aga gac atc tca cta cag ggc cca ggc 367  
Thr Val Ile Gly Ser Ala Ala Arg Asp Ile Ser Leu Gln Gly Pro Gly  
55 60 65

ctg gct cca gag cac tgc tac atc gag aac ctg cgg ggc acc ctc acc 415  
Leu Ala Pro Glu His Cys Tyr Ile Glu Asn Leu Arg Gly Thr Leu Thr  
70 75 80

ctc tac ccc tgt ggc aat gcc tgc act att gat ggg ctc ctg tcc ggc 463  
Leu Tyr Pro Cys Gly Asn Ala Cys Thr Ile Asp Gly Leu Leu Ser Gly  
85 90 95

agc cta ccc ggc tca ctc arn gct gca tgt tgt gsc tgg gtc a 506  
Ser Leu Pro Gly Ser Leu Xaa Ala Ala Cys Cys Xaa Trp Val  
100 105 110

<210> 1462

<211> 393

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 61..393

<400> 1462

agaaacgtgt tcgctgcccc gaagaaggga aggcgcgagt gaggaaggga ggtactgtag 60  
atg ccc tcc aaa tcc ttg gtt atg gaa tat ttg gct cat ccc agt aca 108  
Met Pro Ser Lys Ser Leu Val Met Glu Tyr Leu Ala His Pro Ser Thr  
1 5 10 15

ctc ggc ttg gct gtt gga gtt gct tgt ggc atg tgc ctg ggc tgg agc 156  
Leu Gly Leu Ala Val Gly Val Ala Cys Gly Met Cys Leu Gly Trp Ser  
20 25 30

ctt cga gta tgc ttt ggg atg ctc ccc aaa agc aag acg agc aag aca 204  
Leu Arg Val Cys Phe Gly Met Leu Pro Lys Ser Lys Thr Ser Lys Thr  
35 40 45

cac aca gat act gaa agt gaa gca agc atc ttg gga gac agc ggg gag 252  
His Thr Asp Thr Glu Ser Glu Ala Ser Ile Leu Gly Asp Ser Gly Glu  
50 55 60



<220>  
<221> CDS  
<222> 63..356

<400> 1464  
gttttaagaa tayntcagcg tastagagga tttaagcaga tcgctttgcc tactttaatt 60  
at atg aaa tac cag gag gtc aga tgt tta acc tct ttc aac ata tct 107  
Met Lys Tyr Gln Glu Val Arg Cys Leu Thr Ser Phe Asn Ile Ser  
1 5 10 15  
ggt tct ttt cct gca gaa aca gat gat tat gct gag att ata gat gaa 155  
Val Ser Phe Pro Ala Glu Thr Asp Asp Tyr Ala Glu Ile Ile Asp Glu  
20 25 30  
gaa gat act tac acc atg ccc tca acc agg gat tat gag att caa aga 203  
Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile Gln Arg  
35 40 45  
gam aga ata gaa ctt gga cga tgt att gga gaa ggc caa ttt gga gat 251  
Xaa Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe Gly Asp  
50 55 60  
gta cat caa ggc att yat atg agt cca gag aat cca gct ttg gcg gtt 299  
Val His Gln Gly Ile Xaa Met Ser Pro Glu Asn Pro Ala Leu Ala Val  
65 70 75  
gca att aaa aca tgt aaa aac tgt act kcg gac agc gtg aga gag aaa 347  
Ala Ile Lys Thr Cys Lys Asn Cys Thr Xaa Asp Ser Val Arg Glu Lys  
80 85 90 95  
ttt ctt caa ga 358  
Phe Leu Gln

<210> 1465  
<211> 460  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 217..459

<400> 1465  
acacactgtc agggctagcc tgctgtctta cgcgcgctgc ggattgttgc tccgttgtag 60  
ctgctgggga attcacctcg ttactgcttg atatcttcca ccccttacaa aatcagaaaa 120  
gttggtgtttt ctaataccaa agaggagggtt tggctttctg tgggtgattc ccagacactg 180  
aagtgcaaag aagagaccct cctagaaaag taaaat atg act aaa agc aat gga 234  
Met Thr Lys Ser Asn Gly  
1 5  
gaa gag ccc aag atg ggg ggc agg atg gag aga ttc cag cag gga gtc 282  
Glu Glu Pro Lys Met Gly Gly Arg Met Glu Arg Phe Gln Gln Gly Val  
10 15 20  
cgt aaa cgc aca ctt ttg gcc aag aag aaa gtg cag aac att aca aag 330  
Arg Lys Arg Thr Leu Leu Ala Lys Lys Lys Val Gln Asn Ile Thr Lys  
25 30 35  
gag gat gtt aaa agt tac ctg ttt cgg aat gct ttt gtg ctg ctc aca 378  
Glu Asp Val Lys Ser Tyr Leu Phe Arg Asn Ala Phe Val Leu Leu Thr  
40 45 50

gtc anc gct gtc att gtg ggt aca atc ctt gga ttt anc ctc cga cca 426  
 Val Xaa Ala Val Ile Val Gly Thr Ile Leu Gly Phe Xaa Leu Arg Pro  
 55 60 65 70  
 tac aga atg agc tac cgg gaa gtc aag tac ttc t 460  
 Tyr Arg Met Ser Tyr Arg Glu Val Lys Tyr Phe  
 75 80

<210> 1466  
 <211> 366  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 75..365

<400> 1466  
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 agaacaagga gctg atg gat gaa tat aat cat tta aaa gaa aga atg gat 110  
 Met Asp Glu Tyr Asn His Leu Lys Glu Arg Met Asp  
 1 5 10  
 caa tgt gag aaa gag aaa gca gga aga aaa att gac ctt aca gaa gca 158  
 Gln Cys Glu Lys Glu Lys Ala Gly Arg Lys Ile Asp Leu Thr Glu Ala  
 15 20 25  
 cag gaa act gta cct tca cga tgt cta cat ctg gat gca gag aat gaa 206  
 Gln Glu Thr Val Pro Ser Arg Cys Leu His Leu Asp Ala Glu Asn Glu  
 30 35 40  
 gtt ctt caa ctt caa cag aca tta ttc tct atg aaa gca ata caa aag 254  
 Val Leu Gln Leu Gln Gln Thr Leu Phe Ser Met Lys Ala Ile Gln Lys  
 45 50 55 60  
 caa tgt gaa aca cta cag aag aat aag aag cag ctg aaa caa gaa gta 302  
 Gln Cys Glu Thr Leu Gln Lys Asn Lys Lys Gln Leu Lys Gln Glu Val  
 65 70 75  
 gta aac ctc aaa agt tat atg gaa aga aat atg tta gaa cgt ggt aag 350  
 Val Asn Leu Lys Ser Tyr Met Glu Arg Asn Met Leu Glu Arg Gly Lys  
 80 85 90  
 ctg aat ggc ata aac t 366  
 Leu Asn Gly Ile Asn  
 95

<210> 1467  
 <211> 362  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 28..360

<400> 1467  
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 Met Ala Ala Ala Ala Ala Ala Ala Ala

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gaa	cag	ata	aca	ctt	gtt	att	tgg	gcc	gtg	att	cgc	att	gga	cca	aat				
Glu	Gln	Ile	Thr	Leu	Val	Ile	Trp	Ala	Val	Ile	Arg	Ile	Gly	Pro	Asn				
10					15					20				25					
ggc	tgt	gat	agt	atg	gag	ttt	cat	gaa	agt	ggc	ctg	ctt	cga	tkk	aag				
Gly	Cys	Asp	Ser	Met	Glu	Phe	His	Glu	Ser	Gly	Leu	Leu	Arg	Xaa	Lys				
				30				35					40						
caa	gta	tct	gac	atg	gga	gtg	atc	cac	cct	ctt	tat	aaa	agc	aca	gta				
Gln	Val	Ser	Asp	Met	Gly	Val	Ile	His	Pro	Leu	Tyr	Lys	Ser	Thr	Val				
			45				50					55							
gga	gga	agg	cga	aat	gaa	aat	ttg	gtc	atc	act	ggc	aac	aac	cag	cct				
Gly	Gly	Arg	Arg	Asn	Glu	Asn	Leu	Val	Ile	Thr	Gly	Asn	Asn	Gln	Pro				
		60				65					70								
att	gtt	ttt	cag	caa	ggg	aca	aca	aag	ctc	agt	gta	gas	mac	aac	aaa				
Ile	Val	Phe	Gln	Gln	Gly	Thr	Thr	Lys	Leu	Ser	Val	Xaa	Xaa	Asn	Lys				
	75				80				85										
act	tct	att	aca	agt	gac	atc	ggc	atg	cag	ttt	ttt	gac	ccg	agg	wct				
Thr	Ser	Ile	Thr	Ser	Asp	Ile	Gly	Met	Gln	Phe	Phe	Asp	Pro	Arg	Xaa				
	90				95				100					105					
caa	aat	atc	tta	ttc	agc	ac													
Gln	Asn	Ile	Leu	Phe	Ser														
					110														

<210> 1468  
 <211> 403  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 136..402

<400> 1468  
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 ggtacctcct tcaagctggg agagggtctt agtccctggt tctgaacact ctggggttct 120  
 cgggtgcagg ccgcc atg agc aaa cgg aag gcg ccg cag gag act ctc aac 171  
 Met Ser Lys Arg Lys Ala Pro Gln Glu Thr Leu Asn  
 1 5 10  
 ggg gga atc acc gac atg ctc aca gaa ctc gca aac ttt gag aag aac 219  
 Gly Gly Ile Thr Asp Met Leu Thr Glu Leu Ala Asn Phe Glu Lys Asn  
 15 20 25  
 gtg akc caa gct atc cac aag tac aat gct tas rga aaa gca gca tct 267  
 Val Xaa Gln Ala Ile His Lys Tyr Asn Ala Xaa Xaa Lys Ala Ala Ser  
 30 35 40  
 gtt ata gca aaa tac cca cac aaa ata aag agt gga gct kwa gct aag 315  
 Val Ile Ala Lys Tyr Pro His Lys Ile Lys Ser Gly Ala Xaa Ala Lys  
 45 50 55 60  
 aaa ttg cct gga gta gga aca aaa att gct gaa aag att gat gag ttt 363  
 Lys Leu Pro Gly Val Gly Thr Lys Ile Ala Glu Lys Ile Asp Glu Phe  
 65 70 75  
 tta gca act gga aaa tta cgt aaa ctg gaa aag att cgg c 403  
 Leu Ala Thr Gly Lys Leu Arg Lys Leu Glu Lys Ile Arg  
 80 85

004220" 656ET560

<210> 1469  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 121..387

<400> 1469  
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 gcccgagcgc gggtttctctt aagggttctgc agggcaaggc tgtctgggac aggcttggcc 120  
 atg gat ccg ctc tca gag ctg cag gat gat ctg acc ttg gat gac acc 168  
 Met Asp Pro Leu Ser Glu Leu Gln Asp Asp Leu Thr Leu Asp Asp Thr  
 1 5 10 15  
 agc gag gct ctg aac cag ctg aag ctg gcc tcc atc gat gag aag aac 216  
 Ser Glu Ala Leu Asn Gln Leu Lys Leu Ala Ser Ile Asp Glu Lys Asn  
 20 25 30  
 tgg ccc tcg gat gaa atg cct gac ttc ccc aag tca gat gac tcc aaa 264  
 Trp Pro Ser Asp Glu Met Pro Asp Phe Pro Lys Ser Asp Asp Ser Lys  
 35 40 45  
 agc agc tcc ccg gaa ctt gtc aca cac ctg aag tgg gat gac cca tac 312  
 Ser Ser Ser Pro Glu Leu Val Thr His Leu Lys Trp Asp Asp Pro Tyr  
 50 55 60  
 tat gac atc gcc cgg cac cag atc gtg gag gtg gca gga gat gac aag 360  
 Tyr Asp Ile Ala Arg His Gln Ile Val Glu Val Ala Gly Asp Asp Lys  
 65 70 75 80  
 tat ggg cgg aag atc att gtg ttt agt g 388  
 Tyr Gly Arg Lys Ile Ile Val Phe Ser  
 85

<210> 1470  
 <211> 503  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 100..501

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 agcgtgttca gcctgcctgc ctgcctgcct ctgtgtgtgt gtgagcgtgt gtgcgtgcgt 60  
 ctacttttgta ctgggaagaa cacagcccat gtgctctgc atg gac gtt act gat 114  
 Met Asp Val Thr Asp  
 1 5  
 act ctg ttt agc ttg att ttc nga aaa gca gcc aag atg tcc agc aca 162  
 Thr Leu Phe Ser Leu Ile Phe Xaa Lys Ala Gly Lys Met Ser Ser Thr  
 10 15 20  
 cca cat gac ccc ttc tat tct tct cct ttc ggc cca ttt tat agg agg 210  
 Pro His Asp Pro Phe Tyr Ser Ser Pro Phe Gly Pro Phe Tyr Arg Arg  
 25 30 35

cat aca cca tac atg gta cag cca gag tac cga atc tat gag atg aac	258
His Thr Pro Tyr Met Val Gln Pro Glu Tyr Arg Ile Tyr Glu Met Asn	
40 45 50	
aag aga ctg cag tct cgc aca gag gat agt gac aac ctc tgg tgg gac	306
Lys Arg Leu Gln Ser Arg Thr Glu Asp Ser Asp Asn Leu Trp Trp Asp	
55 60 65	
gcc ttt gcc act gaa ttt ttt gaa gat gac gcc aca tta acc ctt tca	354
Ala Phe Ala Thr Glu Phe Phe Glu Asp Asp Ala Thr Leu Thr Leu Ser	
70 75 80 85	
ttt tgt ttg gaa gat gga cca aag cga tac act atc ggc agg acc ctc	402
Phe Cys Leu Glu Asp Gly Pro Lys Arg Tyr Thr Ile Gly Arg Thr Leu	
90 95 100	
atc ccc cgt tac ttt agc act gtg ttt gaa gga ggg gtg acc gac ctg	450
Ile Pro Arg Tyr Phe Ser Thr Val Phe Glu Gly Gly Val Thr Asp Leu	
105 110 115	
tat tac att ctc aaa cac tcg aaa gag tca tac cac aac tca tcc atc	498
Tyr Tyr Ile Leu Lys His Ser Lys Glu Ser Tyr His Asn Ser Ser Ile	
120 125 130	
acg gt	503
Thr	

<210> 1471  
 <211> 764  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..763

<400> 1471	
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Met	
1	
ttg ggg ttt gtg ggt cgg gtg gcc gct gct ccg gcc tcc ggg gcc ttg	106
Leu Gly Phe Val Gly Arg Val Ala Ala Pro Ala Ser Gly Ala Leu	
5 10 15	
cgg aga ctc acc cct tca gcg tcg ctg ccc cca gct cag ctc tta ctg	154
Arg Arg Leu Thr Pro Ser Ala Ser Leu Pro Pro Ala Gln Leu Leu Leu	
20 25 30	
cgg gcc gct ccg acg gcg gtc cat cct gtc agg gac tat gcg gcg caa	202
Arg Ala Ala Pro Thr Ala Val His Pro Val Arg Asp Tyr Ala Ala Gln	
35 40 45	
aca tct cct tcg cca aaa gca ggc gcc gcc acc ggg cgc atc gtg gcg	250
Thr Ser Pro Ser Pro Lys Ala Gly Ala Ala Thr Gly Arg Ile Val Ala	
50 55 60 65	
gtc att ggc gca gtg gtg gac gtc cag ttt gat gag gga cta cca cca	298
Val Ile Gly Ala Val Val Asp Val Gln Phe Asp Glu Gly Leu Pro Pro	
70 75 80	
att cta aat gcc ctg gaa gtg caa ggc agg gag acc aga ctg gtt ttg	346
Ile Leu Asn Ala Leu Glu Val Gln Gly Arg Glu Thr Arg Leu Val Leu	
85 90 95	
gag gtg gcc cag cat ttg ggt gag agc aca gta agg act att gct atg	394





<210> 1473  
 <211> 440  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 239..439

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 agaaactaaa ctggaagctt gagttttgtg tagcttcttg aaaccttatg aatggattac 120  
 tagaagctga gagccaggag agacctatag gggatgmaag atccctacac attaaaaggg 180  
 ggagaaaagc aggcggaatt cttcttctg gctgtgttat ccctccttcc tgaaatga 238  
 atg gaa ccc aca aga ctc cca gaa ggt gaa gtt aag agc tcc cag act 286  
 Met Glu Pro Thr Arg Leu Pro Glu Gly Glu Val Lys Ser Ser Gln Thr  
 1 5 10 15  
 cat aag gtt att aga aca gca aac tgg cac ccc aaa gaa ctt tac gga 334  
 His Lys Val Ile Arg Thr Ala Asn Trp His Pro Lys Glu Leu Tyr Gly  
 20 25 30  
 gac ttg caa cct atc aac aag ttg gat gag gga tta aaa sct tca aca 382  
 Asp Leu Gln Pro Ile Asn Lys Leu Asp Glu Gly Leu Lys Xaa Ser Thr  
 35 40 45  
 acc aac aac ccc aag cat caa act gaa gga aac att cta acc ttc aca 430  
 Thr Asn Asn Pro Lys His Gln Thr Glu Gly Asn Ile Leu Thr Phe Thr  
 50 55 60  
 gac aga ctg g 440  
 Asp Arg Leu  
 65

<210> 1474  
 <211> 437  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 27..437

<400> 1474  
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 Met Glu Ala Leu Ile Leu Glu Pro Ser  
 1 5  
 ctg tat act gtc aaa gcc atc ctg att ctg gac aat gat gga gat cga 101  
 Leu Tyr Thr Val Lys Ala Ile Leu Ile Leu Asp Asn Asp Gly Asp Arg  
 10 15 20 25  
 ctt ttt gcc aag tac tat gac gac acc tac ccc agt gtc aag gag caa 149  
 Leu Phe Ala Lys Tyr Tyr Asp Asp Thr Tyr Pro Ser Val Lys Glu Gln  
 30 35 40  
 aag gcc ttt gag aag aac att ttc aac aag acc cat cgg act gac agt 197  
 Lys Ala Phe Glu Lys Asn Ile Phe Asn Lys Thr His Arg Thr Asp Ser  
 45 50 55

gaa att gcc ctc ttg gaa ggc ctg aca gtg gta tac aaa agc agt ata	245
Glu Ile Ala Leu Leu Glu Gly Leu Thr Val Val Tyr Lys Ser Ser Ile	
60 65 70	
gat ctc tat ttc tat gtg att ggc agc tcc tat gaa aat gag ctg atg	293
Asp Leu Tyr Phe Tyr Val Ile Gly Ser Ser Tyr Glu Asn Glu Leu Met	
75 80 85	
ctt atg gct gtt ctg aac tgt ctc ttc gac tca ttg agc cag atg ctg	341
Leu Met Ala Val Leu Asn Cys Leu Phe Asp Ser Leu Ser Gln Met Leu	
90 95 100 105	
agg aaa aat gta gaa aag cga gca ctg ctg gag aac atg gag ggg ctg	389
Arg Lys Asn Val Glu Lys Arg Ala Leu Leu Glu Asn Met Glu Gly Leu	
110 115 120	
ttc ttg gct gtg gat gaa att gwa rat gga ggg gtg atc cta gag agt	437
Phe Leu Ala Val Asp Glu Ile Xaa Xaa Gly Gly Val Ile Leu Glu Ser	
125 130 135	

<210> 1475  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 33..320

<400> 1475	
ccacgtcaga gggaaccgng cggasggcca ac atg gcg gaa csc agg aga cac	53
Met Ala Glu Xaa Arg Arg His	
1 5	
aag aag cgg atc cag gaa gtt ggt gaa cca tct aaa gaa gag aag gct	101
Lys Lys Arg Ile Gln Glu Val Gly Glu Pro Ser Lys Glu Glu Lys Ala	
10 15 20	
gtg gcc aag tat ctt cga ttc aac tgt cca aca aag tcc acc aat atg	149
Val Ala Lys Tyr Leu Arg Phe Asn Cys Pro Thr Lys Ser Thr Asn Met	
25 30 35	
atg ggt cac cgg gtt gat tat ttt att gct tca aaa gca gtg gac tgt	197
Met Gly His Arg Val Asp Tyr Phe Ile Ala Ser Lys Ala Val Asp Cys	
40 45 50 55	
ctt ttg gat tca aag tgg gca aag gcc aag aaa gga gag gaa gct tta	245
Leu Leu Asp Ser Lys Trp Ala Lys Ala Lys Lys Gly Glu Glu Ala Leu	
60 65 70	
ttt aca acc agg gag tct gtg gtt gac tac tgc aac agg ctt tta aag	293
Phe Thr Thr Arg Glu Ser Val Val Asp Tyr Cys Asn Arg Leu Leu Lys	
75 80 85	
aag cag ttt ttt cac cga gcc cta aaa gt	322
Lys Gln Phe Phe His Arg Ala Leu Lys	
90 95	

<210> 1476  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<220>  
<221> CDS  
<222> 105..482

<400> 1476

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cactgaccct cgtcccgccc ccgccattcg ccgcctcctc ctgtcccgca gtcggcgctcc      60
agcggctctg cttgttcgtg tgtgtgtcgt tgcaggcctt attc atg ggc tca ccg      116
                               Met Gly Ser Pro
                               1
ctg agg ttc gac ggg cgg gtg gta ctg gtc acc ggc gcg ggg gca gga      164
Leu Arg Phe Asp Gly Arg Val Val Leu Val Thr Gly Ala Gly Ala Gly
5                               10                               15                               20
ttg ggc cga gcc tat gcc ctg gct ttt gca gaa aga gga gcg tta gtt      212
Leu Gly Arg Ala Tyr Ala Leu Ala Phe Ala Glu Arg Gly Ala Leu Val
                               25                               30                               35
gtt gtg aat gat ttg gga ggg gac ttc aaa gga gtt ggt aaa ggc tcc      260
Val Val Asn Asp Leu Gly Gly Asp Phe Lys Gly Val Gly Lys Gly Ser
                               40                               45                               50
tta gct gct gat aag gtt gtt gaa gaa ata aga agg aga ggt gga aaa      308
Leu Ala Ala Asp Lys Val Val Glu Glu Ile Arg Arg Arg Gly Gly Lys
                               55                               60                               65
gca gtg gcc aac tat gat tca gtg gaa gaa gga gag aag gtt gtg aag      356
Ala Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu Lys Val Val Lys
                               70                               75                               80
aca gcc ctg gat gct ttt gga aga ata gat gtt gtg gtc aac aat gct      404
Thr Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val Val Asn Asn Ala
85                               90                               95                               100
gga att ctg agg gat cgt tcc ttt gct agg ata agt gat gaa gac tgg      452
Gly Ile Leu Arg Asp Arg Ser Phe Ala Arg Ile Ser Asp Glu Asp Trp
                               105                               110                               115
gat ata atc cac aga gtt cat ttg cgg ggt t
Asp Ile Ile His Arg Val His Leu Arg Gly
                               120                               125

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<210> 1477  
<211> 338  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 137..337

<400> 1477

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ganaacaaga tggcggggttc gtggtgagaa gccgtcaagc aggagtagaa attggtatgc      60
ttaraagcag attctaaaag cagtttctct tcagaacatc ttttttcata ccacttgata      120
agcatcttka aacacc atg gct gta gct gca gta aaa tgg gtg atg tca aag      172
                               Met Ala Val Ala Ala Val Lys Trp Val Met Ser Lys
                               1                               5                               10
aga act atc ttg aaa cat tta ttt cca gtc caa aat gga gct tta tat      220
Arg Thr Ile Leu Lys His Leu Phe Pro Val Gln Asn Gly Ala Leu Tyr
                               15                               20                               25

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tgt gtt tgt cat aaa tct acg tat tct cct cta cca gat gac tat aat	268
Cys Val Cys His Lys Ser Thr Tyr Ser Pro Leu Pro Asp Asp Tyr Asn	
30 35 40	
tgc aac gta gag cnt gct ctg act tct gat ggc agg aca ata gta tgc	316
Cys Asn Val Glu Xaa Ala Leu Thr Ser Asp Gly Arg Thr Ile Val Cys	
45 50 55 60	
tac cac cct tct gtg gnc att c	338
Tyr His Pro Ser Val Xaa Ile	
65	

<210> 1478  
 <211> 266  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 99..266

<400> 1478	
agctgagcct agagtcgggc tgttggttag agtgggcgcg gatctggtgt ggggaaggcg	60
gcgggactca ggcctgcctg cgaasattgt cctacata atg gta gag gac gaa ctg	116
Met Val Glu Asp Glu Leu	
1 5	
gca ctt ttc gat aaa agc ata aat gaa ttt tgg aat aaa ttc aaa agt	164
Ala Leu Phe Asp Lys Ser Ile Asn Glu Phe Trp Asn Lys Phe Lys Ser	
10 15 20	
acg gac acc tcc tgt cag atg gcg gga cta aga gat acc tac aag gat	212
Thr Asp Thr Ser Cys Gln Met Ala Gly Leu Arg Asp Thr Tyr Lys Asp	
25 30 35	
tcc atc aaa gca ttt gca gaa aag ctg tct gtg aaa tta aag gaa gaa	260
Ser Ile Lys Ala Phe Ala Glu Lys Leu Ser Val Lys Leu Lys Glu Glu	
40 45 50	
gaa cga	266
Glu Arg	
55	

<210> 1479  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 120..410

<400> 1479	
acaacggctc gcggaggctt acgcgtagtg acatcgccgg tggtttgcggg tggttgttgc	60
tctcggggcc gtgtggagta ggtctggacc tggactcacg gctgcttgga gcgtccgcc	119
atg agg aga agt gag gtg ctg gcg gag gag tcc ata gta tgt ctg cag	167
Met Arg Arg Ser Glu Val Leu Ala Glu Glu Ser Ile Val Cys Leu Gln	
1 5 10 15	

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aaa gcc cta aat cac ctt cgg gaa ata tgg gag cta att ggg att cca      215
Lys Ala Leu Asn His Leu Arg Glu Ile Trp Glu Leu Ile Gly Ile Pro
      20                      25                      30
gag gac cag cgg tta caa aga act gag gtg gta aag aag cat atc aag      263
Glu Asp Gln Arg Leu Gln Arg Thr Glu Val Val Lys Lys His Ile Lys
      35                      40                      45
gaa ctc ctg gat atg atg att gct gaa gag gaa agc ctg aag gaa aga      311
Glu Leu Leu Asp Met Met Ile Ala Glu Glu Glu Ser Leu Lys Glu Arg
      50                      55                      60
ctc atc aaa agc ata tcc gtc tgt cag aaa gag ctg aac act ctg tgc      359
Leu Ile Lys Ser Ile Ser Val Cys Gln Lys Glu Leu Asn Thr Leu Cys
      65                      70                      75                      80
agc gag tta cat gtt gag cca ttt cag gaa gaa gga gar ncg acc atc      407
Ser Glu Leu His Val Glu Pro Phe Gln Glu Glu Gly Glu Xaa Thr Ile
      85                      90                      95

ttg c
Leu
      411

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<210> 1480  
 <211> 457  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 88..456

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<400> 1480
ttctctctctcg gcgtttccgc tgtcagggcc ctgcggtgtg actcgcgggc tcagctggtc      60
cggccgtagc acctccgcgc cgtcgcc atg tgc cgg ttt ttc acc acc ggt tgc      114
                        Met Ser Arg Phe Phe Thr Thr Gly Ser
                        1                      5
gac agc gag tcc gag tgc tcc ttg tcc ggg gag gag ctc gtc acc aaa      162
Asp Ser Glu Ser Glu Ser Ser Leu Ser Gly Glu Glu Leu Val Thr Lys
      10                      15                      20                      25
cct gtc gga ggc aac tat ggc aaa cag cca ttg ttg ctg agc gag gat      210
Pro Val Gly Gly Asn Tyr Gly Lys Gln Pro Leu Leu Leu Ser Glu Asp
      30                      35                      40
gaa gaa gat acc aag aga gtt gtc cgc agt gcc aag gac aag agg ttt      258
Glu Glu Asp Thr Lys Arg Val Val Arg Ser Ala Lys Asp Lys Arg Phe
      45                      50                      55
gag gag ctg acc aac ctt atc cgg acc atc cgt aat gcc atg aag att      306
Glu Glu Leu Thr Asn Leu Ile Arg Thr Ile Arg Asn Ala Met Lys Ile
      60                      65                      70
cgt gat gtc acc aag tgc ctg gaa gag ttt gag ctc ctg gga aaa gca      354
Arg Asp Val Thr Lys Cys Leu Glu Glu Phe Glu Leu Leu Gly Lys Ala
      75                      80                      85
tat ggg aag gcc aaa agc att gtg gac aaa gaa ggt gtc ccc cgg ttc      402
Tyr Gly Lys Ala Lys Ser Ile Val Asp Lys Glu Gly Val Pro Arg Phe
      90                      95                      100                      105
tat atc cgc atc ctg gct gac cta gag gac tat ctt aat gag ctt tgg      450
Tyr Ile Arg Ile Leu Ala Asp Leu Glu Asp Tyr Leu Asn Glu Leu Trp
      110                      115                      120

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gaa gat a  
Glu Asp

457

<210> 1481  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 276..428

<400> 1481  
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agcagttctc aataccggga gaggcacaga gctatttcag ccacatgaaa agcatcggaa 120  
ttgagatcgc agctcagagg acaccgggcg ccccttccac cttccaagga gctttgtatt 180  
cttgcatctg gctgcctggg acttcctta ggcagtaaac aaatacataa agcagggata 240  
agactgcatg aatatgtcga aacagccagt ttcca atg tta gag cca tcc agg 293  
Met Leu Glu Pro Ser Arg  
1 5  
caa ata tca ata ttc caa tgg gag cct ttc ggc cag gag cag gtc aac 341  
Gln Ile Ser Ile Phe Gln Trp Glu Pro Phe Gly Gln Glu Gln Val Asn  
10 15 20  
ccc cca gaa gaa aag aat gta ctc ctg aag tgg agg agg gtg ttc ctc 389  
Pro Pro Glu Glu Lys Asn Val Leu Leu Lys Trp Arg Arg Val Phe Leu  
25 30 35  
cca cct cgg atg agg aga aga agc caa ttc cag gag cga 428  
Pro Pro Arg Met Arg Arg Arg Ser Gln Phe Gln Glu Arg  
40 45 50

<210> 1482  
<211> 207  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 48..206

<400> 1482  
atgcctgcct agacggggcca gaaaagccaa acttaagaaa tctgcct atg tac aga 56  
Met Tyr Arg  
1  
aca agt caa cta agg ggt cca tgg agg ctg agg cgg gag aat tgc ttg 104  
Thr Ser Gln Leu Arg Gly Pro Trp Arg Leu Arg Arg Glu Asn Cys Leu  
5 10 15  
ggc ccg gga ggt gga ggt tgc agt gag cca ccg cac tcc agc ctg ggg 152  
Gly Pro Gly Gly Gly Gly Cys Ser Glu Pro Pro His Ser Ser Leu Gly  
20 25 30 35  
gac aga gtg aga ttc cgt ctc agg aga aat aaa aaa act aga tgg aca 200  
Asp Arg Val Arg Phe Arg Leu Arg Arg Asn Lys Lys Thr Arg Trp Thr  
40 45 50

gat aag t  
Asp Lys

207

<210> 1483  
<211> 422  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 114..422

<400> 1483

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accttcgggc aacacccaat actcggggct ccgctcggct tcttcgcgcc gag atg 116  
Met  
1  
cct aag aag gct ggt gcg acg acc aag ggt aaa agc cag agc aag gaa 164  
Pro Lys Lys Ala Gly Ala Thr Thr Lys Gly Lys Ser Gln Ser Lys Glu  
5 10 15  
cca gag aga cca ctt cct ccc tta ggt cct gtg gca gtt gat cct aaa 212  
Pro Glu Arg Pro Leu Pro Pro Leu Gly Pro Val Ala Val Asp Pro Lys  
20 25 30  
gga tgc gtc acc ata gcc atc cat gca aaa cct ggc tcc aaa caa aat 260  
Gly Cys Val Thr Ile Ala Ile His Ala Lys Pro Gly Ser Lys Gln Asn  
35 40 45  
gct gta aca gat ttg aca gca gag gct gta aat gta gct att gca gca 308  
Ala Val Thr Asp Leu Thr Ala Glu Ala Val Asn Val Ala Ile Ala Ala  
50 55 60 65  
cct cca tca gag gga gag gct aat gct gag ctc tgt cgg tat ctt tcc 356  
Pro Pro Ser Glu Gly Glu Ala Asn Ala Glu Leu Cys Arg Tyr Leu Ser  
70 75 80  
aag gtc cta gaa ctc agg aag agt gat gtg gtt ttg gat aag ggt ggt 404  
Lys Val Leu Glu Leu Arg Lys Ser Asp Val Val Leu Asp Lys Gly Gly  
85 90 95  
aaa tct cgt gaa aag gtg 422  
Lys Ser Arg Glu Lys Val  
100

<210> 1484  
<211> 511  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 230..511

<400> 1484

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acccgcgcc tccctccctc cctagctgac ttgctccctc ccgggctgcg gctgctgcaa 120  
aagccagcag cggcagcggg agctgtccgg aggccggcgt cgagggtttg ccgctgtctc 180



tgctattcca tcttccccat aggggctctc tcccctctcc catctcaag atg gca gcc 238  
 Met Ala Ala  
 1  
 agc agc tct gag atc tct gag atg aag ggg gtt gag gag agt ccc aag 286  
 Ser Ser Ser Glu Ile Ser Glu Met Lys Gly Val Glu Glu Ser Pro Lys  
 5 10 15  
 gtt cca ggc gaa ggg cct ggc cat tct gaa gct gaa act ggc cct ccc 334  
 Val Pro Gly Glu Gly Pro Gly His Ser Glu Ala Glu Thr Gly Pro Pro  
 20 25 30 35  
 cag gtc cta gca ggg gta cca gac cag cca gag gcc ccg cag cca ggt 382  
 Gln Val Leu Ala Gly Val Pro Asp Gln Pro Glu Ala Pro Gln Pro Gly  
 40 45 50  
 cca aac acc act gcg gcc cct gtg gac tca ggg ccc aag gct ggg ctg 430  
 Pro Asn Thr Thr Ala Ala Pro Val Asp Ser Gly Pro Lys Ala Gly Leu  
 55 60 65  
 gct cca gaa acc aca gag acc ccg gct ggg gcc tca gaa aca gcc cag 478  
 Ala Pro Glu Thr Thr Glu Thr Pro Ala Gly Ala Ser Glu Thr Ala Gln  
 70 75 80  
 gcc aca gac ctc ags tta agc cca gga ggg gaa 511  
 Ala Thr Asp Leu Xaa Leu Ser Pro Gly Gly Glu  
 85 90

<210> 1485  
 <211> 272  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 117..272

<400> 1485  
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 tccctaataga aggggtaaga ttggactagg taagcatctt acaaccattt gtgggtc atg 119  
 Met

aga gct ggg gtg ggg aag gat tgt cac ttg acc ccc cca gct ctg ttt 167  
 Arg Ala Gly Val Gly Lys Asp Cys His Leu Thr Pro Pro Ala Leu Phe  
 5 10 15  
 caa gtg ctg aaa gag ctc cag gct atg cta cgg gag gag aag cca gct 215  
 Gln Val Leu Lys Glu Leu Gln Ala Met Leu Arg Glu Glu Lys Pro Ala  
 20 25 30  
 act gag gaa aag cca gct act gag aaa aag cgg agt gat tta cca ttc 263  
 Thr Glu Glu Lys Pro Ala Thr Glu Lys Lys Arg Ser Asp Leu Pro Phe  
 35 40 45  
 tcc tcc ccc 272  
 Ser Ser Pro  
 50

<210> 1486  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 196..411

<400> 1486  
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 tcggawtaac ttctgcagc gaccaacagg ctaaagaggg ggaagggatc cagcaccggc 120  
 tcctcctccg gcaaccacgg tgggagcggc ggaggaaatg gacataaacc cggaactct 180  
 gagacgtctc ctggg atg ttt aac ttt gac act ttc tgg aag aat ttt aaa 231  
 Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys  
 1 5 10  
 tcc aag ctg ggt ttc atc aac tgg gat gcc ata aac aag aac cag gtc 279  
 Ser Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asn Gln Val  
 15 20 25  
 ccg ccc ccc agc acc cga gcc ctc ctc tac ttc agc cga ctc tgg gag 327  
 Pro Pro Pro Ser Thr Arg Ala Leu Leu Tyr Phe Ser Arg Leu Trp Glu  
 30 35 40  
 gag ytc aaa cag aac act cct ttc ctc aac tgg aaa gca att att gag 375  
 Glu Xaa Lys Gln Asn Thr Pro Phe Leu Asn Trp Lys Ala Ile Ile Glu  
 45 50 55 60  
 ggt gcg nwc gcg tca tca ctg cag aaa cgt gca ggc a 412  
 Gly Ala Xaa Ala Ser Ser Leu Gln Lys Arg Ala Gly  
 65 70

<210> 1487  
 <211> 590  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 374..589

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